**Supplemental Materials for** “**Detecting hidden diversification shifts in models of trait-dependent speciation and extinction”**

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Figure S1. The uncertainty surrounding estimates of net turnover rate (λ+μ), extinction fraction (μ/λ), and transition rates as a function of tree size. Each row represents a different simulation scenario, all of which are described in detail in Table 1 in the main text. For both turnover rates and extinction fractions the solid green line and green region represent the mean and 95% confidence interval for state 0, the solid blue line and blue region represents the mean and 95% confidence interval for state 1*A*, and the solid red line and red region represents the mean and 95% confidence interval for state 1*B*. In the panels depicting the log-transformed transition rates, the solid purple line and purple region, the solid light purple line and light purple region, represent mean and 95% confidence interval for transition to and from the “hidden” state (i.e., 1*B*), respectively.



Figure S2. Results from the simulations when transforming the estimates of turnover and extinction fraction depicted in Figure S1 to reflect estimates of speciation (λ) and extinction (μ) rates.



Figure S3. The uncertainty surrounding estimates of net diversification rate (λ-μ, obtained from backtransforming net turnover rates and extinction fraction; see main text), extinction fraction (μ/λ), and transition rates as a function of tree size, when the generating model does not contain a hidden state (i.e., a BiSSE model). The specifics of the different simulation scenarios are described in detail in Table 1 from the main text. For both net diversification rates and extinction fractions the solid green line represents and green region represent the mean and 95% confidence interval for state 0, and the solid blue line and blue region represents mean and 95% confidence interval for state 1. In the panels depicting the log-transformed transition rates, the solid black line and surrounding region, and the solid gray line and surrounding region, represent the mean and 95% confidence interval for transitions from state 0 to 1, and state 1 to 0, respectively.



Figure S4. The uncertainty surrounding estimates of net turnover rate (λ+μ) and extinction fraction (μ/λ) when the generating model assumes (a,b) diversification is independent of the observed characters (i.e., null-two model), or (c,d) a hidden state underlies both observed states (i.e., a general HiSSE model). The specifics of the different simulation scenarios are described in detail in Table 2 from the main text. In all panels, the color of dashed line corresponds to the true value under the generating model.

Table S1. Summary of BiSSE model fits only when the generating model is the “worst-case” scenario, which simulated a neutral binary character along trees generated from a complex heterogeneous rate branching process (see main text). As with Tables 1-3, the average Akaike weight (*wi*) for all models assessed the fit.

|  |  |
| --- | --- |
| Model | *wi* |
| BiSSE: τ0=τ1; ε0=ε1 | 0.091 |
| BiSSE: ε0=ε1 | 0.313 |
| BiSSE: Free | 0.596 |
|  |  |
|  |  |
| BiSSE: τ0=τ1; ε0=ε1 | 0.001 |
| BiSSE: ε0=ε1 | 0.005 |
| BiSSE: Free | 0.011 |
| Null-two | 0.983 |

Table S2. The sampling frequencies of clades contained within our phylogeny of the Dipsidae clade. The current diversity estimates were taken from the Angiosperm Phylogeny Website (APWeb; Stevens, 2012).

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| --- | --- | --- |
| Clade | Known diversity | Sampling freq. |
| *Quintinia* | 25 | 0.08 |
| *Paracryphia* | 1 | 1.00 |
| *Sphenostemon* | 10 | 0.10 |
| *Viburnum* | 175 | 0.49 |
| *Sambucus* | 20 | 0.70 |
| *Adoxa* | 1 | 1.00 |
| *Sinadoxa* | 1 | 1.00 |
| *Tetradoxa* | 1 | 1.00 |
| Diervilleae | 16 | 0.81 |
| *Lonicera* | 180 | 0.47 |
| Rest of Caprifolieae | 30 | 0.63 |
| *Heptacodium* | 1 | 1.00 |
| Linnaeeae | 32 | 0.44 |
| *Zabelia* | 5 | 1.00 |
| Morinaceae | 13 | 0.77 |
| *Triplostegia* | 2 | 1.00 |
| Dipsacaceae | 290 | 0.20 |
| Valerianaceae | 350 | 0.34 |

**Supplemental References**

Stevens, P. F. (2001 onwards). Angiosperm Phylogeny Website. Version 12, July 2012 [and more or less continuously updated since].