

Sun et al.—American Journal of Botany 2019 – Appendix S2

Appendix S2a. Summary table for BAMM analyses (also see Appendix S1.2).

Order	9k-tip tree				20k-tip tree				100k-tip tree			
	ES_N_shift	ES_logLik	tree-wide rate	tip rate	ES_N_shift	ES_logLik	tree-wide rate	tip rate	ES_N_shift	ES_logLik	tree-wide rate	tip rate
Brassicales	661.10	534.45	0.7003	0.5881	1359.32	2430.96	0.3953	0.7258	4579.84	20.46	0.4221	0.0893
Celastrales	2737.53	1967.85	0.6262	0.7583	588.06	490.94	0.2910	0.6069	13493.91	227.97	0.3116	0.1369
Crossosomatales	371.53	313.11	0.1722	0.2329	781.13	494.86	0.1771	0.2153	3550.46	2256.42	0.0575	0.1481
Cucurbitales	2507.29	2146.06	0.3319	0.5083	600.01	230.90	0.1576	0.4176	3859.70	204.98	0.3308	0.0680
Fabales	217.63	321.51	0.7193	1.0854	851.79	399.77	0.4219	1.0855	22.90	5.74	0.9133	0.0619
Fagales	37614.85	946.02	2.4111	2.4074	469.09	266.18	1.6606	1.4678	407.51	1892.23	0.3297	0.1291
Geraniales	278.96	203.93	0.4018	0.6493	395.97	241.41	0.5363	0.6265	1484.07	429.74	0.3165	0.1272
Huertales	901.00	901.00	0.0668	0.0514	782.36	995.11	0.0759	0.0497	8418.80	9001.00	0.0451	0.3934
Malpighiales	214.93	347.15	0.5830	0.7354	784.08	2226.57	0.4140	0.7197	139.44	4.75	0.3832	0.0789
Malvales	298.29	349.14	0.7598	1.2517	2946.91	815.99	0.4837	1.2493	10250.54	4915.10	0.3104	0.1140
Myrtales	891.38	599.38	1.0880	1.3626	2015.80	1439.91	1.0803	1.6819	4.84	2.77	0.2143	0.0433
Oxalidales	257011.88	2615.28	0.8868	0.9800	552.70	595.89	0.8116	0.8827	523.91	1024.82	0.3593	0.1454
Picramniales	782.52	901.00	0.2804	0.2911	520.72	251.23	0.2743	0.2846	90224.85	1843.17	0.3092	0.0569
Rosales	400.78	343.11	2.4848	3.2572	901.00	901.00	1.6255	2.4513	376.55	8.51	0.4346	0.0614
Sapindales	685.37	732.94	0.4323	0.6527	560.40	815.48	0.1500	0.4871	7874.50	106.53	0.2942	0.0890
Vitales	901.00	217.16	1.1109	1.1640	272.24	378.22	0.7648	0.9796	7046.82	1646.90	1.1542	0.0561
Zygophyllales	901.00	652.91	0.2535	0.2831	901.00	770.95	0.2026	0.2164	389.49	229.85	0.4687	0.1325
global tree (mean value)	/	/	0.7829	1.1527	/	/	0.5601	1.0731	/	/	0.3914	0.1136

Notes:

“ES_N_shift” and “ES_logLik” mean the number of shifts (ES_N_shift) and the log-Likelihood (ES_logLik); two values used to assess post-burn-in effective sample sizes (>200) and convergence among chains (BAMM manual).

Tree-wide rate is the speciation rate across all tree timeframes including the present, obtained from the rate-through-time matrix; unit

is Myr^{-1} .

Tip rate estimated from the “*getTipRates*” function in BAMMtools; unit is Myr^{-1} .

BAMM analyses for the 100k-tip tree, for which 6 orders (Brassicales, Fabales, Malpighiales, Myrtales, Rosales, and Sapindales) could not reach suitable effective sample sizes despite runs in some cases exceeding 400 million generations.

Appendix S2b. Best models and speciation rates estimated for 9k-, 20k, and 100k-tip trees and each of 17 rosid orders from these trees using RPANDA with nine birth-death models (cf. Appendix S1.1).

Order	9k-tip tree			20k-tip tree			100k-tip tree					
	Model	λ	AICc	AW	Model	λ	AICc	AW	Model	λ	AICc	AW
Brassicales	bvar.dest	0.7079172	3688.8008	0.21165	bvar.dvar	0.9421	10307.214	0.80624	bvar.l.d0	0.0470732	43736.32198	0.73157
Celastrales	bvar.dest	0.8434964	1355.5334	0.27767	bvar.dest	0.7436	1808.7929	0.28739	bvar.l.d0	0.0521688	11284.71122	0.7319
Crossosomatales	bcst.dest	0.3074763	185.80348	0.4336	bcst.dest	0.2968	186.51977	0.42584	bvar.l.d0	0.1289888	532.7036932	0.35819
Cucurbitales	bvar.dvar	0.623294	2945.1235	0.99423	bvar.dvar	0.5014	5275.453	0.8382	bvar.l.dest	0.0295644	23178.99171	1
Fabales	bcst.dest	1.3051584	14884.703	0.37936	bcst.dest	1.2903	31594.913	0.46384	bvar.d0	0.0414453	200995.2753	0.41474
Fagales	bcst.dest	2.5222767	1581.8546	0.44699	bcst.dest	2.026	2539.5318	0.47781	bvar.l.d0	0.0474186	15247.38435	0.73163
Geraniales	bcst.dest	1.1756385	853.5773	0.42802	bvar.dvar	0.8114	1725.0176	0.4725	bvar.l.d0	0.0965253	7219.136959	1
Huerteales	bcst.d0	0.0340313	53.341706	0.66871	bcst.d0	0.0364	52.481626	0.58234	bcst.dvar.l	0.2649092	174.6549247	0.50422
Malpighiales	bvar.dvar	0.9434892	13935.882	0.28884	bvar.dest	0.9758	24684.048	0.21372	bvar.l.d0	0.0182802	157435.2067	0.73093
Malvales	bvar.dest	1.4992228	5011.1028	0.28675	bvar.dest	1.3722	7881.9606	0.32356	bvar.l.d0	-0.001315	49127.59102	0.73125
Myrtales	bcst.dest	2.3182921	4809.0756	0.24044	bvar.dest	2.4124	8268.0079	0.29772	bvar.l.dest	-0.006568	116233.782	1
Oxalidales	bcst.dvar.l	1.4855975	753.60331	0.53209	bcst.dvar.l	1.0214	1388.6102	0.37694	bvar.l.d0	0.0497701	16649.34027	0.73159
Picramniales	bcst.d0	0.0771328	33.297635	0.72901	bcst.d0	0.0765	33.33898	0.73159	bvar.l.dest	0.0372405	370.5424775	0.99659
Rosales	bvar.dvar	4.6098893	4950.3889	0.95931	bcst.dest	3.056	9485.4273	0.44212	bvar.dvar	0.0258025	116962.3346	1
Sapindales	bvar.dvar	0.6382086	5733.1687	0.5147	bvar.dvar	0.5313	8847.7864	0.92422	bvar.l.d0	0.0269303	41719.72204	0.73135
Zygophyllales	bcst.dest	0.4179997	385.42321	0.4215	bcst.dest	0.2635	582.47463	0.40309	bvar.l.d0	0.0257752	2800.561744	0.72948
Vitales	bvar.dvar	11.214279	335.58215	0.99296	bcst.dest	1.5141	832.30451	0.27539	bvar.dvar	0.0188394	9630.261453	0.83137
global tree	bvar.dvar	1.3904588	62217.036	0.38514	bvar.dvar	1.3058	116622.39	0.50235	bvar.l.d0	0.0445547	857591.7899	0.73367

Notes: Model: see Appendix S1.1 for further information.

AICc: the corrected Akaike Information Criterion (AICc) for the fitted model.

AW is Akaike weight (Wagenmakers and Farrell, 2004).

Lambda is the speciation rate (λ) parameter estimated by the fitted birth-death model at the present, see *f.lamb* function in Morlon et al.

(2014); unit is Myr⁻¹.

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Appendix S2c. Summary table for the DR statistic.

Mean DR tip rates were averaged across the 17 orders and the whole of 9k-, 20k-, and 100k-tip rosoid trees, respectively; unit is Myr⁻¹.

Order	9k-tip tree	20k-tip tree	100-k tip tree
Brassicales	0.1216	0.5058	0.1125
Celastrales	0.1854	0.2210	0.0903
Crossosomatales	0.0840	0.0764	0.1005
Cucurbitales	0.2159	0.3055	0.0888
Fabales	0.1778	0.5975	0.1080
Fagales	0.3241	0.5777	0.0808
Geraniales	0.1538	0.3214	0.0915
Huerteales	0.0216	0.0222	0.1133
Malpighiales	0.1284	0.3435	0.0931
Malvales	0.2466	0.4294	0.1129
Myrtales	0.1656	0.4217	0.0727
Oxalidales	0.0894	0.1854	0.1011
Picramniales	0.0303	0.0312	0.0238
Rosales	0.3459	0.6392	0.0599
Sapindales	0.1910	0.2554	0.0804
Vitales	0.1126	0.5672	0.0450
Zygophyllales	0.0555	0.0697	0.0673
global tree (mean value)	0.1889	0.4644	0.0902

Appendix S2d. Summary table for diversification simulations in the Cucurbitaceae test case.

Treatment	Tip no.	RPANDA				Mean DR	BAMM		
		model	λ	AICc	AW		mean tree-wide rate	mean tip rate	
Cucurbitaceae_20k_family	528	bcst.dcst	0.4635	2868.24	0.24	0.3794	0.2408	0.4625	
Cucurbitaceae_20k_genus	123	bvar.d0	0.2687	751.081	0.33	0.1052	0.2571	0.2543	
random drop	Cucurbitaceae_20k_10%	475	bvar.dcst	0.4688	2595.68	1.00	0.3599	0.2466	0.4658
	Cucurbitaceae_20k_30%	370	bcst.dcst	0.5471	2076.03	1.00	0.3282	0.2516	0.4951
	Cucurbitaceae_20k_50%	264	bcst.dcst	0.6283	1539.34	0.93	0.2731	0.2491	0.5010
	Cucurbitaceae_20k_75%	132	bcst.dcst	0.7264	822.306	0.51	0.1910	0.5261	0.6508
backbone addition	Cucurbitaceae_20k_10%	528	bcst.dcst	0.3800	3016	1.00	0.3373	0.3871	0.4054
	Cucurbitaceae_20k_30%	528	bvar.dvar	0.1729	3297	0.96	0.2647	0.8536	0.3662
	Cucurbitaceae_20k_50%	528	bvar.dvar	0.1571	3382	1.00	0.2013	0.9608	0.3661
	Cucurbitaceae_20k_75%	528	bvar.dvar	0.0966	3276	1.00	0.1397	0.9545	0.3412

Appendix S2e. Tukey HSD test across the RPANDA, BAMM, and DR methods for the Cucurbitaceae test case under the random taxon-dropping scenario. p.adj means adjusted *p*-value. Values in boldface are significant.

RPANDA

treatment	diff	lwr	upr	p.adj
Cucurbitaceae 20k 30%—10%	0.0754	-0.0407	0.1916	0.31398
Cucurbitaceae 20k 50%—10%	0.1288	0.0127	0.2450	0.02482
Cucurbitaceae 20k 75%—10%	0.3644	0.2483	0.4806	2.70e-09
Cucurbitaceae 20k 50%—30%	0.0534	-0.0627	0.1695	0.60715
Cucurbitaceae 20k 75%—30%	0.2890	0.1728	0.4051	4.77e-07
Cucurbitaceae 20k 75%—50%	0.2356	0.1194	0.3517	2.10e-05

BAMM tip rate

treatment	diff	lwr	upr	p.adj
Cucurbitaceae 20k 30%—10%	0.0292	0.0029	0.0556	0.022429
Cucurbitaceae 20k 50%—10%	0.0352	0.0060	0.0643	0.010474
Cucurbitaceae 20k 75%—10%	0.1850	0.1476	0.2223	0
Cucurbitaceae 20k 50%—30%	0.0059	-0.0247	0.0365	0.959804
Cucurbitaceae 20k 75%—30%	0.1557	0.1172	0.1942	0
Cucurbitaceae 20k 75%—50%	0.1498	0.1093	0.1903	0

BAMM tree-wide rate

treatment	diff	lwr	upr	p.adj
Cucurbitaceae 20k 30%—10%	0.0050	-0.1111	0.1210	0.999446314
Cucurbitaceae 20k 50%—10%	0.0024	-0.1136	0.1185	0.999933504
Cucurbitaceae 20k 75%—10%	0.2794	0.1634	0.3955	9.22e-07
Cucurbitaceae 20k 50%—30%	-0.0025	-0.1186	0.1136	0.999927428
Cucurbitaceae 20k 75%—30%	0.2745	0.1584	0.3906	1.31e-06
Cucurbitaceae 20k 75%—50%	0.2770	0.1609	0.3931	1.10e-06

DR

treatment	diff	lwr	upr	p.adj
Cucurbitaceae 20k 30%—10%	-0.0317	-0.0497	-0.0137	0.00019
Cucurbitaceae 20k 50%—10%	-0.0868	-0.1048	-0.0688	0
Cucurbitaceae 20k 75%—10%	-0.1689	-0.1869	-0.1509	0.00e+00
Cucurbitaceae 20k 50%—30%	-0.0551	-0.0731	-0.0371	4.75e-09

Cucurbitaceae 20k 75%—30%	-0.1372	-0.1552	-0.1192	0.00e+00
Cucurbitaceae 20k 75%—50%	-0.0821	-0.1001	-0.0641	0.00e+00

Appendix S2f. Tukey HSD test across the RPANDA, BAMM, and DR methods for the Cucurbitaceae test case under the backbone-addition scenario.

p.adj means adjusted *p*-value. Values in boldface are significant.

RPANDA

treatment	diff	lwr	upr	p.adj
Cucurbitaceae 20k 30%—10%	-0.1220	-0.2089	-0.0352	0.00303004
Cucurbitaceae 20k 50%—10%	-0.1993	-0.2862	-0.1124	2.34e-06
Cucurbitaceae 20k 75%—10%	-0.1951	-0.2819	-0.1082	3.49e-06
Cucurbitaceae 20k 50%—30%	-0.0773	-0.1641	0.0096	0.09615573
Cucurbitaceae 20k 75%—30%	-0.0730	-0.1599	0.0138	0.12562993
Cucurbitaceae 20k 75%—50%	0.0042	-0.0826	0.0911	0.99918405

BAMM tip rate

treatment	diff	lwr	upr	p.adj
Cucurbitaceae 20k 30%—10%	-0.0392	-0.0595	-0.0190	3.56e-06
Cucurbitaceae 20k 50%—10%	-0.0393	-0.0595	-0.0191	3.47e-06
Cucurbitaceae 20k 75%—10%	-0.0642	-0.0844	-0.0440	0
Cucurbitaceae 20k 50%—30%	0.0000	-0.0203	0.0202	0.999999951
Cucurbitaceae 20k 75%—30%	-0.0249	-0.0452	-0.0047	0.008276584
Cucurbitaceae 20k 75%—50%	-0.0249	-0.0451	-0.0047	0.00841872

BAMM tree-wide rate

treatment	diff	lwr	upr	p.adj
Cucurbitaceae 20k 30%—10%	0.4664	0.3552	0.5777	1.06E-12
Cucurbitaceae 20k 50%—10%	0.5737	0.4625	0.6849	0
Cucurbitaceae 20k 75%—10%	0.5674	0.4562	0.6786	0
Cucurbitaceae 20k 50%—30%	0.1073	-0.0040	0.2185	0.062090622
Cucurbitaceae 20k 75%—30%	0.1010	-0.0103	0.2122	0.086624821
Cucurbitaceae 20k 75%—50%	-0.0063	-0.1175	0.1049	0.998705281

DR

treatment	diff	lwr	upr	p.adj
Cucurbitaceae 20k 30%—10%	-0.0725	-0.0904	-0.0546	3.11e-12
Cucurbitaceae 20k 50%—10%	-0.1359	-0.1538	-0.1180	0
Cucurbitaceae 20k 75%—10%	-0.1976	-0.2155	-0.1797	0
Cucurbitaceae 20k 50%—30%	-0.0634	-0.0813	-0.0455	1.26e-10

Cucurbitaceae 20k 75%—30%	-0.1251	-0.1429	-0.1072	0
Cucurbitaceae 20k 75%—50%	-0.0617	-0.0795	-0.0438	2.57e-10

Appendix S2g. Summary table for diversification analyses in Cucurbitaceae test case under the representative sampling scenario.

genus tree	RPANDA				BAMM				DR
	Model	lamda	AICc	AW	global sampling		species-specific sampling		mean DR rate
					mean tree-wide	mean tip rate	mean tree-wide	mean tip rate	
Cucurbitaceae 20k genus 1	bvar.d0	0.2970	394.14	0.3164	0.2559	0.2469	0.1780	0.1275	0.0883
Cucurbitaceae 20k genus 2	bvar.d0	0.3072	390.65	0.3188	0.2554	0.2391	0.1774	0.1251	0.0868
Cucurbitaceae 20k genus 3	bvar.d0	0.3061	393.06	0.3193	0.2509	0.2401	0.1730	0.1266	0.0858
Cucurbitaceae 20k genus 4	bvar.d0	0.2998	390.48	0.2950	0.2565	0.2494	0.1785	0.1305	0.0877
Cucurbitaceae 20k genus 5	bvar.d0	0.3044	395.77	0.3145	0.2557	0.2408	0.1781	0.1274	0.0898
Cucurbitaceae 20k genus 6	bvar.d0	0.3055	394.62	0.3367	0.2511	0.2487	0.1746	0.1307	0.0885
Cucurbitaceae 20k genus 7	bvar.d0	0.2998	394.99	0.3244	0.2559	0.2445	0.1783	0.1305	0.0891
Cucurbitaceae 20k genus 8	bvar.d0	0.2968	394.31	0.3151	0.2490	0.2373	0.1751	0.1262	0.0861
Cucurbitaceae 20k genus 9	bvar.d0	0.3020	394.34	0.3263	0.2593	0.2545	0.1766	0.1272	0.0875
Cucurbitaceae 20k genus 10	bvar.d0	0.3030	388.85	0.2934	0.2492	0.2354	0.1746	0.1231	0.0858
mean rates	/	0.3022	/	/	0.2539	0.2437	0.1764	0.1275	0.0875
Cucurbitaceae family tree	best.dcst	0.4635	2868.24	0.2406	0.2408	0.4625	/	/	0.3794