Appendix S3. Justification for comparing speciation rates under different models across different methods.

This Appendix is in three parts. First (Appendix S3a), we report model-weighted averages of speciation rate across RPANDA models. In some cases, model choice was not decisive, so the purpose of this reanalyzed table is to verify that our reported results are not sensitive to choosing among nearly equal-fit models. The results are very similar to best-model values (cf. Appendix S1a). In many cases, Akaike weights are near 1, indicating decisive model choice. In other cases (e.g., Fabales across all three trees), Akaike weights were less conclusive, but the speciation parameter reported is very similar across models.

The last two parts of this Appendix report analyses restricted to pure-birth models, in contrast to the birth-death RPANDA and BAMM models presented in the main text. We present these as sensitivity analyses, as we only consider speciation rates for our exploration of diversification model performance (cf. Methods for justification of this). While not considering extinction in fully parametric diversification models is an atypical approach for most practitioners, it has the advantage of providing a means to examine models more directly compatible with each other. For instance, a pure-birth BAMM model can be compared to RPANDA analyses where a pure-birth models has the best fit, in order to assure more comparable results. For RPANDA, we reduced the pool of already calculated RPANDA models to only pure-birth models, reporting optimal models and recalculating Akaike weights accordingly (Appendix S3b). For

BAMM, we used the 20k-tip tree to rerun BAMM analyses constrained to a pure-birth model following developer instructions (setting the initial extinction value to 0 and disabling MCMC updates on this parameter (Appendix S3c, S3d). Generally, these sensitivity analyses demonstrate similar patterns to birth-death models for tip speciation rates (Appendix S3c). As with other analyses, tip rates proved more robust than other types of rates to different model specifications, providing additional justification for our focus on this metric (cf. Discussion). However, tree-wide rates were quite different in scaling. Rate-through-time plots (Appendix S3d) show that this is driven primarily by differences in overall scaling of speciation rate at early time intervals, while values at present ($t = 0$) are more similar.

Appendix S3a. Model-weighted mean speciation rates estimated for 9k-, 20k, and 100k-tip trees and each of 17 rosid orders using RPANDA with nine birth-death models (cf. Appendix S1a). We calculated a model-weighted mean speciation rate (speciation rate (λ) × Akaike weight summed across models).

Clade	9k-tip tree	20k-tip tree	100k-tip tree
Brassicales	0.7144	0.9271	0.0471
Celastrales	0.8369	0.7453	0.0522
Crossosomatales	0.3005	0.2991	0.1323
Cucurbitales	0.6240	0.5069	0.0296
Fabales	1.2963	1.2913	0.0414
Fagales	2.5766	2.0042	0.0474
Geraniales	1.1517	0.8535	0.0965
Huerteales	0.0348	0.0388	0.3174
Malpighiales	0.9611	0.9769	0.0183
Malvales	1.4992	1.3757	0.0013
Myrtales	2.2453	2.4115	0.0066
Oxalidales	1.5338	1.0266	0.0498
Picramniales	0.1594	0.1655	0.0372
Rosales	4.5903	3.0646	0.0258
Sapindales	0.6592	0.5344	0.0270
Vitales	11.1638	1.6484	0.0191
Zygophyllales	0.3754	0.2624	0.0259
global tree	1.3990	1.3095	0.0446

Appendix S3b. Summary table of speciation rates estimated from RPNADA under three pure-birth models (cf. Methods in Appendix S1a).

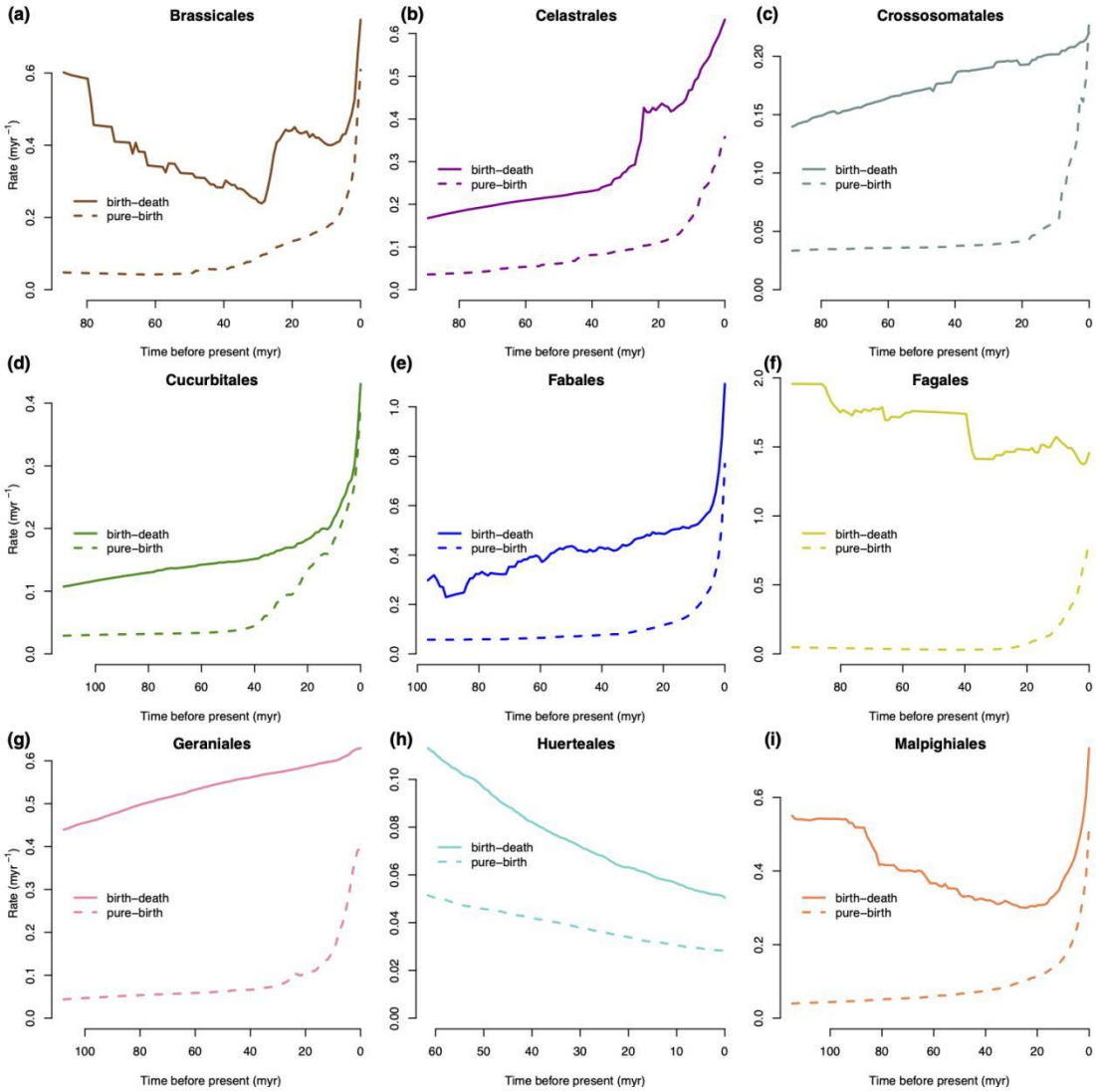
Clade	Model	9k-tip tree		20k-tip tree		100k-tip tree	
		lamda	AICc	lamda	AICc	lamda	AICc
Brassicales	bcstd0	0.1564	3970.2764	0.2409	11291.7494	0.0729	44195.0818
	bvar.d0	0.2653	3759.3472	0.4068	10619.5449	0.0556	43819.7640
	bvar.l.d0	0.2205	3787.5712	0.3077	10826.6908	0.0471	43736.3220
Celastrales	bcstd0	0.1952	1520.0735	0.1936	1994.3127	0.0695	11339.9374
	bvar.d0	0.3665	1372.7525	0.3552	1833.1353	0.0601	11305.8838
	bvar.l.d0	0.2645	1408.8337	0.2605	1879.9468	0.0522	11284.7112
Crossosomatales	bcstd0	0.0602	201.8774	0.0597	201.5109	0.0960	550.3687
	bvar.d0	0.1409	189.8818	0.1389	190.7729	0.1419	533.4104
	bvar.l.d0	0.1049	191.5032	0.0914	194.6991	0.1290	532.7037
Cucurbitales	bcstd0	0.2066	3248.1228	0.2111	5598.7111	0.0643	24950.9114
	bvar.d0	0.3547	2965.8946	0.3262	5306.3942	0.0323	24198.3544
	bvar.l.d0	0.2637	3045.4506	0.2579	5389.7681	0.0313	24373.8209
Fabales	bcstd0	0.1766	17082.6974	0.2512	36411.2554	0.0428	201015.8026
	bvar.d0	0.3511	15559.4793	0.4771	33185.9076	0.0414	200995.2753
	bvar.l.d0	0.2710	15833.4321	0.3549	34136.7378	0.0414	200996.0848
Fagales	bcstd0	0.2152	2175.1509	0.3133	3348.9589	0.0682	15339.8582
	bvar.d0	0.5895	1731.1818	0.7304	2647.4577	0.0590	15290.6216
	bvar.l.d0	0.3434	1877.0250	0.4537	2903.7101	0.0474	15247.3844
Geraniales	bcstd0	0.1269	1024.4885	0.2149	2002.0945	0.0666	7644.1400
	bvar.d0	0.3037	897.5662	0.4418	1750.0863	0.0526	7586.1561
	bvar.l.d0	0.1948	938.5702	0.2831	1857.2251	0.0965	7219.1370
Huerteales	bcstd0	0.0340	53.3417	0.0364	52.4816	0.0588	201.4799
	bvar.d0	0.0236	57.2549	0.0193	55.9275	0.1375	191.6220
	bvar.l.d0	0.0406	56.4587	0.0488	54.3704	0.0983	189.0625
Malpighiales	bcst.d0	0.1469	15767.0844	0.1913	27825.9404	0.0634	162063.7479
	bvar.d0	0.2886	14403.6833	0.3598	25624.2147	0.0460	159722.4805
	bvar.l.d0	0.2149	14709.3851	0.2678	26345.6577	0.0183	157435.2067
Malvales	bcst.d0	0.2273	5794.3818	0.2483	9076.1751	0.0949	52668.8427
	bvar.d0	0.4367	5238.2738	0.4667	8264.4406	0.0644	51217.2303
	bvar.l.d0	0.2938	5435.2560	0.3249	8589.0617	0.0013	49127.5910

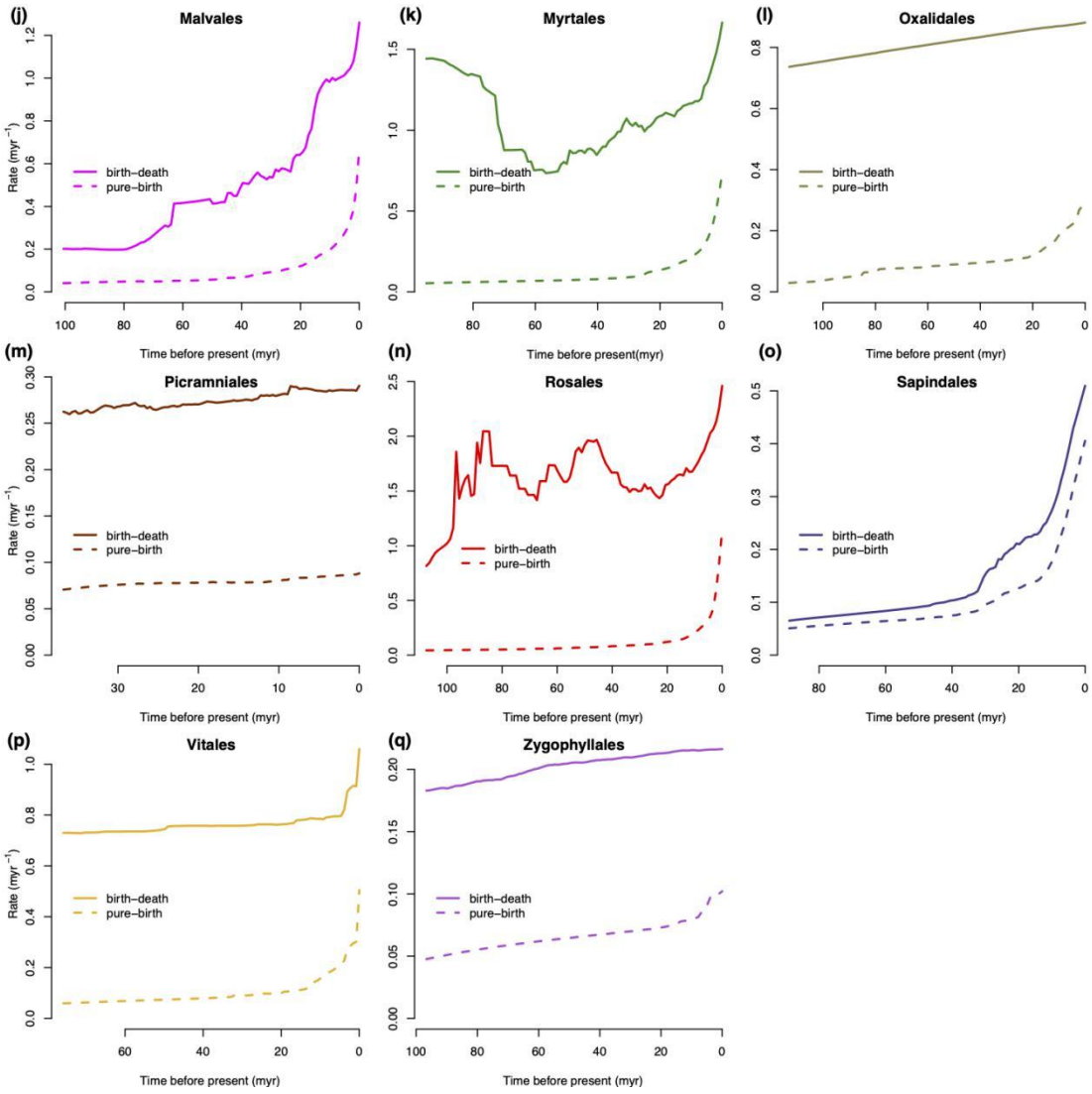
	bcst.d0	0.2080	5717.0573	0.2730	10113.4779	0.0505	125889.5715
Myrtales	bvar.d0	0.4400	5077.4518	0.5839	8834.0057	0.0233	119260.9675
	bvar.l.d0	0.3258	5238.8693	0.3815	9307.2210	0.0030	116364.9189
	bcst.d0	0.1523	904.2727	0.1631	1590.7540	0.0661	16740.3727
Oxalidales	bvar.d0	0.3555	775.1138	0.3308	1422.6776	0.0551	16670.1458
	bvar.l.d0	0.2326	813.4359	0.2334	1472.4350	0.0498	16649.3403
	bcst.d0	0.0771	33.2976	0.0765	33.3390	0.0246	453.6749
Picramniales	bvar.d0	0.2254	37.7802	0.2225	37.9161	0.0040	393.1063
	bvar.l.d0	0.1533	37.9626	0.1501	38.2132	0.0206	381.9055
	bcst.d0	0.1860	6691.5289	0.2867	12609.0191	0.0274	125274.7839
Rosales	bvar.d0	0.5034	5742.5722	0.7019	10588.9277	0.0201	124562.9518
	bvar.l.d0	0.3037	6100.8188	0.4094	11492.3028	0.0505	123451.0228
	bcst.d0	0.1998	6175.3200	0.2075	9430.4204	0.0618	42588.6735
Sapindales	bvar.d0	0.3373	5790.9788	0.3362	8909.3196	0.0433	41993.2414
	bvar.l.d0	0.2776	5848.4990	0.2829	9017.1770	0.0269	41719.7220
	bcst.d0	0.1425	445.4461	0.0756	608.9782	0.0334	11141.7598
Vitales	bvar.d0	0.3633	395.9158	0.1300	589.7110	0.0049	10011.3497
	bvar.l.d0	0.2211	410.6484	0.1001	595.9946	0.0498	10250.6331
	bcst.d0	0.0811	415.5112	0.1503	985.5402	0.0559	2853.6877
Zygophyllales	bvar.d0	0.1611	391.7703	0.3397	892.6860	0.0366	2810.7790
	bvar.l.d0	0.1335	388.3089	0.2199	928.0631	0.0258	2800.5617
	bcst.d0	0.1762	72491.7990	0.2308	135337.7719	0.0491	858296.7190
Whole tree	bvar.d0	0.3580	65352.1952	0.4460	122542.2358	0.0456	857711.7141
	bvar.l.d0	0.2517	67402.6815	0.3140	127081.6083	0.0446	857591.7899

Appendix S3c. Rate comparison for 20k-tip tree under birth-death model and pure-birth model in BAMM analysis. The procedures are the same as it described in Appendix S1a, except using pure-birth model (setting "updateRateMu0 = 0" and "muInit0 = 0.0"; see BAMM project website: http://bamm-project.org/advanced.html#modeling-less-complex-evolutionary-scenarios).

Order	Birth-death model		Pure-birth model	
	tree-wide rate	tip rate	tree-wide rate	tip rate
Brassicales	0.3953	0.7258	0.0973	0.5903
Celastrales	0.2910	0.6069	0.0935	0.3429
Crossosomatales	0.1771	0.2153	0.0484	0.2244
Cucurbitales	0.1576	0.4176	0.0733	0.3909
Fabales	0.4219	1.0855	0.1060	0.7670
Fagales	1.6606	1.4678	0.0908	0.8060
Geraniales	0.5363	0.6265	0.0880	0.3882
Huerteales	0.0759	0.0497	0.0385	0.0268
Malpighiales	0.4140	0.7197	0.0872	0.5068
Malvales	0.4837	1.2493	0.0987	0.6544
Myrtales	1.0803	1.6819	0.1179	0.7076
Oxalidales	0.8116	0.8827	0.0949	0.3003
Picramniales	0.2743	0.2846	0.0789	0.0813
Rosales	1.6255	2.4513	0.1128	1.1257
Sapindales	0.1500	0.4871	0.1052	0.3892
Vitales	0.7648	0.9796	0.1045	0.4914
Zygophyllales	0.2026	0.2164	0.0663	0.0926
global tree (mean value)	0.5601	1.0731	0.0884	0.4639

Appendix S3d. Comparison of rate-through-time plots for each of the 17 rosid orders from 20k-tip tree under birth-death model (solid line) and pure-birth model (dashed line), respectively.




(j)
Malvales
(k)
Myrtales
(l)
Oxalidales
(m)
Picramniales
(n)
Rosales
(o)
Sapindales
(p)
Vitales
(q)
Zygophyllales
Rate (myr⁻¹)
birth–death
pure–birth
Time before present (myr)
Time before present(myr)