Supplementary information

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Supplementary Text S1. Ecological and biogeographical characteristics of angiosperms, palms and ferns relevant to the hypothesized relationships between environmental factors and phylogenetic diversity and structure (Fig. 1).

Angiosperms overall. Dispersal modes in angiosperms range widely in their chance of long distance dispersal, from wind and ocean dispersal to underground fruits depositing seeds next to parent plants. Some angiosperm families show remarkably little variation in dispersal modes¹ and seed mass is often conserved within genera and families² and larger lineages³. Many basal lineages also show conserved physiological tolerances and habitat affinities^{4,5}, with half of all families being restricted to the tropics, mainly because they lack adaptations to tolerate coldness and frost⁶. Together, these features make angiosperms an ideal model group for investigating dispersal and environmental filtering. Angiosperms also include many spectacular examples of radiations on archipelagos (e.g. Hawaiian lobeliads⁷) or large single islands (e.g. *Dypsis* on Madagascar⁸), and of relict endemic island lineages, even at the taxonomic rank of families (e.g. Amborellaceae on New Caledonia⁹).

Palms. Many species of the angiosperm family of palms (Arecaceae) are characterized by larger fruits and seeds than most other angiosperm families³. Only a few species with floating fruits (e.g. *Cocos*, *Nypa*) or fruits eaten by large-bodied flying birds are capable of intermediate- to long-distance dispersal; most species are strongly dispersal limited¹⁰. For example, species with large fruits that are predominantly dispersed by non-volant mammals¹⁰ rarely reach remote islands. Accordingly, many higher-level palm taxa are restricted to certain biogeographic regions or islands¹¹. Palms are characterized by a strictly subtropical to tropical distribution with a strong temperature and precipitation-dependent diversity gradient increasing towards the inner tropics¹²⁻¹⁴. The vast majority of higher-level palm taxa cannot survive seasonality and cold because of their soft and water-rich tissue, inability to undergo dormancy and lack of frost tolerance, particularly of the apical meristems^{11,12}. Palms include many island radiations (e.g. *Pritchardia* on Hawaii⁷, *Dypsis* on Madagascar⁸, *Coccothrinax* and *Copernicia* on Cuba¹⁰) and show evidence of cladogenesis even on small islands (e.g. *Howea* on Lord Howe Island¹⁵).

Ferns. Few fern clades include island radiations that reach the magnitude of angiosperms (but see *Cibotium* and *Diellia* on Hawaii¹⁶). The lower tendency of ferns to show high *in-situ* speciation rates is likely due to their high dispersal ability¹⁶⁻¹⁸. Ferns have small wind-dispersed spores, and most species produce bisexual gametophytes capable of self-fertilization¹⁹. Consequently, ferns tend to have lower diversification rates and larger ranges than angiosperms, and speciation through hybridization and polyploidization makes up a larger part of fern speciation events^{17,19}. Hence, dispersal filtering and *insitu* speciation should be of minor importance for phylogenetic diversity of island ferns. However, environmental filtering might play an important role in ferns due to their strong dependence on humidity which is known to have a particularly strong limiting influence on species richness in this group²⁰. Very few fern lineages have evolved adaptations to drought, which may be explained by eco-

physiological constraints like their lack of active stomatal control, their need for water for sperm movement and their comparatively simple xylem anatomy^{21,22}. Accordingly, fern floras on islands may be unbalanced compared to mainland floras, with an overrepresentation of families characterized by adaptations to islands' ecological niches¹⁸.

Supplementary Methods S1. Floras and phylogenies.

We assembled plant species lists for marine islands from floras, checklists and online databases. Based on the more than 1000 species lists in our database, we only included lists which claimed completeness in our analysis (see Supplementary References S1). The final selection covered 393 islands, 375 for all angiosperms (flowering plants), 386 for palms and 328 for ferns. All species names (including subspecies name and author information if available) were matched to the working list of all known plant species, the Plant List, version 1.0 (www.theplantlist.org/1/). Genus names not found in the Plant List were manually checked for mistakes and validity according to Mabberley's Plant-Book²³. Species names were matched to the Plant List using fuzzy matching and replaced by names accepted by the Plant List if they were found to be synonyms. If a name could not be matched or its taxonomic status in the Plant List was unresolved, we used the Taxonomic Name Resolution Service provided by iPlant (tnrs.iplantcollaborative.org, accessed May 2, 2013) for taxonomic match-up. Species names that were matched but not resolved by either service or that were not matched at all were used in their matched or original form, respectively (97.7% matched / 85.8% resolved for angiosperms, 97.2% matched / 65.3% resolved for ferns, 99.8% matched / resolved for palms; in total 95% using the Plant List, 5% using iPlant). All names entered further analyses at the species level. Family assignment followed the Plant List, which corresponds to the Angiosperm Phylogeny Group (APG) classification III²⁴. To match the taxonomic concepts of the fern phylogeny, and to acknowledge recent advances in fern taxonomy, all fern names were additionally subjected to a comprehensive and careful taxonomic check (by M.K. and S.L.) so that genus and family assignments were up to date.

In order to link the species from the island checklists to the phylogenetic trees, phylogenies were pruned to family level (angiosperms and ferns) or genus level (palms and ferns) and species added as polytomies according to their family or genus membership.

For angiosperms, the original phylogeny²⁵ considered DNA sequence data for 560 species from 335 families and 45 orders, and was simultaneously estimated and dated using Bayesian methods based on 35 fossils and an additional age constraint for the root of the tree²⁵. For comparison with ferns, we pruned the phylogeny to family level (Supplementary Fig. S4). Five pairs of families that would otherwise not be monophyletic were merged (Supplementary Fig. S4). 60 families representing 935 species were missing from the phylogeny and were manually added to the tree according to ref. 26, the Angiosperm Phylogeny Group (APG) classification III²⁴, and information on the Angiosperm Phylogeny Website²⁷. In the cases of Achatocarpaceae, Alismataceae, Butomaceae, Cymodoceaceae, Juncaginaceae, Posidoniaceae, Potamogetonaceae and Scheuchzeriaceae the position in the tree and ages relative to adjacent clades could be adopted from ref. 26. In all other cases, age estimates were not available (Anisophylleaceae, Campynemataceae, Centrolepidaceae, Clusiaceae, Connaraceae, Brunelliaceae, Calceolariaceae, Campynemataceae, Centrolepidaceae, Clusiaceae, Connaraceae, Response of the set of the set of the case of the case, Centrolepidaceae, Clusiaceae, Connaraceae, Connaraceae, Campynemataceae, Centrolepidaceae, Clusiaceae, Connaraceae, Connaraceae, Campynemataceae, Centrolepidaceae, Clusiaceae, Connaraceae, Campynemataceae, Centrolepidaceae, Clusiaceae, Connaraceae, Campynemataceae, Centrolepidaceae, Clusiaceae, Connaraceae, Campynemataceae, Cam

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Corsiaceae, Cynomoriaceae, Cytinaceae, Dipentodontaceae, Dirachmaceae, Elatinaceae, Gisekiaceae, Gyrostemonaceae, Haemodoraceae, Hydatellaceae, Joinvilleaceae, Linderniaceae, Lophiocarpaceae, Loranthaceae, Mayacaceae, Mitrastemonaceae, Montiaceae, Nartheciaceae, Nitrariaceae, Nothofagaceae, Olacaceae, Pandaceae, Paracryphiaceae, Pennantiaceae, Pentaphragmataceae, Peraceae, Phrymaceae, Phyllanthaceae, Picramniaceae, Rhipogonaceae, Ruppiaceae, Salvadoraceae, Schlegeliaceae, Siparunaceae, Sphenocleaceae, Stegnospermataceae, Tetrachondraceae, Tovariaceae, Trimeniaceae, Triuridaceae, Xyridaceae). Families thought to be the sister clade of a family in the tree were added at 2/3 of the stem age of the family in the tree. Families thought to be sister to larger clades were added half way between nodes. For the calculation of phylogenetic community metrics, the 32,446 angiosperm species from the island checklists were added to the family-level phylogeny as polytomies at 1/3 of the family stem node ages. The final phylogeny pruned to include only species present in the considered island floras comprised 315 families and merged groups (Supplementary Fig. S4).

The palm phylogeny was based on a complete genus-level supertree of palms, dated using a Bayesian relaxed molecular clock approach with uncorrelated rates and calibrated using four palm fossil taxa and a stem node age constrained to 110 to 120 Ma²⁸. For comparison with ferns, we pruned the phylogeny to genus level (Supplementary Fig. S5). For the calculation of phylogenetic community metrics, the 1143 palm species from the island checklists were added to the phylogeny as polytomies at 2/3 of the genus stem node ages¹⁰. All palm species included in the species checklists were represented by genera in the phylogeny. The final phylogeny pruned to only include species present in the considered island floras comprised 118 genera (Supplementary Fig. S5).

For ferns, we used a dated phylogeny based on a global fern $phylogeny^{29}$. This dataset was updated by querying GenBank release 184 (June 15 2011), complemented with additional data not included in the queried release (KJ628500-KJ628963; KJ716370-KJ716414), and filtered to retain only those taxa that were represented in the dataset by at least two genes (one of which had to be *rbcL*) and more than 1000 base pairs of sequence data. Furthermore, the most similar taxa (defined by the pairwise distance of aligned sequences) were removed until no pair of taxa had pairwise distance less than 0.5%. This resulted in a taxonomically broad sample of 1118 taxa representing most extant fern genera. Molecular dating was based on uncorrelated exponential relaxed clock analysis in Beast $1.7.3^{30}$, using 42 fossil calibrated nodes and a partially constrained starting tree produced in RAxML 7.3.0^{31,32}. For comparison with angiosperms, we pruned the phylogeny to family level following the classification from ref. 33, and for comparison with palms, we pruned the phylogeny to genus level (Supplementary Fig. S6). A group of nine genera that would otherwise not be monophyletic was merged (Polypodiaceae A in Supplementary Fig. S6: Lemmaphyllum, Lepidomicrosorium, Lepisorus, Leptochilus, Microsorum, Neocheiropteris, Neolepisorus, Paragramma and Tricholepidium). The genus Odontosoria was split into an old world clade and a new world clade to avoid polyphyly. 25 missing genera representing 146 species were added to the tree manually according to information

from the literature (Supplementary Fig. S6). Genera thought to be located inside genera in the tree were merged with the already present genera. Genera thought to be the sister clade of a genus in the tree were added at 2/3 stem age of the genus in the tree (Aenigmopteris, Austrogramme, Cerosora, Cheiroglossa, Oenotrichia, Paraselliguea, Scoliosorus, Syngramma, Taenitis and Vaginularia). Genera thought to be sister to larger clades were added half way between nodes (Ananthacorus and Trachypteris). The genus Adenoderris (one species with one occurrence on Jamaica) was excluded due to its unknown phylogenetic position. For the calculation of phylogenetic community metrics, the 3689 fern species from the island checklists were added to the family-level phylogenies as tips at 1/3 of the family stem node ages and to the genus-level phylogenies as polytomies at 2/3 of the genus stem node ages. We chose 1/3 in the family phylogenies to account for the higher discrepancy between stem node ages of families and species when compared to genera and species in the genus-level phylogenies (2/3 stem node age). However, comprehensive sensitivity analyses of the palm phylogeny show that the specific age thresholds for polytomies do not qualitatively affect patterns and determinants of phylogenetic community structure¹⁰ because the metrics are predominantly influenced by long branch lengths in the older parts of the phylogeny. The final phylogenies pruned to include only species present in the considered island floras comprised 42 families and 168 genera (Supplementary Fig. S6).

Angiosperms, palms and ferns differ in age, number of species and major clades, and number of islands inhabited. However, the fern phylogeny encompasses a similar time span to the angiosperm phylogeny and an intermediate number of species compared to angiosperms and palms (Supplementary Figs S4, S5 and S6). In contrast to common belief, extant fern diversity is not older than angiosperm diversity; the largest fern lineages diversified in response to diversification in angiosperms³⁴. Differences between angiosperms, palms and ferns in the importance of dispersal, environmental filtering and diversification for phylogenetic assembly can therefore directly be compared and linked to differences in dispersal- and speciation-related traits.

The comparison between family- and genus-level analyses for ferns enabled us to scrutinize the sensitivity of our analyses towards the resolution of the phylogenies. Both levels, however, provide sufficient detail to address our hypotheses (Fig. 1) and to disentangle patterns and determinants of phylogenetic structure of island floras as most variation in branch lengths is in basal parts of phylogenies. Thus, higher resolution in relationships among species is not expected to considerably influence general patterns and dependencies (compare sensitivity analyses in ref. 10). In addition, dispersal-related traits and environmental adaptations are phylogenetic structure independent of whether family- or genus-level phylogenies have been used. Furthermore, usually young island radiations³⁵ are clearly distinguishable from relict lineages which often go back way beyond genus and even family level (e.g. Amborellaceae⁹) even in genus or family-level phylogenies with species appended as polytomies. In fact, there are plenty of examples of island radiations producing up to hundreds of closely related species^{7,36}, leading to clustered island assemblages.

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Our hypotheses on dispersal and environmental filtering as drivers of phylogenetic patterns assume phylogenetic signals in traits which vary with phylogenetic scale³⁷. The more of the tree of life is encompassed, the more conservative the traits should be⁴. However, if traits of clades of different biogeographic regions have converged, conservatism may diminish^{4,37}, hampering comparisons among phylogenies. In fact, we could not test for a phylogenetic signal of traits in the phylogenies, but previous studies suggest that dispersal related traits like seed size and dispersal mode, and adaptations to climates are phylogenetically conserved in many large and old clades^{2,3,6,38} (Supplementary Text S1). Furthermore, our results may help to understand patterns arising from different levels of phylogenetic signal in traits. The environmental models explained varying proportions of variance for angiosperms, palms and ferns (Table 1) suggesting differences in both predominant traits and levels of trait conservatism.

Tree editing was performed with R statistical software version 3.0.1 (R development Core Team, available at cran.r-project.org) using the package ape^{39} . Phylogenetic community metrics were calculated using the package *picante*⁴⁰.

Supplementary Methods S2. Statistical models and spatial autocorrelation.

To account for spatial autocorrelation in model residuals of the best non-spatial model of each plant group, we applied spatial eigenvector filtering⁴¹. We applied principal coordinate analysis to a neighbourhood matrix (PCNM) to deconstruct geographic distances between island centroids into orthogonal spatial eigenvectors. Spatial distances were truncated by exchanging distances larger than 1000 km by 4000 km to emphasize spatial autocorrelation at relatively small scales⁴¹. All eigenvectors with positive eigenvalues were considered as they represent positive spatial autocorrelation at different spatial scales. Following ref. 42, we consecutively added spatial filters as linear effects to the best models until residual spatial autocorrelation was no longer significant. In each round, the spatial filter that best reduced residual Moran's *I* values was retained in the model for the next round. Moran's *I* values were calculated for varying neighbourhood structures considered. Afterwards, the model selection procedure to find the best model and model averaging based on Akaike's Information Criterion corrected for small sampling sizes were repeated, with the identified set of spatial eigenvectors included in each model.

Analyses were performed with R statistical software version 3.0.1 (R development Core Team, available at cran.r-project.org) using packages $mgcv^{43}$ for Generalized Additive Models, $MuMIn^{44}$ for model selection and averaging, $vegan^{45}$ for PCNM and $spdep^{46}$ for spatial autocorrelation assessment.

Supplementary Table S1. Pearson correlations of phylogenetic community metrics within angiosperms, palms and ferns on islands worldwide. Metrics were calculated for angiosperms based on the dated family-level phylogeny from ref. 25, and for palms based on a dated genus-level phylogeny. For comparison, metrics for ferns were calculated using phylogenies at both family and genus levels. MPD_{es} = standardized effect size of mean pairwise phylogenetic distance, PD_{es} = standardized effect size of phylogenetic diversity (PD). n = 363 islands for all angiosperms, n = 71 islands for palms and n = 234 islands for ferns. Coefficients and p-values were corrected for spatial autocorrelation following ref. 47. Significance: * p < 0.05, ** p < 0.01, *** p < 0.001.

Taxon	Metric	log ₁₀ SR	log ₁₀ PD	PDes
Angiosperms	log10 PD	0.99 ***		
	PDes	-0.39 ***	-0.29 **	
	MPDes	0.04	0.10	0.56 **
Ferns (family)	log ₁₀ PD	0.96 ***		
	PDes	0.03	0.23 ***	
	MPD _{es}	0.07	0.24 ***	0.86 ***
Palms	log ₁₀ PD	0.83 ***		
	PDes	-0.36 **	0.04	
	MPD _{es}	-0.59 ***	-0.32 **	0.84 ***
Ferns (genus)	log10 PD	0.97 ***		
_	PDes	-0.03	0.17 *	
	MPDes	0.05	0.22 ***	0.86 ***

Supplementary Table S2. Pearson correlations of phylogenetic community metrics among angiosperms, palms and ferns on islands worldwide. Metrics were calculated for angiosperms based on two dated family-level phylogenies^{25,26}, and for palms based on a dated genus-level phylogeny. For comparison, metrics for ferns were calculated using phylogenies at both family and genus levels. MPD_{es} = standardized effect size of mean pairwise phylogenetic distance, PD_{es} = standardized effect size of phylogenetic diversity (PD). n = 363 islands for all angiosperms, n = 71 islands for palms and n = 234 islands for ferns. Coefficients and p-values were corrected for spatial autocorrelation following ref. 47. Significance: * p < 0.05, ** p < 0.01, *** p < 0.001.

Metric	Taxon	Angiosperms (Davies <i>et al</i> .)	Angiosperms (Bell <i>et al</i> .)	Ferns (family)	Ferns (genus)
PD	Angiosperms (Bell et al.)	1.00 ***	()		
	Ferns (family)	0.71 ***	0.71 ***		
	Ferns (genus)	0.71 ***	0.70 ***	1.00 ***	
	Palms	0.83 ***	0.83 ***	0.78 ***	0.78 ***
PDes	Angiosperms (Bell et al.)	0.98 ***			
	Ferns (family)	0.08	0.01		
	Ferns (genus)	-0.01	-0.07	0.91 ***	
	Palms	0.04	0.22	-0.27	-0.11
MPDes	Angiosperms (Bell et al.)	0.99 ***			
	Ferns (family)	0.31 ***	0.30 **		
	Ferns (genus)	0.30 ***	0.29 **	0.99 ***	
	Palms	0.41 **	0.40 **	-0.28	-0.28

Supplementary Table S3. Best Generalized Additive Models based on Akaike's Information Criterion corrected for small sampling sizes of the relationships of the standardized effect size of phylogenetic diversity (PD_{es}) of angiosperms, palms and ferns with environmental factors on islands. In addition to the parameters shown here, the models included spatial eigenvectors to account for spatial autocorrelation. For angiosperms, PD_{es} was calculated based on a dated family-level phylogeny, and for palms based on a dated genus-level phylogeny. For comparison, PD_{es} of ferns was calculated using phylogenies at both family and genus levels (n = 363 islands for all angiosperms, n =71 islands for palms and n = 234 islands for ferns). R² is a partial R² for the predictor variables, removing the effect of the spatial eigenvectors; edf = effective degrees of freedom; column t/F-value contains t-values in case of intercepts and linear effects (edf =1) and F-values in case of smooth terms (edf > 1); MLSR = Mainland species richness, SLMP = surrounding landmass proportion, CCVT = Late Quaternary climate change velocity.

Term	Estimate	Std. error	edf	t/F-value	p-value	R ²
Angiagnamma						0.49
Angiosperms Intercept	-4.185	0.093	1.000	-45.003	< 0.001	0.49
Elevation range (m)	-4.105	0.075	1.318	3.064	0.061	
\log_{10} Area (km ²)			1.852	19.346	< 0.001	
MLSR			1.000	28.613	< 0.001	
Precipitation (mm)			1.926	30.367	< 0.001	
-1 x log ₁₀ SLMP			1.870	32.029	< 0.001	
Temperature (°C)			1.997	26.865	< 0.001	
Temperature range (°C)			1.855	28.384	< 0.001	
Ferns (family)						0.15
Intercept	0.253	0.072	1.000	3.518	0.001	0110
Elevation range (m)			1.751	4.600	0.012	
\log_{10} Area (km ²)			1.000	5.536	0.019	
$\log_{10} \text{CCVT} (\text{m/y})$			1.901	6.551	0.002	
MLSR			1.000	19.900	< 0.001	
Precipitation (mm)			1.775	8.257	< 0.001	
Palms						0.52
Intercept	-1.06	0.184	1.000	-5.776	< 0.001	
log ₁₀ Årea (km ²)			1.933	13.852	< 0.001	
MLSR			1.000	11.596	0.001	
-1 x log ₁₀ SLMP			1.000	13.384	0.001	
Variation in precipitation			1.656	7.603	0.001	
Temperature range (°C)			1.951	7.447	0.001	
Ferns (genus)						0.18
Intercept	0.271	0.067	1.000	4.025	< 0.001	
Elevation range (m)			1.859	5.521	0.005	
\log_{10} Area (km ²)			1.000	4.783	0.030	
MLSR			1.894	8.016	< 0.001	
Precipitation (mm)			1.000	9.083	0.003	
Temperature (°C)			1.902	12.679	< 0.001	
Variation in precipitation			1.000	5.376	0.021	

Supplementary Table S4. Variable importance estimated from all possible multi-predictor Generalized Additive Models for the standardized effect size of mean pairwise phylogenetic distance (MPD_{es}) of angiosperms, palms and ferns on islands in dependence on environmental predictors. Importance was assessed as the sum of Akaike's Information Criterion corrected for small sampling sizes (AIC_c) weights of all models in which a variable was included. Apart from island predictor variables, all candidate models also included spatial eigenvectors to account for spatial autocorrelation. Angiosperm MPD_{es} was calculated based on a dated family-level phylogeny, and palm MPD_{es} based on a dated genus-level phylogeny. Fern MPD_{es} was based on dated phylogenies at both family and genus levels (n = 363 islands for all angiosperms, n = 71 islands for palms and n = 234 islands for ferns). Columns Disp (dispersal filtering), Spec (*in-situ* speciation) and Env (environmental filtering) indicate which hypothesized process the variables relate to. Values larger than 0.8 are printed in bold.

	Pr	ocess (Fi	g. 1)	Family-level phylogeny Genus-leve		el phylogeny	
Variable	Disp	Spec	Env	Angiosperms	Ferns	Palms	Ferns
Mainland species richness (MLSR)	Х			0.93	0.99	0.3	1
Geologic history (fragment, shelf, oceanic)	Х	Х		0.7	0.59	0.67	0.46
-1 x log ₁₀ Surrounding landmass proportion (SLMP)	Х	Х		0.93	0.78	0.84	1
log ₁₀ Island area (km ²)		Х		1	0.97	1	1
Elevation range (m)		Х	Х	0.97	1	0.85	1
Annual mean temperature (°C)			Х	0.4	0.95	0.94	0.5
Temperature seasonality (annual range; °C)			Х	0.99	0.36	0.35	0.85
Annual precipitation (mm)			Х	1	0.81	0.2	0.31
Precipitation seasonality (coefficient of variation)			X	0.31	0.44	0.88	0.26
log ₁₀ Late Quaternary climate change velocity in temperature (m y ⁻¹ ; CCVT)			Х	0.67	0.94	0.3	1

Supplementary Table S5. Best Generalized Additive Models based on Akaike's Information Criterion corrected for small sampling sizes of the relationships of the standardized effect size of mean pairwise phylogenetic distance (MPD_{es}) of angiosperms, palms and ferns with environmental factors on islands. Models included spatial eigenvectors to account for spatial autocorrelation. For angiosperms, MPD_{es} was calculated based on a dated family-level phylogeny, and for palms based on a dated genus-level phylogeny. For comparison, MPD_{es} of ferns was calculated using phylogenies at both family and genus levels. (n = 363 islands for all angiosperms, n = 71 islands for palms and n = 234 islands for ferns). Estimates for factor levels of geologic history are given relative to continental fragments. R² is a partial R² for the predictor variables, removing the effect of the spatial eigenvectors; edf = effective degrees of freedom; column t/F-value contains t-values in case of intercepts and linear effects (edf =1) and F-values in case of smooth terms (edf > 1); MLSR = Mainland species richness, SLMP = surrounding landmass proportion, CCVT = Late Quaternary climate change velocity.

Term	Estimate	Std. error	edf	t/F-value	p-value	R ²
Angiosperms						0.37
Intercept	-1.559	0.248	1.000	-6.290	< 0.001	
Geologic history (oceanic)	0.278	0.288	1.000	0.966	0.335	
Geologic history (shelf)	0.819	0.351	1.000	2.330	0.020	
Elevation range (m)			1.000	7.955	0.005	
log10 Area (km ²)			1.000	18.066	< 0.001	
log ₁₀ CCVT (m/y)			1.000	3.869	0.050	
MLSR			1.882	3.893	0.022	
Precipitation (mm)			1.935	18.350	< 0.001	
-1 x log ₁₀ SLMP			1.660	5.064	0.008	
Temperature range (°C)			1.940	7.226	0.001	
Ferns (family)						0.25
Intercept	1.030	0.234	1.000	4.406	< 0.001	
Geologic history (oceanic)	-0.617	0.279	1.000	-2.212	0.028	
Geologic history (shelf)	-0.525	0.321	1.000	-1.634	0.104	
Elevation range (m)			1.862	8.794	< 0.001	
log ₁₀ Area (km ²)			1.384	6.389	0.005	
log ₁₀ CCVT (m/y)			1.937	6.154	0.003	
MLSR			1.550	7.668	0.001	
Precipitation (mm)			1.000	5.789	0.017	
-1 x log ₁₀ SLMP			1.615	2.838	0.065	
Temperature (°C)			1.000	13.984	< 0.001	
Variation in precipitation			1.000	2.138	0.145	
Palms						0.59
Intercept	-3.027	0.791	1.000	-3.828	< 0.001	
Geologic history (oceanic)	0.269	1.152	1.000	0.233	0.816	
Geologic history (shelf)	4.918	1.913	1.000	2.571	0.013	
Elevation range (m)			1.705	4.959	0.011	
\log_{10} Area (km ²)			2.000	21.465	< 0.001	
$-1 \ge \log_{10} \text{SLMP}$			1.000	5.648	0.021	
Temperature (°C)			1.931	5.746	0.005	
Variation in precipitation			1.000	7.352	0.009	
Ferns (genus)						0.24
Intercept	0.585	0.078	1.000	7.545	< 0.001	0.24
Elevation range (m)	0.505	0.070	1.867	8.278	< 0.001	
\log_{10} Area (km ²)			1.000	35.587	< 0.001	
\log_{10} CCVT (m/y)			1.948	16.175	< 0.001	
MLSR			1.707	14.465	< 0.001	
-1 x log ₁₀ SLMP			1.935	9.101	< 0.001	
Temperature (°C)			1.000	2.720	0.101	
Temperature (°C)			1.288	4.856	0.101	
remperature range (°C)			1.200	4.000	0.017	

Supplementary Table S6. Pearson correlations among predictor variables used to explain phylogenetic structure of island floras (n = 393). Correlations with island age were calculated for a subset of n = 202 oceanic islands with information on the age of emergence. Coefficients and p-values were corrected for spatial autocorrelation following ref. 47. MLSR = mainland species richness, -SLMP = -1 x log₁₀ surrounding landmass proportion, Area = log₁₀ island area (km²), Elev = elevation range (m), Temp = annual mean temperature (°C), varT = annual temperature range (°C), Prec = annual precipitation (mm), varP = variation in monthly precipitation, CCVT = log₁₀ Late Quaternary climate change velocity (m/y), Age = island age (my). Coefficients larger than 0.7 are printed in bold. Significance: * p < 0.05, ** p < 0.01, *** p < 0.001.

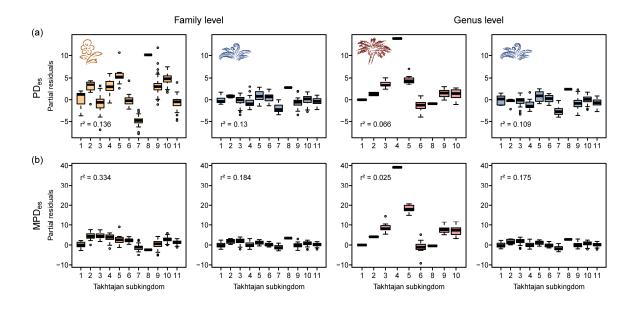
	MLSR	- SLMP	Area	Elev	Temp	varT	Prec	varP	CCVT
- SLMP	0.09								
Area	0.04	-0.08							
Elev	0.01	-0.01	0.78***						
Temp	0.55***	0.23	-0.10	-0.07					
varŤ	-0.30*	-0.70***	-0.02	-0.04	-0.55**				
Prec	0.22	0.43***	0.28***	0.43***	0.19	-0.29**			
varP	-0.07	-0.32*	-0.17*	-0.18*	0.31*	0.05	-0.48***		
CCVT	-0.22*	-0.34**	-0.48***	-0.48***	-0.43***	0.47***	-0.26**	-0.07	
Age	0.12	-0.12	0.14	-0.14	0.20*	-0.26***	-0.14	0.16*	-0.08

Supplementary Table S7. Pearson correlations among phylogenetic community metrics calculated with a global island species pool and three different regional species pool delineations (standardized effect size of phylogenetic diversity (PD_{es}) and mean pairwise phylogenetic distance (MPD_{es})). Regional species pools include all species of all islands that 1) belong to a particular floristic realm after Takhtajan⁴⁸ (Regions; Australis included in Holantarctis), 2) belong to a major ocean basin (Oceans; i.e. Pacific, Atlantic, Indian Ocean), or 3) are located within 10,000 km around each target island⁴⁹ (Circular; see Supplementary Fig. S9). Coefficients and p-values were corrected for spatial autocorrelation⁴⁷. Significance: * p < 0.05, ** p < 0.01, *** p < 0.001.

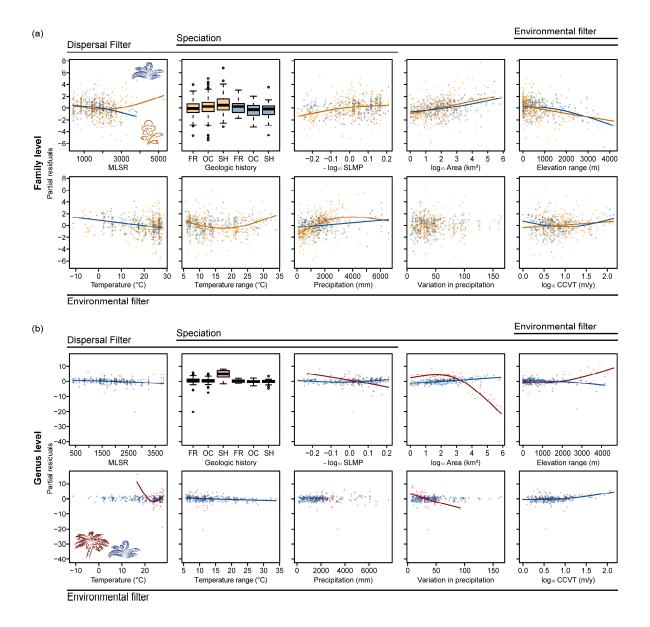
Metric	Taxon	Regions	Oceans	Circular
PDes	Angiosperms	0.87 ***	0.96 ***	0.96 ***
	Ferns (family)	0.93 ***	0.98 ***	0.99 ***
	Ferns (genus)	0.95 ***	0.97 ***	0.99 ***
	Palms	0.96 ***	0.94 ***	0.97 ***
MPD _{es}	Angiosperms	0.94 ***	0.90 ***	0.91 ***
	Ferns (family)	0.86 ***	0.99 ***	0.99 ***
	Ferns (genus)	0.87 ***	0.99 ***	0.99 ***
	Palms	0.97 ***	0.97 ***	0.97 ***

Supplementary Table S8. Variation explained by Generalized Additive Models (GAM) of the standardized effect size of phylogenetic diversity (PD_{es}) and mean pairwise phylogenetic distance (MPD_{es}) of angiosperms overall, palms and ferns on islands based on a global island species pool (Global) and three different regional species pool delineations (Regions, Oceans, Circular) as response variables and environmental predictor variables. Results are shown for the best models retained after a model selection procedure based on Akaike's Information Criterion corrected for small sampling sizes (see methods for the set of environmental predictors included). In addition to the environmental predictors, the models included spatial eigenvectors to account for spatial autocorrelation. Here, we report pseudo R²-values derived from linear models of observed vs. predicted values from the GAMs, disregarding the spatial filters in the predictions, to estimate variation explained by environmental predictors alone. Regional species pools included all species of all islands that 1) belong to a particular floristic realm after Takhtajan⁴⁸ (Regions; Australis included in Holantarctis), 2) belong to a major ocean basin (Oceans; i.e. Pacific, Atlantic, Indian Ocean), or 3) are located within 10,000 km around each target island⁴⁹ (Circular; see Supplementary Fig. S9).

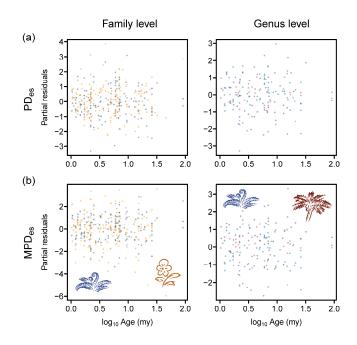
Metric	Taxon	Global	Regions	Oceans	Circular
PDes	Angiosperms	48.6	34.3	45.7	48.3
	Ferns (family)	15.1	16.7	13.5	11.9
	Ferns (genus)	18.1	18.8	18.8	19.7
	Palms	51.6	54.6	53.4	52.0
MPD _{es}	Angiosperms	36.8	33.2	34.3	39.7
	Ferns (family)	25.3	15.6	24.0	17.0
	Ferns (genus)	24.1	13.0	26.8	17.2
	Palms	58.8	52.4	48.7	47.5



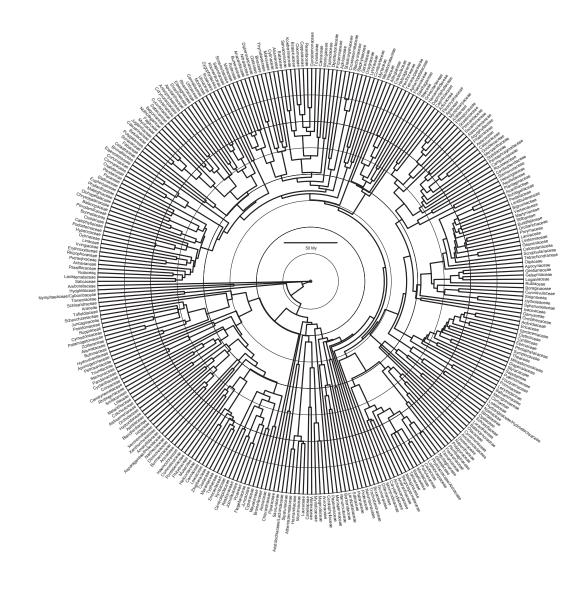
Supplementary Figure S1. Partial residual plots for Takhtajan's floristic subkingdoms derived from averaged Generalized Additive Models of the relationships of the standardized effect sizes of (a) phylogenetic diversity (PD_{es}) and (b) mean pairwise phylogenetic distance (MPD_{es}) of angiosperms, palms and ferns with environmental factors on islands. In addition to Takhtajan's floristic subkingdoms⁴⁸, models included ten environmental predictors as well as spatial eigenvectors to account for spatial autocorrelation. PD_{es} and MPD_{es} were calculated based on a dated family-level phylogeny for angiosperms (orange) and based on a dated genus-level phylogeny for palms (red). Metrics for ferns (blue) were calculated based on a dated family-level phylogeny for comparison with angiosperms (column 2), and based on a dated genus-level phylogeny for comparison with palms (column 4). Only islands with at least two species of the focal group were included in models (n = 363 for all angiosperms, n = 71 for palms only and n = 234 for ferns). Takhtajan's floristic subkingdoms: 1 = African, 2 = Australian, 3 = Boreal, 4 = Holantarctic, 5 = Indomalesian, 6 = Madagascan, 7 = Madrean, 8 = Neocaledonian, 9 = Neotropical, 10 = Polynesian, 11 = Tethyan.



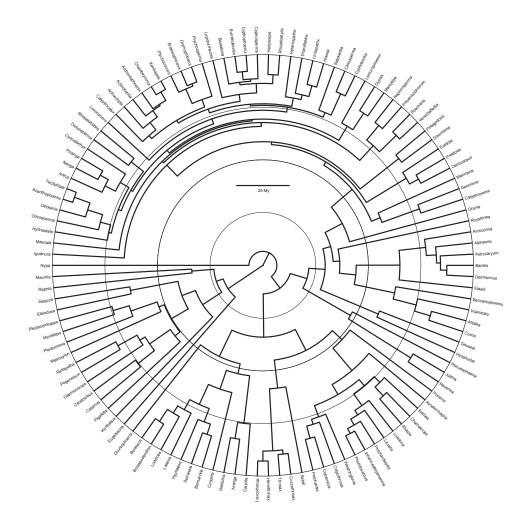
Supplementary Figure S2. Partial residual plots from averaged Generalized Additive Models of the relationships of the standardized effect size of mean pairwise phylogenetic distance (MPD_{es}) of angiosperms, palms and ferns with environmental factors on islands. Models included spatial eigenvectors to account for spatial autocorrelation. Regression lines are shown if the variable was significant in the averaged model. In (a), MPD_{es} was based on dated family-level phylogenies of angiosperms (orange) and ferns (blue). In (b), MPD_{es} was based on dated genus-level phylogenies of palms (red) and ferns (blue). Only islands with at least two species of the focal group are shown (n = 363 for all angiosperms, n = 71 for palms and n = 234 for ferns). MLSR = Mainland species richness, SLMP = surrounding landmass proportion, CCVT = Late Quaternary climate change velocity; Geologic island types: FR = continental fragment, OC = oceanic island (volcanic islands, atolls, uplifted sea floor), SH = continental shelf islands.



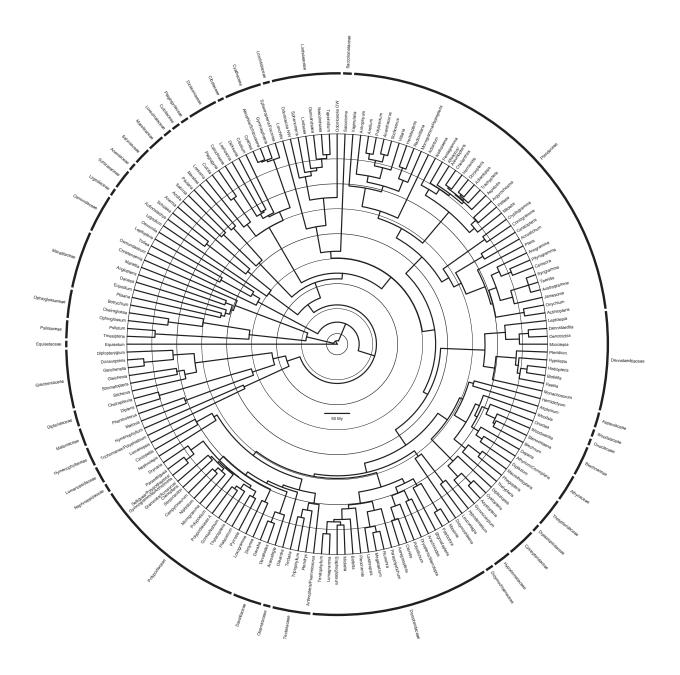
Supplementary Figure S3. Partial residual plots for island geologic age derived from averaged Generalized Additive Models of the relationships of the standardized effect sizes of (a) phylogenetic diversity (PD_{es}) and (b) mean pairwise phylogenetic distance (MPD_{es}) of angiosperms, palms and ferns with environmental factors on islands. In addition to island age, the full models included ten environmental predictors and spatial eigenvectors to account for spatial autocorrelation. The effect of island age was not significant in any averaged model (p > 0.05). Regression lines are therefore not plotted. PD_{es} and MPD_{es} were calculated based on a dated family-level phylogeny for angiosperms (orange) and based on a dated genus-level phylogeny for comparison with angiosperms (column 1), and based on a dated genus-level phylogeny for comparison with angiosperms (column 1), and based on a dated genus-level phylogeny for comparison with palms (column 2). Only islands with at least two species of the focal group and with information on island age were included in models (n = 187 islands for all angiosperms, n = 31 islands for palms only and n = 138 islands for ferns).



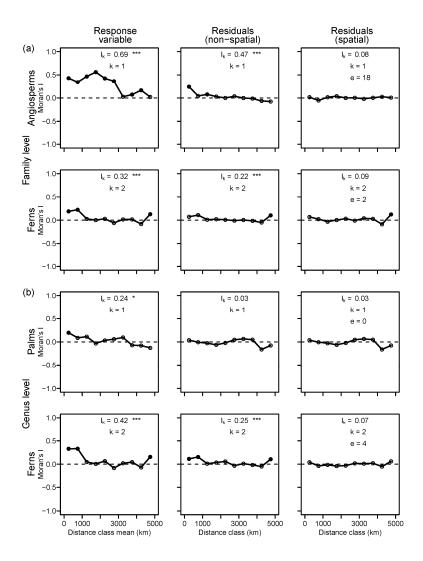
Supplementary Figure S4. Dated angiosperm phylogeny used to analyse the phylogenetic structure of island floras. The original phylogeny²⁵, including 560 angiosperm species from 335 families, was pruned to family level and to only include families present in the considered island floras (315 families and merged groups). Five pairs of families that would otherwise not be monophyletic were merged (names at tree tips separated by slash). 60 families missing from the phylogeny were manually added according to the phylogeny from ref. 26, the angiosperm phylogeny group²⁴ classification III and information on the angiosperm phylogeny website²⁷ (see Supplementary Methods S1 for details).



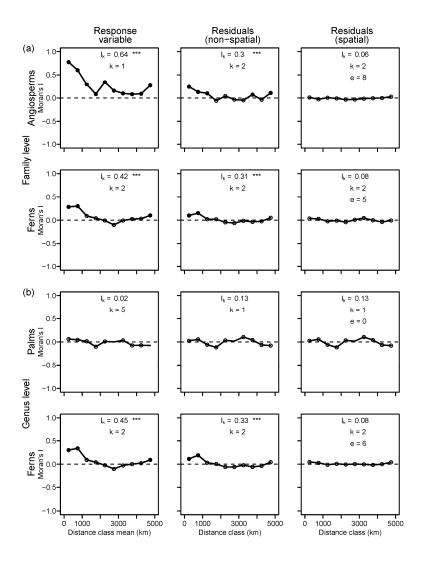
Supplementary Figure S5. Dated palm phylogeny used to analyse the phylogenetic structure of island floras. The original phylogeny²⁸ was pruned to genus level and only includes genera present in the considered island floras (118 genera; see Supplementary Methods S1 for details).



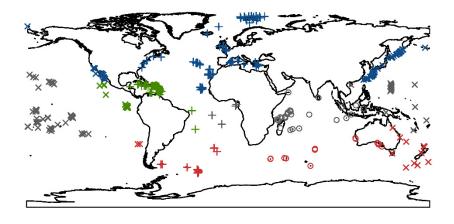
Supplementary Figure S6. Dated fern phylogeny used to analyse the phylogenetic structure of island floras. The original phylogeny including 1,118 fern species was pruned to genus level and to only include genera present on the considered islands (168 genera, 42 families). 25 genera were placed manually to the tree according to literature information (see Supplementary Methods S1 for details). The genus *Odontosoria* was split into an old world clade (*Odontosoria* OW) and a new world clade (*Odontosoria* NW). Genus names separated by slashes and the label "Polypodiaceae A" indicate groups of merged genera. The outside ring of lines and names indicates how fern families were delimited in the family-level phylogeny.



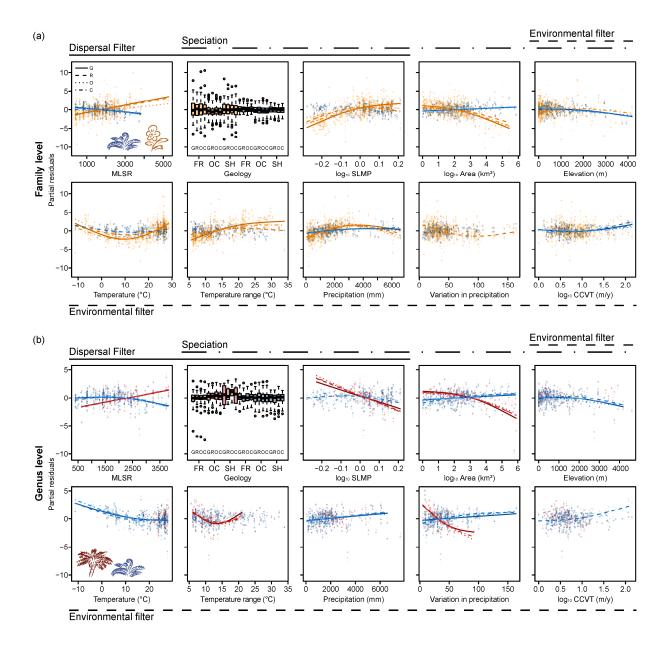
Supplementary Figure S7. Moran's *I* correlograms of spatial autocorrelation for the standardized effect size of phylogenetic diversity (PD_{es}; Response variable) of angiosperms, palms and ferns on islands; residuals from the best Generalized Additive Models of PD_{es} in dependence on environmental predictors (Residuals (non-spatial)); and residuals from best spatial models (Residuals (spatial)) including a set of *e* spatial eigenvectors to reduce spatial autocorrelation (see Supplementary Methods S2 for details). In (a), PD_{es} was calculated based on dated family-level phylogenies of angiosperms and ferns. In (b), PD_{es} was calculated based on dated genus-level phylogenies of palms and ferns. Filled circles indicate spatial autocorrelation significant at p < 0.05; open circles indicate non-significant autocorrelation. I_k values are Moran's *I* values based on row standardized neighbourhood lists of k neighbours per island. We show the highest Moran's *I* value out of values for k = 1 to k = 25. Significance of I_k: * p < 0.05, *** p < 0.001.



Supplementary Figure S8. Moran's *I* correlograms of spatial autocorrelation for the standardized effect size of mean pairwise phylogenetic distance (MPD_{es}; Response variable) of angiosperms, palms and ferns on islands; residuals from the best Generalized Additive Models of MPD_{es} in dependence on environmental predictors (Residuals (non-spatial)); and residuals from bes spatial models (Residuals (spatial)) including a set of e spatial eigenvectors to reduce spatial autocorrelation (see Supplementary Methods S2 for details). In (a), MPD_{es} was calculated based on dated family-level phylogenies of angiosperms and ferns. In (b), MPD_{es} was calculated based on dated genus-level phylogenies of palms and ferns. Filled circles indicate spatial autocorrelation significant at p < 0.05 in contrast to non-significant autocorrelation (open circles). I_k values are Moran's *I* values based on row standardized neighbourhood lists of k neighbours per island (I_k). We show the highest Moran's *I* value out of values for k = 1 to k = 25. Significance of I_k: * p < 0.05, *** p < 0.001.



Supplementary Figure S9. Three different delineations of regional species pools used in sensitivity analyses. Colours indicate floristic realms after Takhtajan⁴⁸ (Australis included in Holantarctis): blue = Holarctis, green = Neotropis, grey = Palaeotropis, red = Holantarctis (including Australis); Symbols indicate regions delimited after the major ocean basins: x = Pacific, + = Atlantic, $\circ = Indian$. In addition, we used all plants on all islands within 10,000 km around each target island as circular regional species pools⁴⁹. The map was created in R⁵⁰.



Supplementary Figure S10. Species pool sensitivity analyses for environmental predictors of phylogenetic structure in island floras. Equivalent to Fig. 4, partial residual plots from averaged Generalized Additive Models show the standardized effect size of phylogenetic diversity (PD_{es}) of angiosperms overall, palms and ferns as a function of environmental predictors. Here, however, results are shown based on different regional species pool delineations in addition to the global island species pool (denoted G; solid lines, symbol •). Regional species pools include all species of all islands that 1) belong to a particular floristic realm after Takhtajan⁴⁸ (denoted R; dashed lines; symbol *; Australis included in Holantarctis), 2) belong to a major ocean basin (denoted O; dashed lines; symbol -; i.e. Pacific, Atlantic, Indian Ocean), or 3) are located within 10,000 km around each target island⁴⁹ (denoted C; dashed lines; symbol +; see Supplementary Fig. S9). Models included spatial eigenvectors to account for spatial autocorrelation. Regression lines are shown if the variable was significant in the

averaged model for the given species pool delineation. In (a), PD_{es} was based on dated family-level phylogenies of angiosperms (orange) and ferns (blue). In (b), PD_{es} was based on dated genus-level phylogenies of palms (red) and ferns (blue). Only islands with at least two species of the focal group are shown (363 islands for all angiosperms, 71 for palms and 234 for ferns). MLSR = Mainland species richness, SLMP = surrounding landmass proportion, CCVT = Late Quaternary climate change velocity; Geologic island types: FR = continental fragment, OC = oceanic island, SH = continental shelf islands.

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