**Table S3** Tail probabilities of asymmetric values for the among-lineage diversification rate variation in the phylogenetic topologies reconstructed from total samples and Taiwanese samples, respectively, inferred from the species tree (BEAST).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | *IC* | *MΠ\** | *MΠ* | *MΣ\** | *MΣ* |
| Total sample |  |  |  |  |  |
| Min ERM | 136 | -1.516 | 1.84E-10 | 0.268 | 5.879 |
| Max ERM | 6 | 0 | 1 | 1 | 17 |
| Observed | 58 | -0.674 | 4.83E-04 | 0.604 | 12.321 |
| Tail Prob. | 0.030 | 0.044 | 0.035 | 0.033 | 0.026 |
| Taiwan *Scutellaria* |  |  |  |  |  |
| Min ERM | 15 | -0.640 | 0.044 | 0.573 | 3.9 |
| Max ERM | 2.000 | 0 | 1.000 | 1.000 | 6.000 |
| Observed | 9.000 | -0.332 | 0.222 | 0.742 | 4.833 |
| Tail Prob. | 0.333 | 0.378 | 0.333 | 0.222 | 0.333 |

*IC* is the Colless’s tree imbalance index; *MΠ* and *MΣ* are the nodal probability product and nodal probability sum of the tree, respectively; *MΠ*\* and *MΣ*\* are modified versions of *MΠ* and *MΣ* obtained through differential weighting of the individual equal-rate Markov nodal probabilities according to their species diversity. These indices display the diversification rate variation of the whole tree.