

**Limitations of phylogenomic data can drive inferred speciation rate shifts**

***Supplementary Material***

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**Table S1.** Summary statistics from TESS and TreePar analyses of site-poor and site-rich timetrees of suboscine birds.

	Site-poor pruned	Site-rich pruned	Site-rich full
Species fraction ( $\rho$ )	0.60	0.60	1.00
<b>TESS (Bayesian)</b>			
Rate shifts of $2 \times \ln(\text{BF}) > 6$	0	1	1
Speciation rate hyperprior shape	normal	normal	normal
Speciation rate hyperprior mean	0.16	0.18	0.25
Speciation rate hyperprior SD	0.03	0.02	0.03
Extinction rate hyperprior shape	normal	lognormal	normal
Extinction rate hyperprior mean*	0.02	-6.17	0.07
Extinction rate hyperprior SD*	0.04	1.40	0.05
<b>Best TreePar (ML) Model</b>			
Number of rate shifts	1	1	1
Speciation rate ( $\lambda$ )	0.12	0.13	0.23
Extinction rate ( $\mu$ )	0.00	0.00	0.03
Diversification rate	0.12	0.13	0.19
Turnover rate ( $\epsilon$ )	0.00	0.00	0.15

**Note:** Species fractions ( $\rho$ ) are estimated based on the information provided in Jetz et al. (2012) and Harvey et al. (2020). Asterisks (\*) mark means and standard deviations (SD) generated from log-transformed distributions. BF: Bayes Factor (Jeffreys 1961; Kass and Raftery 1995; Lakens et al. 2020) at a threshold of  $2 \times \ln(\text{BF}) > 6$ , following the recommended settings in the TESS documentation (Höhna et al. 2016) Given that a Bayes factor of  $2 \times \ln(\text{BF}) > 3$  is generally a more stringent cutoff than a traditional p-value of 0.05, comparable to a p-value of 0.01, the confidence threshold we use here is more strict than that commonly used in conventional hypothesis testing (Jeon and De Boeck 2017). We defined unique rate shifts as a spike above  $2 \times \ln(\text{BF}) = 6$  preceded and typically followed by a return to baseline, not by a continued increase.

**References**

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