

Additional File 3. Posterior probabilities for the speciation models sampled by BPP, using the different algorithms and fine-tune parameters (ϵ , a and m). Priors were kept constant: $\theta \sim G(1.5, 300)$ and $\tau_0 \sim G(1.5, 30)$. Each speciation model is represented using 0-1 flags for the interior nodes, with 0 indicating a collapsed node and 1 a resolved node. Nodes are ordered as in Figure 1, with the first flag corresponding to node a , the second to node b , and so on up to node l . Each cell has the posterior probability for two replicate runs of BPP, which started with different speciation models. NS: model not sampled.

speciation model	algorithm 0		algorithm 1			
	$\epsilon = 5$	$\epsilon = 20$	$a = 0.5; m = 1$	$a = 0.5; m = 2$	$a = 2; m = 1$	$a = 2; m = 2$
111111111111	0.997; 0.996	1; 1	0.996; 0.991	0.998; 1	0.995; 0.999	0.994; 0.986
111101111111	2.7E-3; 3.7E-3	NS	4.1E-3; 8.7E-3	2.1E-3; NS	5.5E-3; 1.2E-3	6.2E-3; 0.014