

Opposing community assembly patterns for dominant and non-dominant plant species in herbaceous ecosystems globally

Appendices 1 and 2

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Appendix 1. Complementary figures and tables

Complementary figures

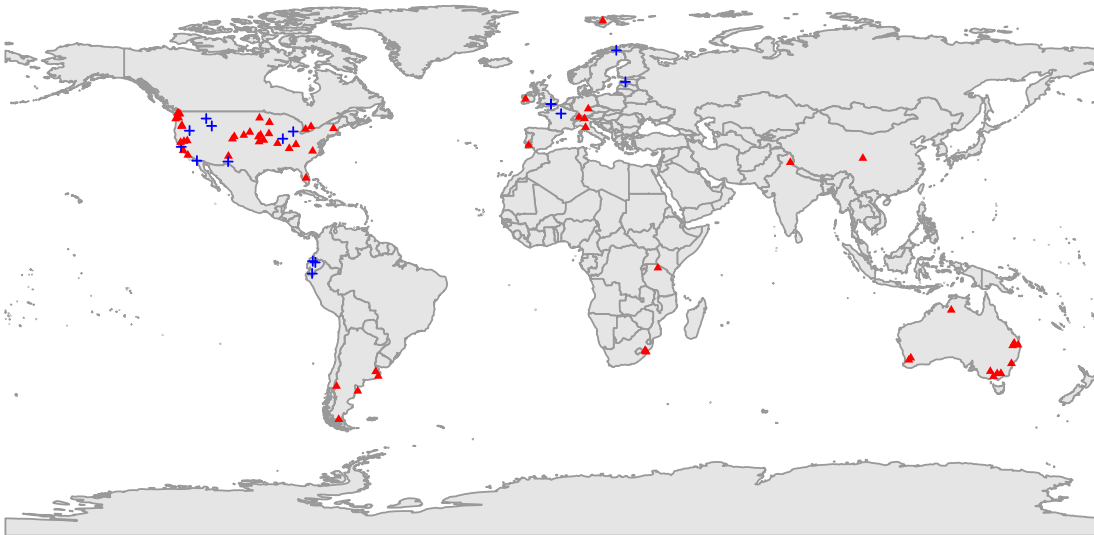


Figure A1: Global distribution of the study sites. In blue, sites with cover information only, in red sites with cover and biomass info. Sites were distributed in North America (41 cover, 33 with biomass info), Europe (12 cover, 7 with biomass info), Oceania (11 cover and with biomass info), South America (8 cover, 5 with biomass info), Africa (3, all with biomass info) and Asia (3, all with biomass info).

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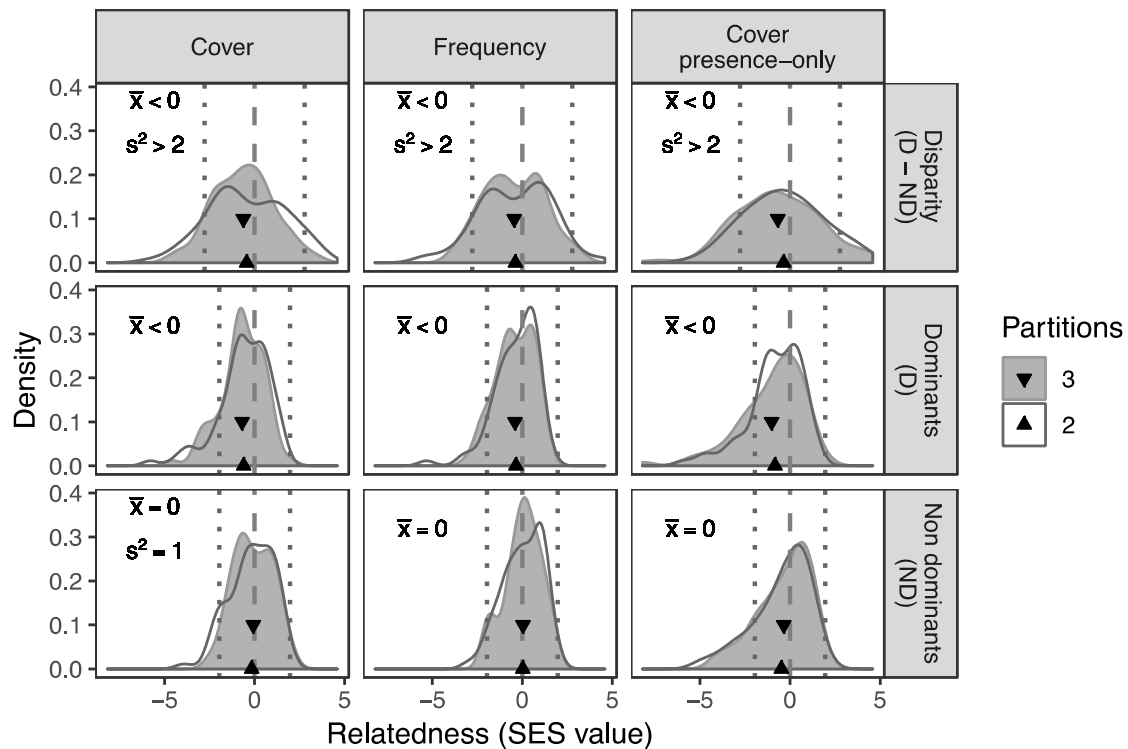


Figure A2: Relatedness disparity between dominants and non-dominant plants, and the relatedness of these partitions. The relatedness in each site and partition is the standardized effect size of the mean phylogenetic distance (MPD). The columns represent different ways to measure the dominance of the species. We partitioned the community into two (clear) and three (grey) partitions. Vertical dashed line represents zero (random) assortment, and vertical dotted line represent the limit for an independent site to be considered equal to zero. The distribution for three partitions was tested for normality, when non-normal we tested whether the mean (\bar{x}) was lower or higher than 0. If normal, we also tested if the variance (s^2) was lower or higher than the expected variance (2 for disparity, 1 for relatedness). All tests done at $p < 0.05$.

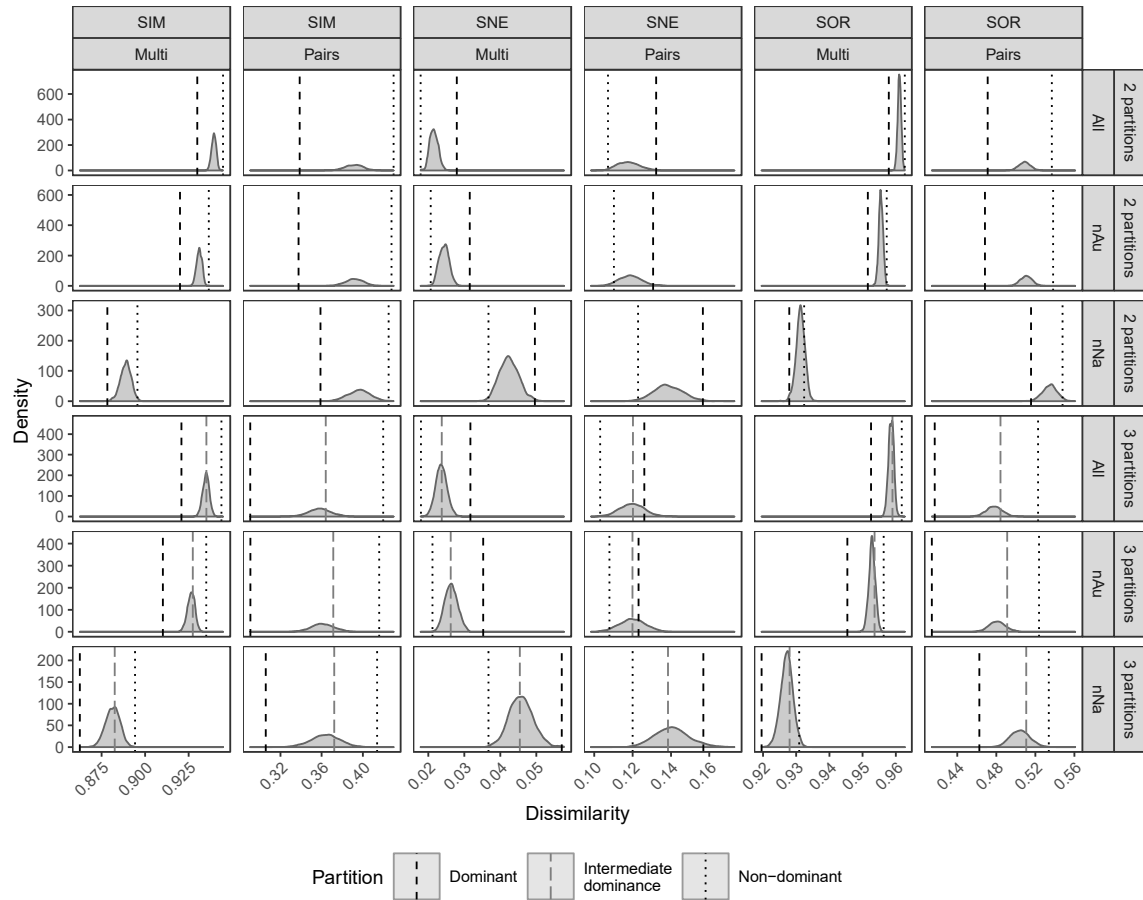


Figure A3: Phylogenetic dissimilarities among sites when each site is partitioned in two or three dominance partitions. Two dominance partitions include dominant and non-dominant (species, each with half of the species in the site). Three dominance partitions include also an intermediate dominance, each with a third of the species in the site. The phylogenetic dissimilarity is measured as the multisite Sørensen (SOR – multi) and as the mean pairwise Sørensen dissimilarity (SOR – pairs). In both cases, the indices were decomposed in their turnover (SIM) and nestedness (SNE) fractions. Dashed lines represent the observed value when dominance is assigned base on observed mean species cover per plot, while the densities represent the expected value when the species are randomly distributed in the two or three partitions. Rows 1 and 3 include all sites (All), 2 and 4 exclude Australian sites (nAu), and 3 and 6 exclude sites in North America (nNA).

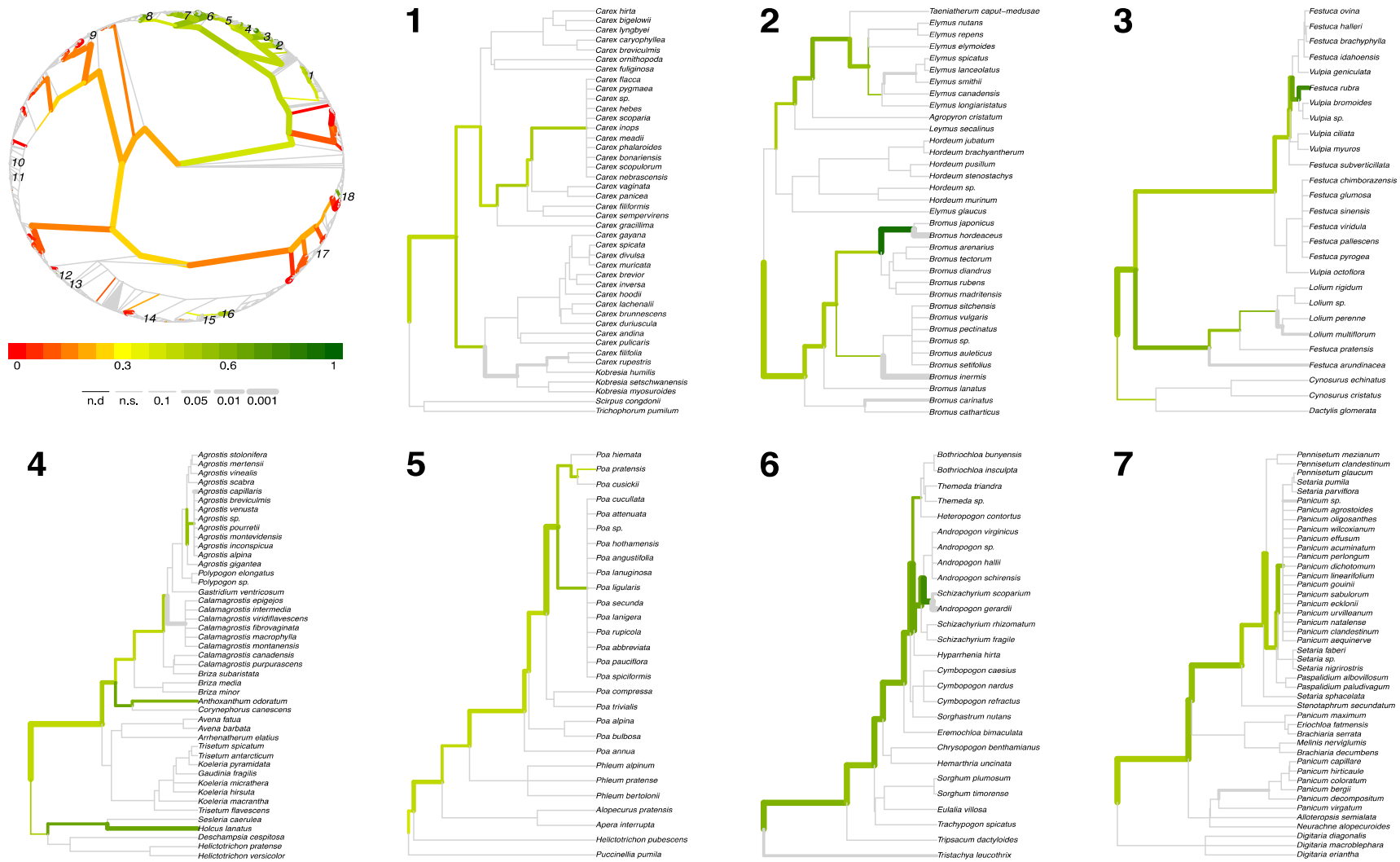
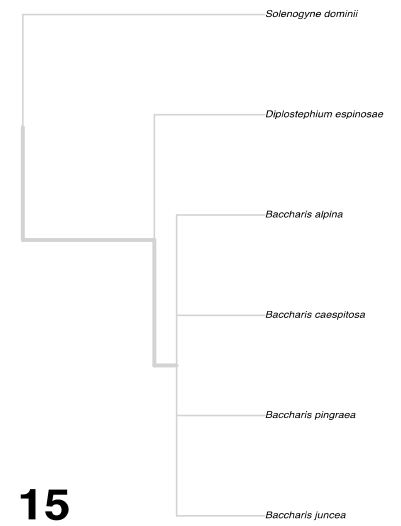
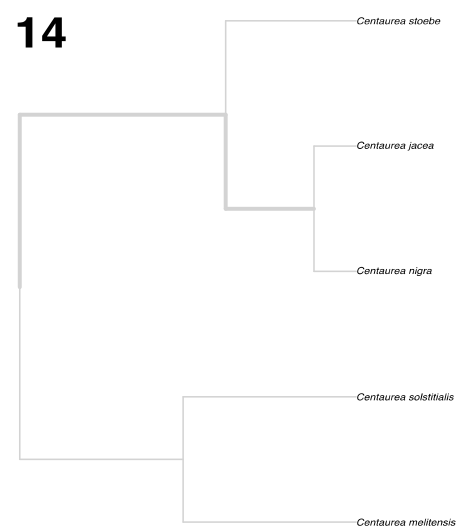
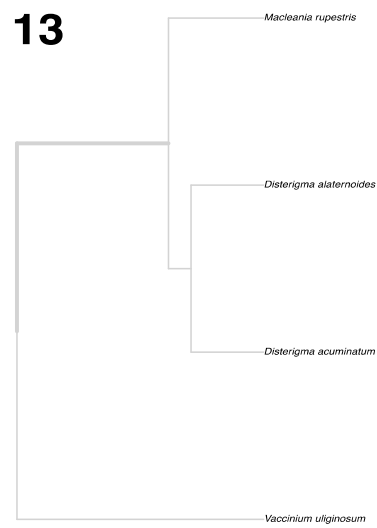
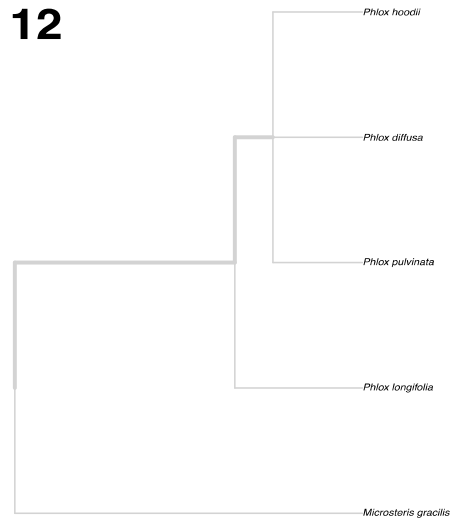
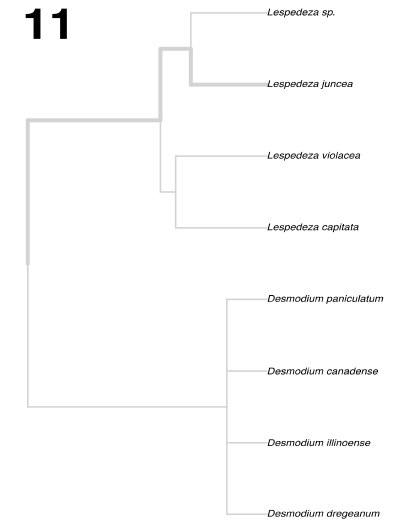
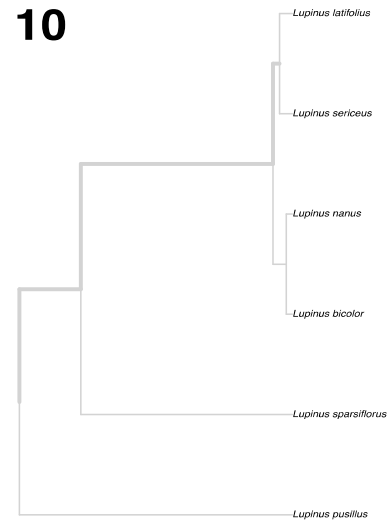
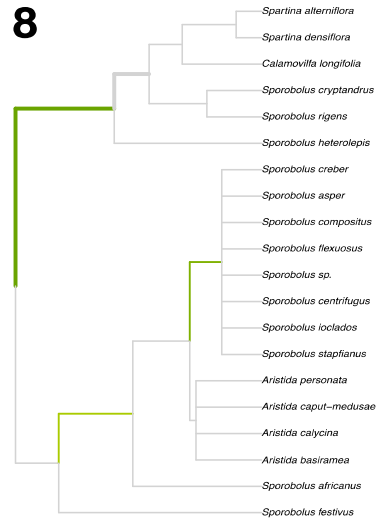
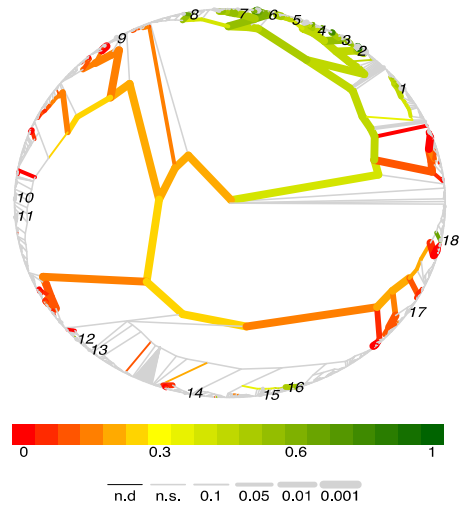
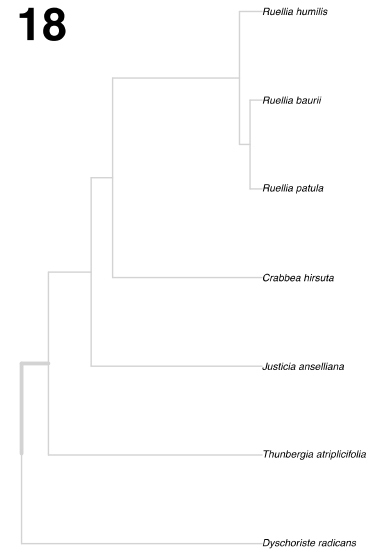
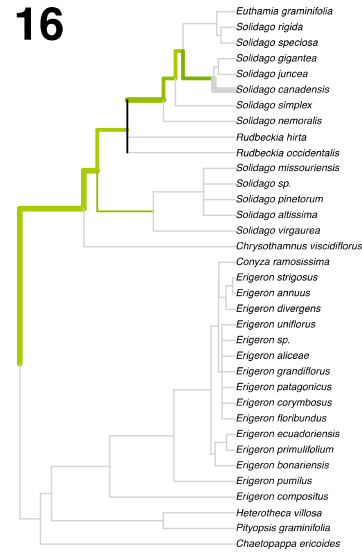
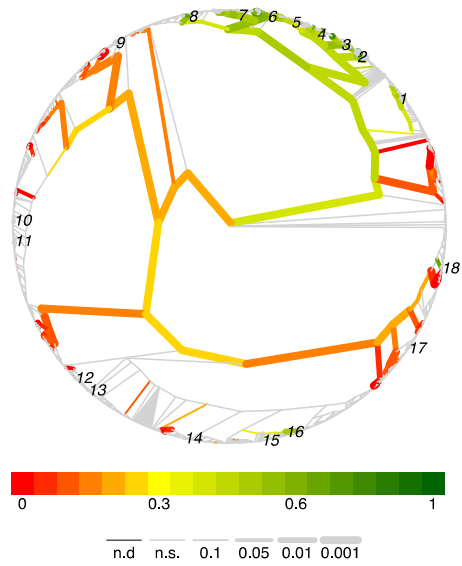


Figure A4: Details of the lineages with species more likely to be dominant. The numbers in the phylogenetic tree in the top-left of each panel represent the location of the detailed section in the whole tree. Detailed trees are provided for lineages with $p < 0.05$.

(Figure A4b cont. Node 9 corresponds to species *Erodium botrys*)



(Figure A4c cont. Node 17 corresponds to species *Galium_verum*)



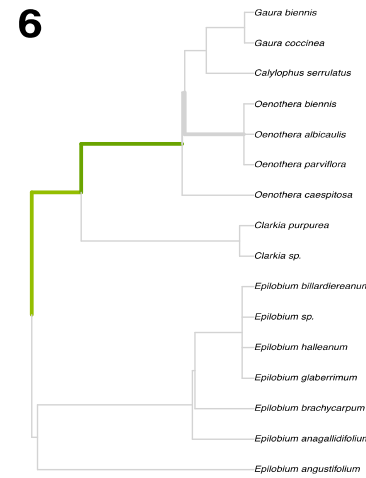
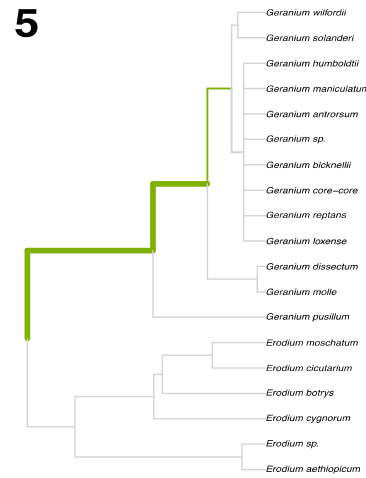
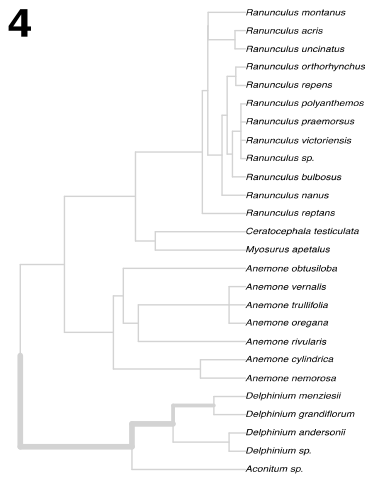
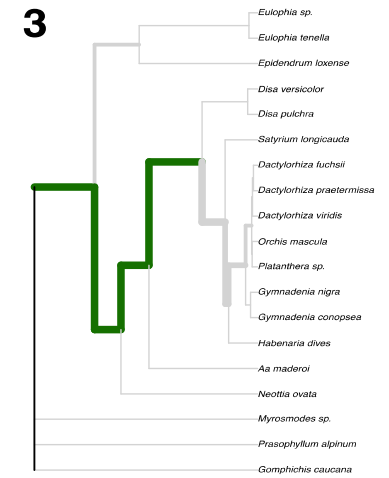
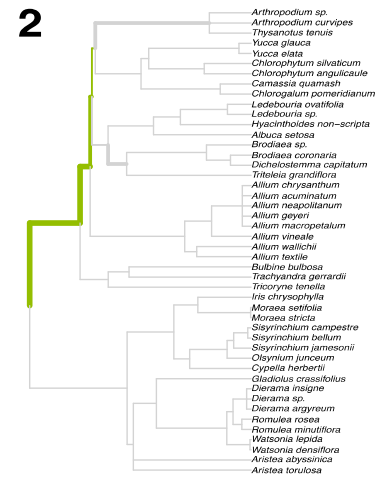
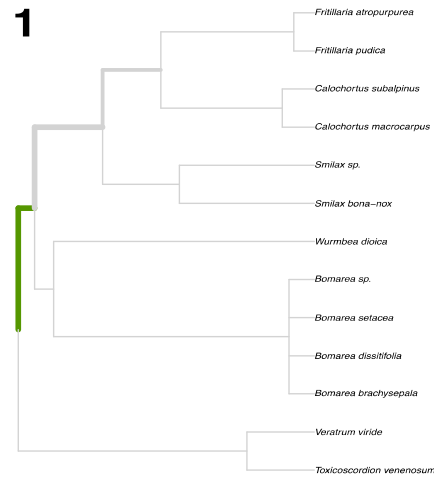
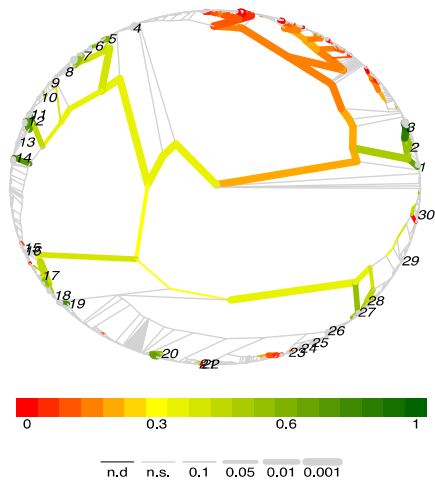
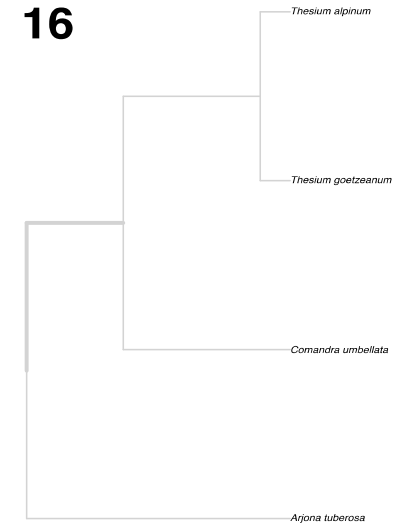
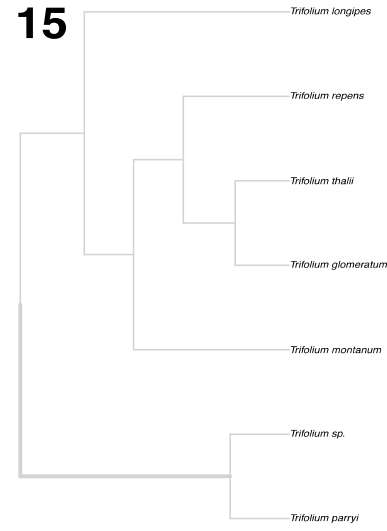
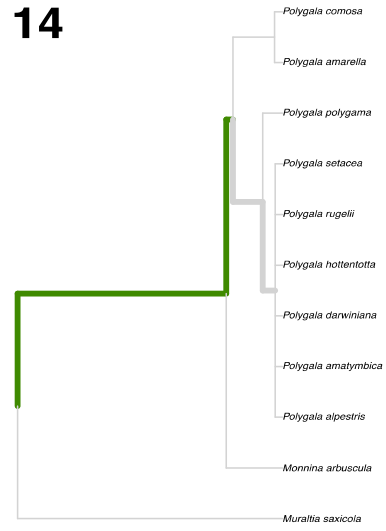
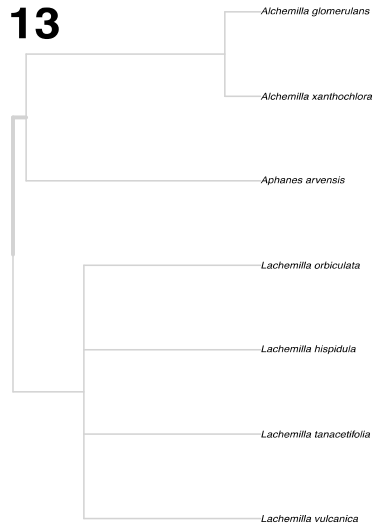
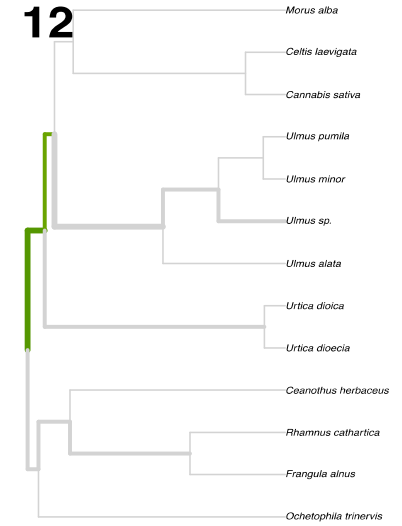
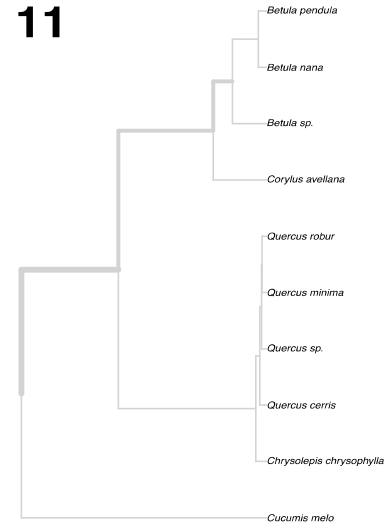
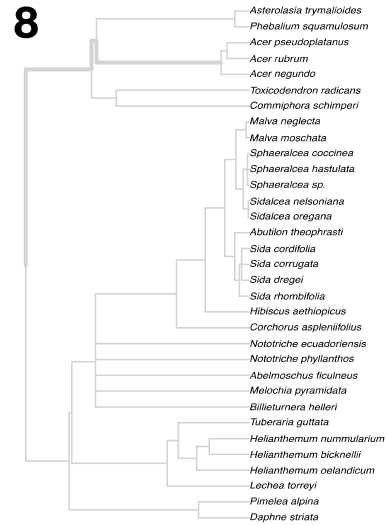
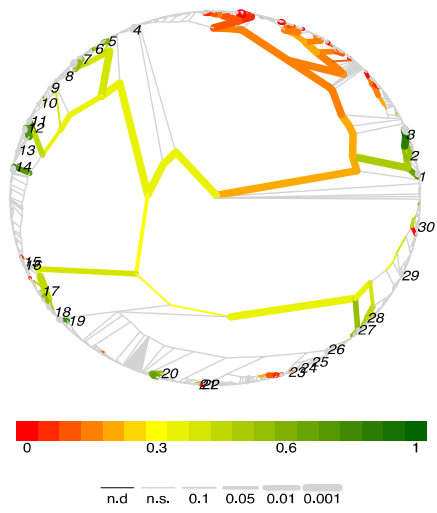
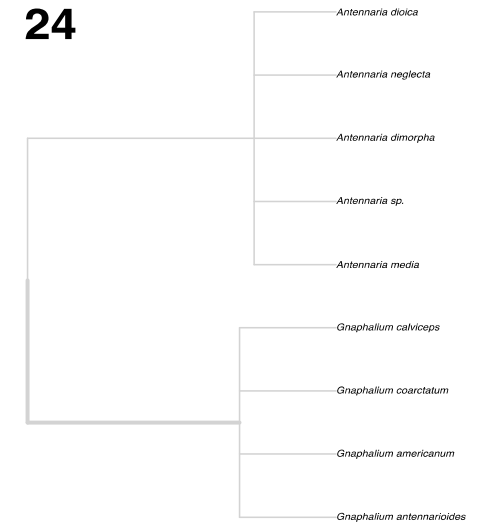
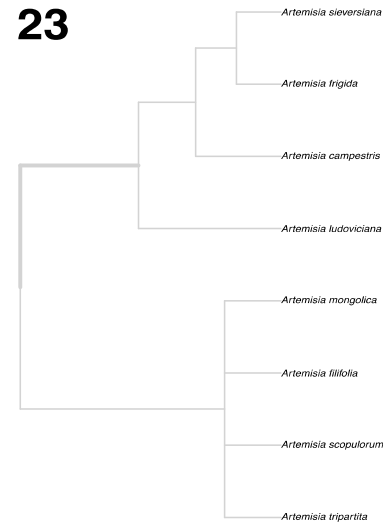
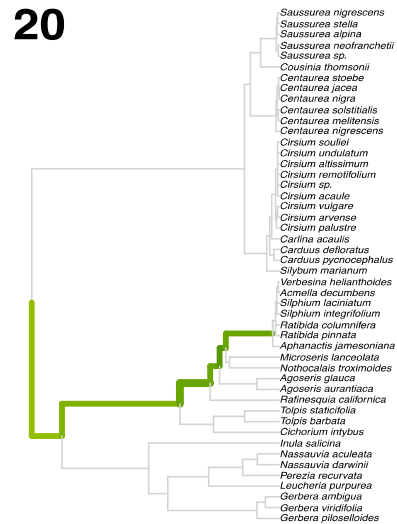
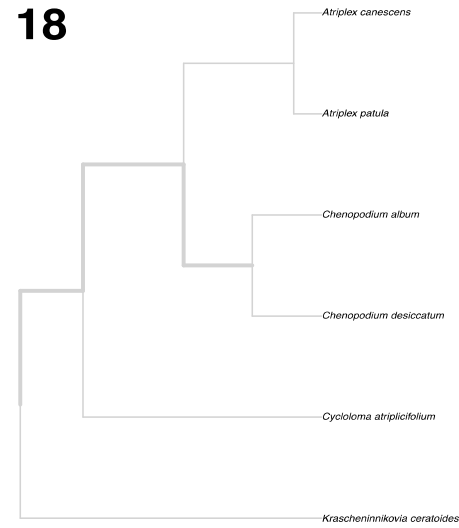
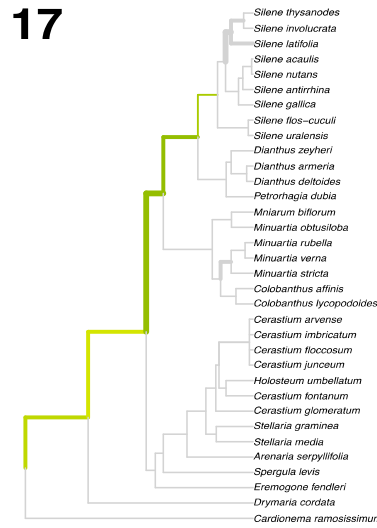
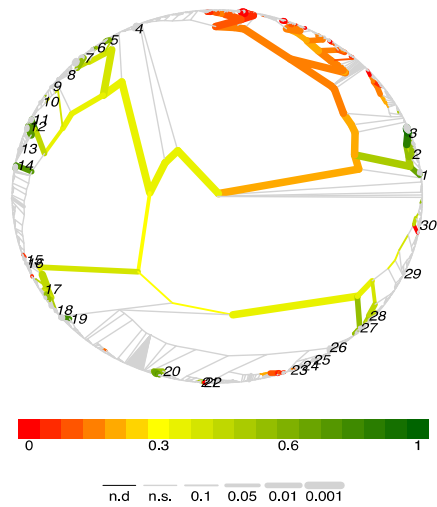


Figure A5: Details of the lineages with species more likely to be non-dominant. The numbers in the phylogenetic tree in the top-left of each panel represent the location of the detailed section in the whole tree. Detailed trees are provided for lineages with $p < 0.05$.

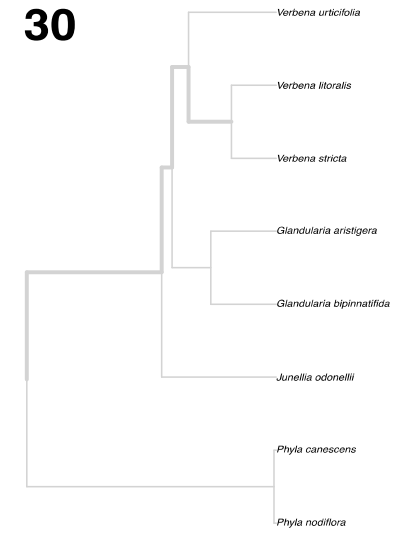
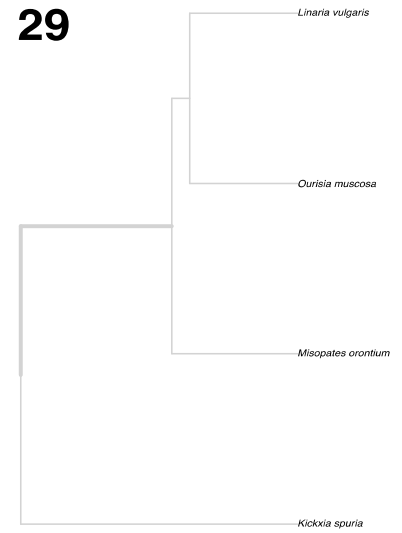
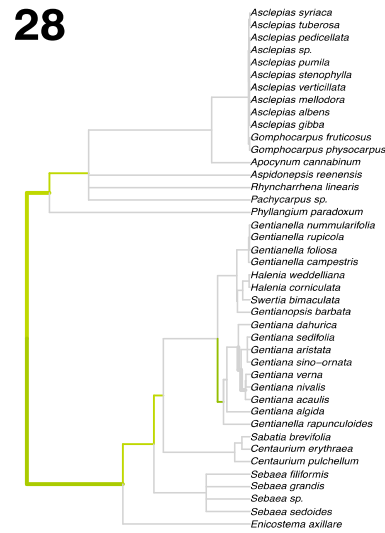
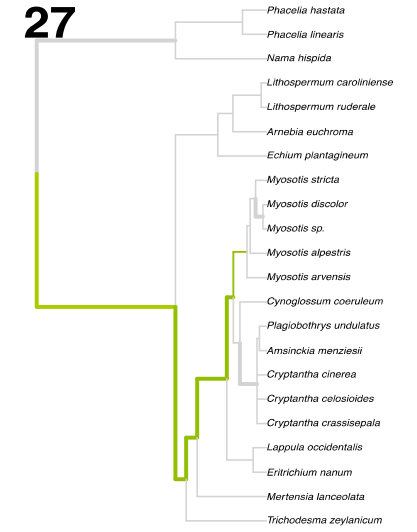
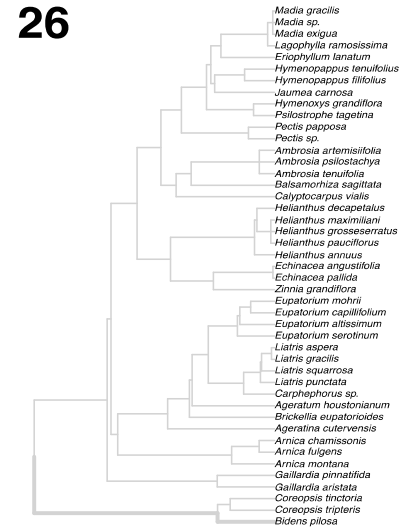
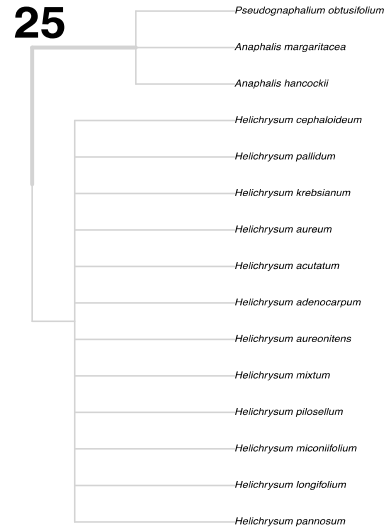
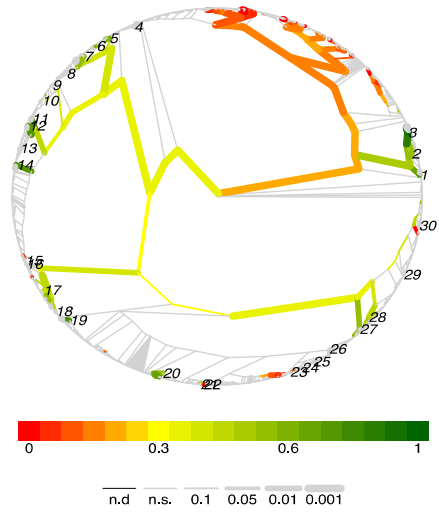
(Figure A5 cont. Node 9 and 10 correspond to species *Oxalis* spp. and *Viola* spp. respectively.)



(Figure A5 cont.. Node 22 corresponds to the species *Taraxacum campyloides*.)



(Figure A5 cont.)



Complementary tables

Table A1: Evaluation of the seven assumptions and potential caveats identified by Gerhorld et al. (2015). Each assumption is commented in the context of relatedness disparity (the difference in the phylogenetic relatedness of dominant and non-dominant species), and a potential interpretation of a negative or a positive disparity is presented when relevant.

Assumption*	Caveat*	Comments about the applicability of the assumption/caveat to relatedness disparity	Alternative scenario if disparity exists (either positive or negative) and the assumption is wrong	
			Negative†	Positive
“Phylogenetic dispersion reflects dispersion of phylogenetically conserved functional traits”	“Community assembly processes can select for related dissimilar species (or the inverse)”	If there is no consistent trend between phylogeny and trait dispersion, we should expect no disparity between dominant and non-dominant species.	Dominants are dissimilar and closely related and non-dominants are similar and distantly related. → Competition is stronger than filtering among dominants, and the opposite for non-dominants. <i>A1</i>	Dominants are similar and distantly related and non-dominants are dissimilar and closely related. → Competition is stronger than filtering among non-dominants, and the opposite for dominants.
“A single ecological function can only be performed by a single trait state or combination of trait states”	“Multiple traits, occurring in multiple lineages, may serve the same function”	Relatedness disparity assumes that different sets of traits are relevant for dominant and non-dominant species.	Any key ecological function related to survival (associated to either competition or filtering) is performed by a combination of traits in dominants in a lineage and by several multiple traits in multiple lineages in non-dominants. → Dominance is not determined by the traits defining the ecological function, but by a different suit of traits. <i>A2</i>	Same ecological function is performed by several multiple traits in dominants in different lineages and by a combination of some traits in few non-dominant lineages. → Dominance is not determined by the traits defining the ecological function, but by a different suit of traits.
“Trait similarity causes enhanced competition”	“Trait similarity might facilitate coexistence”	The question extends to the dominant/non-dominant partition: if similarity facilitates coexistence (either by filtering or facilitated coexistence), are dominants and non-dominants equally sorted?††	Dominants are similar and related, which facilitates their coexistence. Filtering can also play a role. Low similarity to dominant species is a possible cause for non-dominance, but cannot explain non-dominant overdispersion if present. <i>A3</i>	Non-dominant species are similar and related, which facilitate each other. Filtering can also play a role.

Assumption*	Caveat*	Comments about the applicability of the assumption/caveat to relatedness disparity	Alternative scenario if disparity exists (either positive or negative) and the assumption is wrong	
			Negative†	Positive
“Competition necessarily causes exclusion” (re-interpreted as: <i>Species interactions necessarily causes exclusions at the species level</i>)	“Competition (<i>and facilitation</i>) may be symmetric and without losers or winners <i>predictable at the species level.</i> ”	This assumption/caveat is grounded on the comparison between an existent community with a potential species pool. When comparing among dominants and non-dominants the comparison is between existent species only.	Filtering causes dominant species to be clustered. In the absence of consistent species interactions, the more random pattern in the non-dominants indicates weaker filtering acting on them. A4	Filtering causes non-dominant species to be clustered. In the absence of consistent species interactions, the more random pattern in the dominants indicates weaker filtering acting on them.
“The system is at ‘rest’ such that the process of assembly has played out”	“Not enough time has elapsed to lead to exclusion of species”	No assumption of system at rest: the dominants can be transient, same for non-dominants.		
“Habitat filtering and competition are alternative processes, not operating together nor interacting”	“Habitat filtering and competition are independent, increase in parallel or mutually imply each other”	We do not assume that they are negatively correlated, but that one (or the other) can prevail. If both mechanisms have similar effect, we expect that relatedness disparity will be close to 0.		
“Community phylogenetic dispersion depends on local and present-day processes only; without such local processes, phylogenetic dispersion is random”	“Community phylogenetic dispersion reflects habitat species pools, not local processes”	Dominant and non-dominant species are present in the same locality, and therefore the dispersion filter is similar for both. Potential habitat selection bias at the global scale, but not applicable at the local scale.		

A5

Notes: * quoted text obtained as it is from original text, unless otherwise stated; *italics* indicate text added by the authors. † Scenarios compatible with our observed results (negative disparity) are indicated (A1-A5) and discussed in the main text. †† Mayfield & Levine (2010) proposed a model in which this pattern holds, but their model is based on asymmetric competition under a limiting resource (i.e., light), and therefore is consistent with our finding of dominant species being clustered because of a strong environmental filter.

Table A2: Variables used to model the difference in the phylogenetic dispersion of dominants and non-dominant plants and the sources of information used to measure them. Range of observed values is also reported for the independent variables.

Variables	Definition	Source*
Response variables		
D _{SES.MNTD}	Phylogenetic dispersion (measured as the standardized effect size of the mean nearest taxonomic distance) of the third most dominant plant species in each site. Dominance defined as the mean cover per plot.	Based on NutNet cover and Qian and Jin (2016)
ND _{SES.MNTD}	Phylogenetic dispersion (measured as the standardized effect size of the mean nearest taxonomic distance) of the third least dominant plant species in each site. Dominance defined as the mean cover per plot.	Based on NutNet cover and Qian and Jin (2016)
Δ _{SES.MNTD}	Difference in the phylogenetic dispersion of dominants minus non-dominants (D _{SES.MNTD} – ND _{SES.MNTD})	Based on NutNet cover and Qian and Jin (2016)
Climatic variables*		
T	Mean annual temperature Range: -7.6 – 27.3 °C	Worldclim 2
TR	Temperature annual range Range: 14.6 – 46.6 °C	Worldclim 2
DR	Mean diurnal temperature range (mean of monthly range) Range: 5.1 – 19.6 °C	Worldclim 2
P	Total annual precipitation in mm (log transformed) Range: 5.38 – 7.71	Worldclim 2
PV	Variance of the monthly precipitation in mm Range: 11.2 – 111.82	Worldclim 2
Location variables		
Elev	Altitude above sea level Range: 0 – 4241 m	Worldclim 2
Management		
Gz	Is the site subject to grazing? Range: [0,1]	NutNet description
An	Is the site of anthropogenic origin? (e.g., restored) Range: [0,1]	NutNet description
Fr	Is the site subject to prescriptive fire? Range: [0,1]	NutNet description
Biomass variables		
pGr	Proportion of graminoid biomass in the site Range: 0.14 – 1	Based on NutNet biomass
BM	Total aboveground biomass in g by m ² (log transformed) Range: 3.27 – 7.12	Based on NutNet biomass
LM	Legume aboveground biomass in g by m ² (log + 1 transformation) Range: 0 – 4.24	Based on NutNet biomass

Variables	Definition	Source*
Tree topology and phylogenetic information		
Rec	Proportion of the phylogenetic information of the site tree contained in the site tree tips Range: 0.45 – 0.74	Based on NutNet cover and Qian and Jin (2016)
S	Number of species present in the site Range: 13 – 94	Based on NutNet cover
PD	Site level Faith's Phylogenetic Diversity (Faith, 1992), obtained as the sum of the branches of the site tree. Range: 1200 – 4238	Based on NutNet cover and Qian and Jin (2016)
MPD	Observed site level Mean Phylogenetic Diversity (Webb <i>et al.</i> , 2002) Range: 220 – 336	Based on NutNet cover and Qian and Jin (2016)
MNTD	Observed site level Mean Nearest Taxonomic Diversity (Webb <i>et al.</i> , 2002) Range: 38 – 131	Based on NutNet cover and Qian and Jin (2016)
Gm	Site level Gamma statistics (Pybus and Harvey, 2000), that measures the temporal distribution of the nodes: negative values indicate deeper nodes, while positive values indicate shallower nodes. Obtained as the mean of a hundred randomly generated binary trees based on the site tree. Range: -1.15 – 5.75	Based on NutNet cover and Qian and Jin (2016)
Bal	Site level Colless statistics (Mooers and Heard, 1997), that measures the symmetry in the branching pattern (balance): negative values indicate balanced nodes, while positive values indicate unbalanced nodes. Obtained as the mean of a hundred randomly generated binary trees based on the site tree. Range: 17 – 541	Based on NutNet cover and Qian and Jin (2016)

Notes: * All Worldclim 2 (Fick and Hijmans, 2017) variables were included in the model, but discarded because they (1) were correlated among each other or (2) they were poor predictors. Variables listed here but not present in the final model were discarded for similar reasons.

Table A3: Genera observed in the study more likely to be a dominant (a), intermediate -dominant (b) or non-dominant (c).

a. Genera most likely to contain dominant species

Family	Genus	Number of species	Number of species and sites per partition			Probability (proportion of dominants = 1/3)
			Dominant	Intermediate dominance	Non-dominant	
Asteraceae	<i>Baccharis</i>	4	4	1	0	0.045
	<i>Hypochaeris</i>	4	13	8	2	0.025
	<i>Solidago</i>	12	18	9	2	0.002
Cyperaceae	<i>Carex</i>	37	31	22	11	0.016
	<i>Kobresia</i>	4	4	0	0	0.012
Fabaceae	<i>Lespedeza</i>	4	5	0	2	0.045
Poaceae	<i>Andropogon</i>	5	11	4	0	0.002
	<i>Anthoxanthum</i>	1	8	3	1	0.026
	<i>Bromus</i>	17	29	14	8	0.001
	<i>Calamagrostis</i>	8	7	2	0	0.008
	<i>Chondrosium</i>	4	5	2	0	0.045
	<i>Diheteropogon</i>	2	4	0	0	0.012
	<i>Elymus</i>	9	14	7	4	0.020
	<i>Festuca</i>	14	24	5	6	0.000
	<i>Holcus</i>	1	8	3	0	0.009
	<i>Panicum</i>	24	22	13	3	0.003
	<i>Poa</i>	21	29	12	15	0.004
	<i>Sporobolus</i>	13	12	3	4	0.012
	<i>Tristachya</i>	1	3	0	0	0.037
	Polemoniaceae	<i>Phlox</i>	4	4	1	0

b. Genera most likely to contain intermediate dominance species

Family	Genus	Number of species	Number of species per partition			Probability (proportion of intermediate dominance = 1/3)
			Dominant	Intermediate dominance	Non-dominant	
Apiaceae	<i>Zizia</i>	2	0	3	0	0.037
Caryophyllaceae	<i>Cerastium</i>	6	3	11	5	0.029
Asteraceae	<i>Antennaria</i>	7	3	8	1	0.026
	<i>Saussurea</i>	5	0	4	1	0.045
	<i>Sonchus</i>	2	0	3	0	0.037
Convolvulaceae	<i>Ipomoea</i>	4	0	5	1	0.018
	<i>Polymeria</i>	3	0	3	0	0.037
Equisetaceae	<i>Equisetum</i>	2	0	3	0	0.037
Euphorbiaceae	<i>Acalypha</i>	3	0	3	0	0.037
Onagraceae	<i>Epilobium</i>	7	0	7	3	0.020
Poaceae	<i>Dactyloctenium</i>	3	0	3	0	0.037
Ranunculaceae	<i>Ranunculus</i>	12	3	11	5	0.029
Solanaceae	<i>Physalis</i>	4	1	6	1	0.020

c. Genera most likely to contain non-dominant species

Family	Genus	Number of species	Number of species per partition			Probability (proportion of non-dominants = 1/3)
			Dominant	Intermediate dominance	Non-dominant	
Amaranthaceae	<i>Chenopodium</i>	2	0	1	4	0.045
Betulaceae	<i>Betula</i> †	3	0	0	3	0.037
Boraginaceae	<i>Cryptantha</i>	3	0	0	3	0.037
Brassicaceae	<i>Brassica</i>	2	0	0	4	0.012
	<i>Descurainia</i>	3	0	0	3	0.037
Asteraceae	<i>Bidens</i>	1	0	0	3	0.037
	<i>Gnaphalium</i>	4	0	0	4	0.012
Fabaceae	<i>Argyrolobium</i>	4	0	0	4	0.012
Geraniaceae	<i>Geranium</i>	13	3	3	12	0.005
Onagraceae	<i>Oenothera</i>	4	0	1	5	0.018
Polygalaceae	<i>Polygala</i>	9	0	2	8	0.003
Primulaceae	<i>Anagallis</i>	1	0	0	4	0.012
	<i>Lysimachia</i>	3	0	0	3	0.037
Ranunculaceae	<i>Delphinium</i>	4	0	0	5	0.004
Sapindaceae	<i>Acer</i> †	3	0	0	3	0.037
Ulmaceae	<i>Ulmus</i> †	4	0	1	6	0.007
Urticaceae	<i>Urtica</i>	2	0	0	3	0.037
Verbenaceae	<i>Verbena</i>	3	0	0	4	0.012

Table A4: Life-form, number of species and global distribution of the genera more likely to contain non-dominant species in the study. In grey genus composed mostly of trees and/or shrubs.

Family	Genus	Life-form	Species in the genus	Distribution	Source†
Amaranthaceae	<i>Chenopodium</i>	Herbs, annual or perennial (rarely suffruticose, or small trees)	170	Almost worldwide, but most frequent in temperate and subtropical zones	Dinghushan
Betulaceae	<i>Betula</i>	Trees or shrubs	60	Found in the North temperate and the Arctic regions of Europe and Asia and the Andes in South America	Flora of Pakistan
Boraginaceae	<i>Cryptantha</i>	Annual, biennial, or perennial herbs	121	Amphitropic distribution (some species in the Northern and other in the Southern hemisphere).	††
Brassicaceae	<i>Brassica</i>	Herbs annual, biennial, or perennial, rarely subshrubs or shrubs, often glaucous.	40	Primarily in the Mediterranean region, especially SW Europe and NW Africa; six species in China.	Dinghushan
	<i>Descurainia</i>	Herbs annual or perennial, rarely shrubs.	40	Mainly in North and South America (30 species) and Macaronesia (seven species), one species a cosmopolitan weed.	IBSC
Asteraceae	<i>Bidens</i>	Annuals or perennials.	150-250	Widespread, especially in subtropical, tropical, and warm-temperate North and South America; ten species (one endemic, one introduced) in China.	IBSC
	<i>Gnaphalium</i>	Herbs, annual or perennial.	80	Cosmopolitan	Dinghushan
Fabaceae	<i>Argyrolobium</i>	Herbs, rarely small shrubs.	130	North, tropical and South Africa, Madagascar, South of Europe, West of Asia and Indo-Pakistan subcontinent.	Flora of Pakistan

Family	Genus	Life-form	Species in the genus	Distribution	Source†
Geraniaceae	<i>Geranium</i>	Annual or perennial herbs.	400	Mainly distributed in the temperate zone of Northern Hemisphere, but also in the tropics.	Flora of Pakistan
Onagraceae	<i>Oenothera</i>	Annual, biennial or perennial herbs	125	Native to North and South America, with some species widely introduced as escapes from cultivation throughout the world.	Flora of Pakistan
Oxalidaceae	<i>Oxalis</i>	Herbs (subshrubs, shrubs, or vines)	700	North America, Mexico, West Indies, Central America, South America, Eurasia, Africa, Atlantic Islands, Indian Ocean Islands, Pacific Islands, Australia; introduced in Bermuda.	FNA
Polygalaceae	<i>Polygala</i>	Annual or perennial herbs, or shrubs or small trees, rarely small, woody climbers.	500	Widespread worldwide	Dinghushan
Primulaceae	<i>Anagallis</i>	Herbs, annual or perennial,	20	North America, Mexico, West Indies (Jamaica), Central America, South America, Eurasia, Africa.	FNA
	<i>Lysimachia</i>	Herbs (shrubs), perennial,	160	Nearly worldwide; chiefly north temperate, especially Asia.	FNA
Ranunculaceae	<i>Delphinium</i>	Herbs, perennial, from fasciculate roots or rhizomes.	300	North temperate and arctic subtropical and, in Eastern Hemisphere, tropical mountains (South of equator in Africa).	FNA
Sapindaceae	<i>Acer</i>	Trees or shrubs.	129	Widespread in both temperate and tropical regions of Northern Africa, Asia, Europe, and Central and North America	FNA
Ulmaceae	<i>Ulmus</i>	Deciduous trees	45	Northern hemisphere.	Flora of Pakistan
Urticaceae	<i>Urtica</i>	Herbs, annual or perennial	45	Nearly worldwide.	FNA
Verbenaceae	<i>Verbena</i>	Herbs or subshrubs, annual or perennial.	250	Chiefly in tropical America	Dinghushan

Family	Genus	Life-form	Species in the genus	Distribution	Source†
Violaceae	<i>Viola</i>	Herbs, annual or perennial,	400-600	Nearly worldwide, temperate regions, also South America, Pacific Islands (Hawaii, Philippines, Taiwan).	FNA

Notes: † Databases accessed through web portal eFloras (www.efloras.org, accessed on 2019-01-11). †† Genera not available on eFloras, information obtained from <http://www.sci.sdsu.edu/plants/cryptantha/cryptax.html> (accessed on 2019-01-11).

Table S5 Correlation between graminoid prevalence and relatedness disparity, dominance relatedness, and non-dominant relatedness. Relatedness was measured using mean taxonomic nearest distance ($\Delta_{SES.MNTD}$, $D_{SES.MNTD}$, $ND_{SES.MNTD}$) and mean phylogenetic distance ($\Delta_{SES.MPD}$, $D_{SES.MPD}$, $ND_{SES.MPD}$).

Predictor	MNTD			MPD		
	$\Delta_{SES.MNTD}$	$D_{SES.MNTD}$	$ND_{SES.MNTD}$	$\Delta_{SES.MPD}$	$D_{SES.MPD}$	$ND_{SES.MPD}$
(Intercept)	0.449	0.023	-0.426	1.427 *	1.177 *	-0.25
Graminoid prevalence	-2.788 **	-1.310 *	1.479 *	-2.938 **	-2.671 ***	0.268
R ²	0.138	0.083	0.103	0.147	0.205	0.003

Table S6: Proportion of the variance in relatedness disparity ($\Delta_{SES.MNTD}$, $\Delta_{SES.MPD}$), dominant ($D_{SES.MNTD}$, $D_{SES.MPD}$) and non-dominant relatedness ($ND_{SES.MNTD}$, $ND_{SES.MPD}$) explained by different categories of drivers. The proportion was estimated as the difference between the final predicted model R² and the R² of a similar model without the variables in each category.

Relatedness response variable	Variance explained by category of variable				Full model R ²
	Tree topology and phylogenetic information	Environment (location, climate, management)	Aboveground biomass	Graminoid prevalence	
Mean nearest taxonomic distance (more sensitive to the tips of the phylogeny)					
$\Delta_{SES.MNTD}$	0%	8%	0%	11%	22%
$D_{SES.MNTD}$	13%	11%	0%	6%	27%
$ND_{SES.MNTD}$	0%	14%	3%	5%	29%
Mean phylogenetic distance (more sensitive to the basal part of the phylogeny)					
$\Delta_{SES.MPD}$	7%	16%	0%	6%	38%
$D_{SES.MPD}$	7%	12%	0%	8%	44%
$ND_{SES.MPD}$	8%	22%	4%	0%	30%

Appendix 2. Methods details

Adaptation of the phylogenetic tree

We found that 45.6% of the observed species were not present in Qian and Jin (2016) phylogenetic tree. If the genus was present, (41.2% of the observed species), we looked for the other species of the same genus, found the tip distance (branch length of the species terminal node to the closest node), identified the species closest to the median of the tip distances and included the missing species as a sister species of the species closest to the median. If the genus was absent, the new species was linked to the family node (4.3%).

Tests of phylogenetic dispersion

This test aimed to assess if dominant relatedness ($D_{SES.MNTD}$), non-dominant relatedness ($ND_{SES.MNTD}$) and dominance disparity ($\Delta_{SES.MNTD}$) were different from zero globally, regardless the identity of the species in each site. We assumed each site's $D_{SES.MNTD}$ value represents an independent observation and used a Shapiro-Wilks normality test first. If the site $D_{SES.MNTD}$ were not normally distributed we used a Wilcoxon signed rank test to decide if the mean of the site $D_{SES.MNTD}$ was lower, equal or higher than zero. If normal, we used a Kolmogorov-Smirnoff goodness-of-fit test (KS-test) to assess if the site $D_{SES.MNTD}$ followed a normal distribution with mean 0 and variance 1, indicating random species sorting. If this KS-test was rejected, we kept the sign of the mean site $D_{SES.MNTD}$ to indicate whether clustering or overdispersion prevails. Then, we removed the mean site $D_{SES.MNTD}$ and did a second KS-test with the same parameters to confirm that the lack of fit was caused only by the mean. If the second KS-test was rejected we recorded if the variance was larger or smaller than 1. We repeated the analysis for $ND_{SES.MNTD}$ and for $\Delta_{SES.MNTD}$. In the latter case, we used mean 0 and variance 2, assuming $\Delta_{SES.MNTD}$ was the difference of two normally distributed variables with mean 0 and variance 1.

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