

Supporting Information

Kerkhoff et al. 10.1073/pnas.1308932111

SI Text

Alternative Models of Evolution

Our ancestral estimates of the tropicality index (TI) were drawn from a random walk (RW) model of character evolution, with the parameter $\lambda = 0.76$. Based on an Akaike's information criterion (AIC) analysis, the RW model fit better than three alternatives: (i) a white noise model (WN), which ignores phylogenetic branch lengths; (ii) Brownian motion (BM), which assumes constant variation with no trend; and (iii) the Ornstein–Uhlenbeck model (OU), which adds selection in proportion to the distance of the trait from an optimum value (Table S2). We also compared our results with those of Felsenstein's contrast method (PIC), which also assumes a BM model of character evolution.

Although the RW model provides the best fit, the character estimates from all of the methods (not including WN) were highly correlated (Table S3) and all of the ancestral reconstruction results were qualitatively similar (Fig. S3). Most temperate lineages always originated relatively recently. In the OU model, the selection toward the optimum tropicality value made the deeper temperate lineages (which are well documented in the fossil record) disappear and the deeper nodes seem unrealistically static. These results highlight the caution that must be exercised in drawing conclusions based on models of trait evolution and ancestral character reconstruction.

Additional Taxonomic Analyses

For comparison with previous results, we also analyzed our data based on family ages (1, 2). Specifically, we examined whether family age varied systematically with several distributional measures derived from the species' latitudinal limits. For family age estimates, we relied on the stem-group estimates of Davies et al. (3).

First, at the coarsest scale, we assigned each of the 12,521 species to one of six latitudinal zones depending on their latitudinal range boundaries: species present only in the northern temperate zone, those present only in the southern temperate zone, those spanning from the tropics into the northern temperate zone, those spanning from the tropics into the southern temperate zone, those spanning from the northern temperate zone through to the southern temperate zone, and those present only in the tropics. On a finer scale, we divided the species into 5° latitudinal bands based on their range midpoints, from –50° S to 70° N. These two alternative classifications emphasize different aspects of the species' distributions (midpoint vs. boundaries), but in both cases, each species only occupies a single bin or zone, eliminating the problem of pseudoreplication that arises in many studies of geographical ranges along the latitudinal gradient (4).

To test whether temperate species tend to be from younger families, we used a null model to compare the mean family ages of the species in each band and zone with what would be expected from a random distribution. In the null model, we shuffled the ages of species' families without replacement, while holding constant the number of species in each zone or band. We then calculated the randomized mean age for each zone or band and repeated this process for a total of 999 repetitions. The actual mean age was then compared with this distribution of ages. If the actual age was in the lower or upper 2.5% of the random distribution ($\alpha = 0.05$), it was considered significantly older or younger.

For a complementary test, we divide families based on their geological epoch of origin and calculated the mean TI across species for each epoch. We then used a null model randomizing TI and holding constant the number of species in each family (and thus in each epoch) to determine if the species from younger families were more temperate than would be expected, based again on the distribution of mean TIs from 1,000 randomizations, as described above.

We found that species distributed in the northern temperate zone were consistently drawn from younger than expected families. When species were divided into 5° bands based on their midpoints, those with their midpoints between 15–45° N, 50–55° N, and 60–0° N were from younger than expected families (Fig. S1; $P \leq 0.03$), whereas the species with midpoints between 10° S and 10° N were from significantly older families ($P = 0.012$). Species with range midpoints from 15–20° S were also from younger than expected families. Based on their range boundaries, species present only in the northern temperate zone and those that span from the tropics into either the northern temperate zone or southern temperate zone were from younger than expected families, as were species that span from the southern temperate zone to the northern temperate zone (Fig. S1; $P = 0.002$ and $P < 0.001$, respectively). Surprisingly, 9,500 of 12,521 total species isolated to the tropics were still drawn from older than expected families ($P < 0.001$). All other latitudinal zones had mean family ages that were indistinguishable from the randomized expectation.

In qualitative agreement with the tropical conservatism hypothesis (TCH), species from families originating in the more recent geological epochs (since the Paleocene) are more temperate than expected (Fig. S2; $P < 0.001$), whereas those from families originating in the Cretaceous are more tropical than expected ($P < 0.001$). However, based on family ages, the transition to a more temperate habitat appears to occur earlier than the Oligocene cooling highlighted by the TCH. Further discussion is provided in the main text.

1. Hawkins BA, DeVries PJ (2009) Tropical niche conservatism and the species richness gradient of North American butterflies. *J Biogeogr* 36(9):1698–1711.
2. Hawkins BA, Rodriguez MA, Weller SG (2011) Global angiosperm family richness revisited: Linking ecology and evolution to climate. *J Biogeogr* 38(7):1253–1266.

3. Davies TJ, et al. (2004) Darwin's abominable mystery: Insights from a supertree of the angiosperms. *Proc Natl Acad Sci USA* 101(7):1904–1909.
4. Weiser MD, et al. (2007) Latitudinal patterns of range size and species richness of New World woody plants. *Glob Ecol Biogeogr* 16(5):679–688.

Table S1. Distribution of tropical (TI \geq 0) and temperate (TI < 0) species and the percentage of temperate species across different clades

Clade	Species counts		Temperate, %
	Tropical	Temperate	
Angiospermae (169)	10,638	1,883	15.0%
Magnoliidae (12)	858	40	4.5%
Monocotyledonae (12)	1,112	62	5.3%
Basal eudicots (8)	154	45	22.6%
Superasteridae (62)	4,055	744	15.5%
Lamiidae (20)	2,140	290	11.9%
Campanuliidae (11)	1,006	259	20.5%
Superrosidae (73)	4,437	991	18.3%
Malvidae (22)	1,656	146	8.1%
Fabidae (48)	2,743	815	22.9%
Magnoliidae			
Laurales (5)	343	15	4.2%
Magnoliales (3)	255	14	5.2%
Piperales (2)	258	11	4.1%
Canellales (2)	2	0	0%
Monocotyledonae			
Arecales (1)	396	20	4.8%
Asparagales (3)	17	22	56.4%
Poales (2)	142	4	2.7%
Zingiberales (3)	101	1	1.0%
Liliales (1)	19	15	44.1%
Pandales (1)	39	0	0%
Alismatales (1)	398	0	0%
Basal eudicots			
Buxales (1)	3	0	0%
Proteales (2)	21	5	19.2%
Sabiales (1)	30	0	0%
Ranunculales (4)	100	40	28.6%
Superasteridae			
Dilleniales (1)	23	1	4.2%
Santalales (5)	38	1	2.6%
Berberidopsidales (1)	0	1	100%
Caryophyllales (8)	191	74	27.9%
Cornales (2)	8	26	76.5%
Ericales (14)	649	92	12.4%
Lamiidae			
Garryales+ (3)	9	7	43.8%
Solanales (2)	422	77	15.4%
Gentianales (5)	937	53	5.4%
Lamiales (10)	772	153	16.5%
Campanuliidae			
Asterales (2)	836	218	20.7%
Escalloniales (1)	10	1	9.1%
Aquifoliales (4)	52	17	24.6%
Dipsacales (1)	22	14	38.9%
Apiales (2)	82	8	8.9%
Bruniales (1)	4	1	20.0%
Superrosidae			
Saxifragales (2)	2	3	60.0%
Vitales (1)	36	27	42.9%
Malvidae			
Brassicales (2)	61	2	3.2%
Malvales (3)	266	48	15.3%
Huertales (2)	7	0	0%
Sapindales (6)	540	76	12.3%
Picramniales (1)	15	0	0%
Crossosomatales (1)	3	2	40%
Myrtales (6)	763	18	2.3%
Geraniales (1)	1	0	0%

Table S1. Cont.

Clade	Species counts		
	Tropical	Temperate	Temperate, %
Fabidae			
Zygophyllales (1)	6	1	14.3%
Fabales (3)	932	172	15.6%
Rosales (7)	379	220	36.7%
Cucurbitales (3)	78	2	2.5%
Fagales (6)	72	163	69.4%
Celastrales (1)	99	9	8.3%
Oxalidales (5)	111	6	5.1%
Malpighiales (22)	1,066	3	18.5%

Numbers in parentheses are the number of families represented in each lineage.

Table S2. Comparison of different models of character evolution fit to the tropicity data

Model	AIC	Δ AIC
RW	19,674.48	0
OU	20,718.34	1,072
BM	22,601.15	2,965
WN	25,844.4	6,170

AIC, Akaike's information criterion; BM, Brownian motion; OU, Ornstein-Uhlenbeck; PIC, Felsenstein's contrast method; RW, Pagel's random walk.

Table S3. Correlation matrix for 1,329 ancestral tropicity values drawn from maximum likelihood estimates from the alternative models of character evolution

	Correlation among estimates			
	RW	OU	BM	PIC
RW	1.0	0.95	0.98	0.95
OU	0.95	1.0	0.96	0.93
BM	0.98	0.93	1.0	0.99

BM, Brownian motion; OU, Ornstein-Uhlenbeck; PIC, Felsenstein's contrast method; RW, Pagel's random walk.