

4. Results with different relaxed clock models and node-age priors

Dataset (no. taxa)	#Genes	Length (bp)	Grouping	<i>LogN/Yule</i>		<i>Exp/Yule</i>		<i>Exp/Birth-death</i>		<i>LogN/Birth-death</i>		<i>No fossils</i>	
				Trees	<i>p</i>	trees	<i>p</i>	trees	<i>p</i>	trees	<i>p</i>	trees	<i>p</i>
1. (113 <i>sp</i>)	full	4732	Palaeoptera	14907	0.99	14779	0.99	14817	0.99	14885	0.99	14820	0.99
			Chiastomyaria	93	0.01	221	0.01	183	0.01	115	0.01	180	0.01
			Metapterygota	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
	composition bias corrected	4372	Palaeoptera	14375	0.96	14187	0.95	14176	0.95	14328	0.96	13107	0.87
			Chiastomyaria	605	0.04	797	0.05	809	0.05	648	0.04	1878	0.13
			Metapterygota	20	>0.01	16	>0.01	15	>0.01	24	>0.01	15	>0.01
	nuclear only; composition bias corrected	3935	Palaeoptera	14629	0.98	14624	0.98	14651	0.98	14660	0.98	14134	0.94
			Chiastomyaria	348	0.02	350	0.02	328	0.02	319	0.02	857	0.06
			Metapterygota	23	>0.01	26	>0.01	21	>0.01	21	>0.01	9	>0.01
2. (38 <i>sp</i>)	full	6381	Palaeoptera	4595	0.31	3817	0.25	3922	0.26	4448	0.30	5176	0.35
			Chiastomyaria	4121	0.27	4549	0.31	4433	0.30	4177	0.28	3790	0.25
			Metapterygota	6284	0.42	6634	0.44	6645	0.44	6375	0.42	6034	0.40
	composition bias corrected	6145	Palaeoptera	3296	0.22	2531	0.17	2477	0.17	3236	0.22	2822	0.19
			Chiastomyaria	11411	0.76	12189	0.81	12240	0.82	11490	0.76	11975	0.80
			Metapterygota	293	0.02	280	0.02	283	0.02	274	0.02	203	0.01
	nuclear only; composition bias corrected	4890	Palaeoptera	4221	0.28	3576	0.24	3736	0.25	4210	0.30	1405	0.09
			Chiastomyaria	9330	0.62	10164	0.68	9971	0.66	9405	0.61	12464	0.83
			Metapterygota	1449	0.10	1260	0.08	1293	0.09	1385	0.09	1131	0.07

Note. Variable substitution rates were modelled with either an uncorrelated exponential distribution (Exp) or an uncorrelated lognormal distribution (LogN); Prior expectations on node ages were modelled with either a birth-death model of cladogenesis (Birth-death) or a Yule process (Yule). Full details of all models are found in Drummond *et al.*, (2006). The “no fossils” run uses the standard birth-death and lognormal models (as in Table 2), but excludes all fossil calibrations except that placed on the base of the Pterygota (necessary to impose an absolute temporal scale). Shown are the number of trees in the posterior sample, and the corresponding posterior *p*-value of each phylogenetic hypothesis (Fig. 1). All other details are as for Table 2.