

Supporting Information

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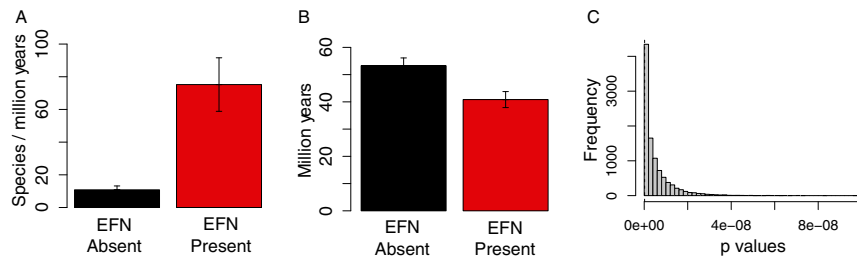


Fig. S1. Mean (\pm SE) species per million years (A) and mean (\pm SE) age (B) of families without EFNs (black) vs. with EFNs (red). (C) Histogram of P values from 10,000 tests that each randomly “discover” EFNs in 10 non-EFN families. The dotted line marks the P value from the nonsimulated test.

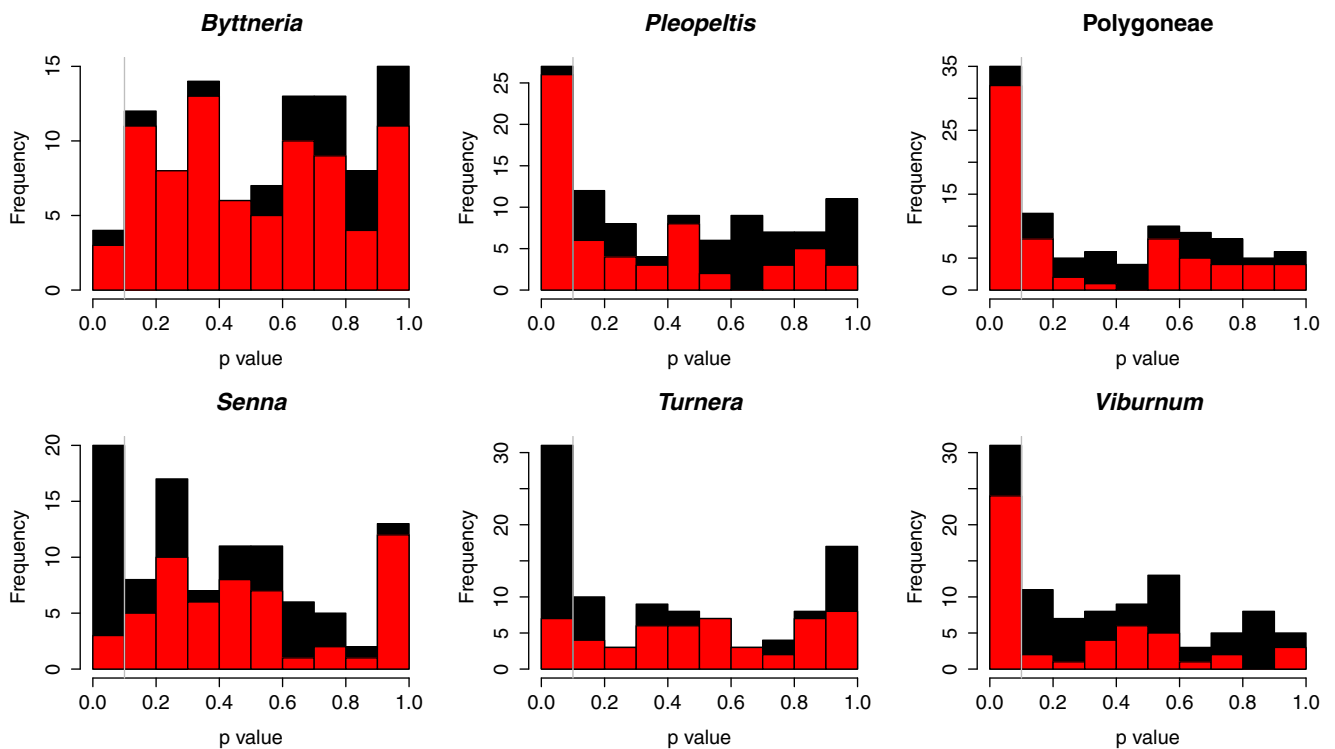


Fig. S2. Distribution of P values from ML-BiSSE analyses on simulated data. Black bars represent the total frequency of P values from the simulations (regardless of the directionality of the outcome). Red bars represent only those simulations where EFN rates were higher than non-EFN rates. The gray line marks the 0.1 significance level.

Table S1. Relationship between net diversification rates and the presence of species with EFNs in a family

e	+EFN	-EFN	F(1, 423)	P
APGIII megatree (minimum estimates)				
0	0.203 (0.023)	0.099 (0.008)	28.133	<0.0001
0.1	0.203 (0.023)	0.099 (0.008)	28.163	<0.0001
0.5	0.198 (0.022)	0.104 (0.008)	23.359	<0.0001
0.9	0.147 (0.018)	0.069 (0.006)	27.126	<0.0001
APGIII megatree (maximum estimates)				
0	0.203 (0.023)	0.101 (0.008)	27.504	<0.0001
0.1	0.203 (0.023)	0.1 (0.008)	27.532	<0.0001
0.5	0.198 (0.022)	0.104 (0.008)	23.619	<0.0001
0.9	0.147 (0.018)	0.069 (0.006)	27.449	<0.0001

Diversification rates were calculated following the method of Magallon and Sanderson (1) assuming no extinction ($e = 0$), and extinction fractions of 0.1, 0.5, and 0.9. Ages were derived from the APGIII megatree. In all analyses, diversification rates are higher in families that contain at least one species with EFNs. Mean diversification rates (SEs) for families that contain instances of EFNs (+) and for those families that do not (-), F statistics, and P values are reported for each test.

1. Magallón S, Sanderson MJ (2001) Absolute diversification rates in angiosperm clades. *Evolution* 55(9):1762–1780, and erratum (2006) 60(11):2411.

Table S2. Relationship between net diversification rates and the presence of species with EFNs in a family

E	+EFN	-EFN	F(1, 414)	P
Zanne et al., megatree (minimum estimates)				
0	0.085 (0.005)	0.039 (0.002)	87.972	<0.0001
0.1	0.085 (0.005)	0.039 (0.002)	88.031	<0.0001
0.5	0.083 (0.005)	0.041 (0.002)	81.081	<0.0001
0.9	0.062 (0.004)	0.027 (0.002)	93.921	<0.0001
Zanne et al., megatree (maximum estimates)				
0	0.085 (0.005)	0.04 (0.002)	85.825	<0.0001
0.1	0.085 (0.005)	0.04 (0.002)	85.882	<0.0001
0.5	0.083 (0.005)	0.041 (0.002)	80.923	<0.0001
0.9	0.063 (0.004)	0.027 (0.002)	93.745	<0.0001

Diversification rates were calculated following the method of Magallon and Sanderson (1) assuming no extinction ($e = 0$), and extinction fractions of 0.1, 0.5, and 0.9. Ages were derived from the Zanne et al. (2) megatree. In all analyses, diversification rates are higher in families that contain at least one species with EFNs. Mean diversification rates (SEs) for families that contain instances of EFNs (+) and those families that do not (-), F statistics, and P values are reported for each test.

1. Magallón S, Sanderson MJ (2001) Absolute diversification rates in angiosperm clades. *Evolution* 55(9):1762–1780, and erratum (2006) 60(11):2411.

2. Zanne AE, et al. (2014) Three keys to the radiation of angiosperms into freezing environments. *Nature* 506(7486):89–92.

Table S3. Summary of parameter estimates from post-burn-in MCMC for BiSSE analyses

Plant group	<i>Byttneria</i>	<i>Pleopeltis</i>	Polygoneae	<i>Senna</i>	<i>Turnera</i>	<i>Viburnum</i>
λ_0	232.9 (85.97)	128.56 (27.58)	77.44 (13.34)	144.51 (57.58)	15.4 (11.2)	456.75 (108.47)
λ_1	288.07 (78.79)	146.12 (23.59)	39.62 (8.42)	387.92 (74.28)	48.6 (11.2)	760.13 (138.1)
μ_0	115.6 (95.45)	112.19 (30.96)	63.77 (16.81)	101.14 (68.22)	18.66 (17.57)	385.24 (128.79)
μ_1	157.32 (103.45)	35.03 (28.67)	12.73 (11.19)	273.79 (92.55)	20.46 (14.91)	470.07 (184.43)
q_{01}	54.13 (42.69)	0.56 (0.48)	0.44 (0.36)	18.54 (13.51)	11.22 (12.51)	7.38 (6.5)
q_{10}	10.82 (11.28)	2.68 (2.64)	1.39 (1.47)	1.83 (1.85)	12.37 (8.9)	5 (5.16)
$P(q_{01} > q_{10})$	0.8839	0.1721	0.2474	0.9595	0.4228	0.6371
$r_1 - r_0$	13.46 (103.92)	94.72 (22.15)	13.23 (12.55)	70.75 (44.77)	31.39 (23.3)	218.55 (93.48)

The mean (and SD) of BiSSE estimates are reported. 0, EFN absent; 1, EFN present. λ_i , speciation rate; μ_i , extinction rate; q_{01} , rate of EFN gain; q_{10} , rate of EFN loss; $P(q_{01} > q_{10})$, proportion of MCMC steps where the rate of EFN gain was higher than the rate of EFN loss; $r_1 - r_0$, difference between EFN and non-EFN state-specific net diversification rates [$(\lambda_1 - \mu_1) - (\lambda_0 - \mu_0)$].

Table S4. Summary of diversification results from post-burn-in MCMC for BMM analyses and ML-estimated character transition rates used in marginal ancestral character state reconstructions

Plant group	<i>Byttneria</i>	<i>Pleopeltis</i>	Polygoneae	<i>Senna</i>	<i>Turnera</i>	<i>Viburnum</i>
λ_0	644.56 (247.65)	90.02 (21.67)	64.32 (10.4)	233.51 (75.93)	41.30 (14.01)	418.37 (101.61)
λ_1	569.4 (163.55)	146.97 (29.56)	44.37 (10.39)	360.80 (78.53)	51.91 (12.22)	591.77 (97.47)
μ_0	432.15 (283.84)	58.52 (27.12)	30.9 (13.82)	182.8 (80.97)	23.08 (15.44)	304.17 (121.68)
μ_1	397.14 (187.07)	81.86 (39.55)	20.71 (12.77)	247.26 (93.18)	27.67 (14.4)	325.15 (129.5)
q_{01}	14.71	0.31	0.25	6.33	3.73	3.087
q_{10}	4.69	<0.001	0.001	<0.001	8.04	<0.001
$r_1 - r_0$	-40.15 (107.74)	33.61 (20.02)	-9.76 (8.93)	62.83 (35.57)	6.01 (6.55)	152.43 (70.2)

The mean (and SD) of BMM estimates are reported.

Table S5. Substitution models for BEAST analyses

Plant group	Region	Substitution model (AIC)
<i>Byttneria</i>	trnL	HKY + G
	matK	GTR + I
<i>Pleopeltis</i>	rbcl	GTR + G
	rps4	GTR + G
Polygoneae	trnL-trnF	GTR + G
	ITS	GTR + G
	matK	GTR + G
	rbcl	GTR + G
<i>Senna</i>	trnL-trnF	GTR + G
	rpl16	GTR + G
	rpS16	GTR + G
	trnK-matK	GTR + G
<i>Turnera</i>	ITS	GTR + G
<i>Viburnum</i>	ITS	GTR + G
	matK	GTR + I
	rbcl	GTR + I
	rpl32-trnL	GTR + G
	trnH-psbA	HKY + G
	trnK	GTR + G

AIC, Akaike's information criterion; G, gamma distribution; GTR, general time reversible; HKY, Hasegawa-Kishino-Yano; I, proportion of invariable sites; ITS, internal transcribed spacer; matK, maturase K gene; psbA, photosystem Q(B) protein gene; rbcl, ribulose-biphosphate carboxylase gene; rpl16, ribosomal protein L16 gene; rpl32, ribosomal protein L32 gene; rpS16, ribosomal protein S16 gene; trnH, tRNA-His gene; trnK, chloroplast trnK gene; trnL, tRNA-Leu gene.

Table S6. Number of species included in the phylogenetic analyses for each clade, along with estimates for total numbers of species

Plant group	Phylogeny (EFN ⁺ /EFN ⁻)	Total (EFN ⁺ /EFN ⁻)
<i>Byttneria</i>	35 (27/8)	204 (141/63)
<i>Pleopeltis</i>	125 (35/90)	173 (75/98)
Polygoneae	104 (49/55)	160 (89/71)
<i>Senna</i>	94 (85/9)	400 (362/38)
<i>Turnera</i>	35 (30/5)	137 (129/8)
<i>Viburnum</i>	117 (71/41)	165 (103/62)

Numbers of species with/without EFNs are included parenthetically.