

**Additional file 1 for “Hostplant change and paleoclimatic events explain diversification shifts in skipper butterflies (Family: Hesperiidae).”**

**(Detailed legends are given along with respective figure or table)**

**Figure S1:** Comparison of ultrametric trees of contrasting topologies calibrated using one time unit as the crown age.

**Table S1:** Fitting of models of diversification to the lineage accumulation pattern in MCC tree.

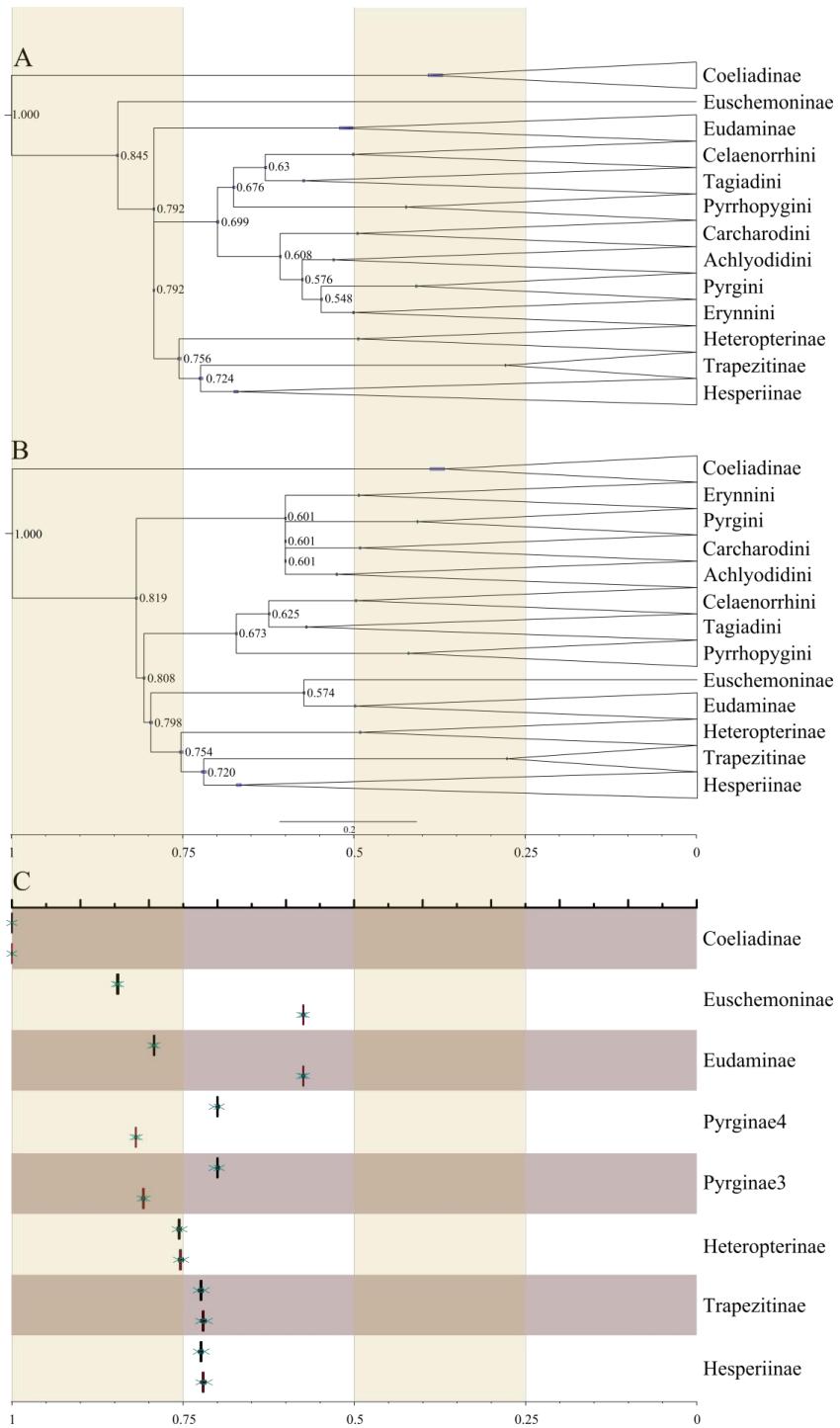
**Figure S2:** 95% credibility shift configurations with the configuration frequencies summarized with the posteriors from the BAMM analysis.

**Figure S3:** Posterior distributions of speciation and extinction rates of dicot- and monocot-feeding lineages from the BiSSE analysis.

**Figure S4:** Graphs showing the relative positions of AIC values from the BiSSE analysis of the MCC tree on the distribution of the AIC values from 100 random posterior trees from the dating analysis.

**Table S2:** Exploring the effect of hidden states on the diversification rate estimation.

**Appendix S1:** Data References



**Figure S1:** Comparison of ultrametric trees of contrasting topologies (A) and (B) calibrated using one time unit as the crown age of the skipper phylogeny. These two trees are random samples from the ultrametric trees derived from the calibration of 105 ML trees from the concatenated dataset from Sahoo et al. (2016) with gene-partitions. Node values represent the median age calculated from 48 and 57 time trees respectively for (A) and (B). The distribution of all node ages estimated from the contrasting topologies (black and red for A and B respectively; cross mark represents the average value) are in (C). N.B: Pyrginae4 is the clade containing four tribes of Pyrginae and Pyrginae3 is the clade containing 3 tribes.

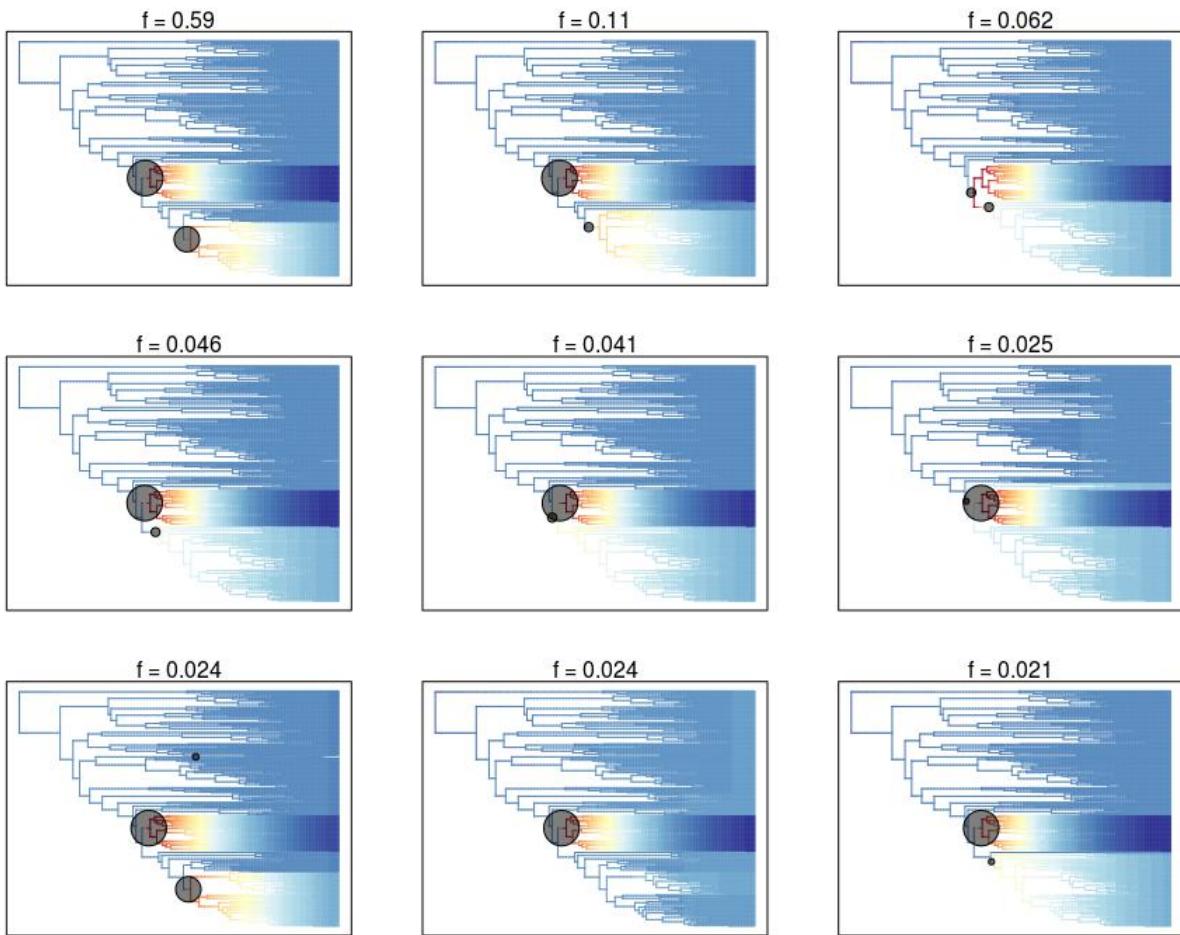
**Table S1:** Comparison of different models of diversification fitted to the diversification pattern in the MCC tree. Pure Birth is a pure birth or Yule model of diversification, Birth Death is a constant birth death model of diversification, SPVAR considers a variable speciation rate and constant extinction rate, EXVAR considers a variable extinction rate and constant speciation rate, yule2rate assumes an abrupt change in diversification rate. DDX and DDL fit exponential and logistic variants of the density-dependent speciation rate model respectively. AIC = Akaike information criteria; logLik = log-likelihood;  $\lambda$ ,  $\mu$  are speciation and extinction rates.

	Pure Birth	Birth Death	SPVAR	EXVAR	yule2rate	DDX	DDL
logLik	92.994	92.994	165.266	91.441	202	139.474	136.947
AIC	-183.987	-185.987	-324.531	-176.882	-398.01	-274.948	-269.894
$\lambda$	0.034	0.034	0.43	0.035	0.044	0.497	0.054
$\mu$	-	0	0.001	0.001	0.001	-	-

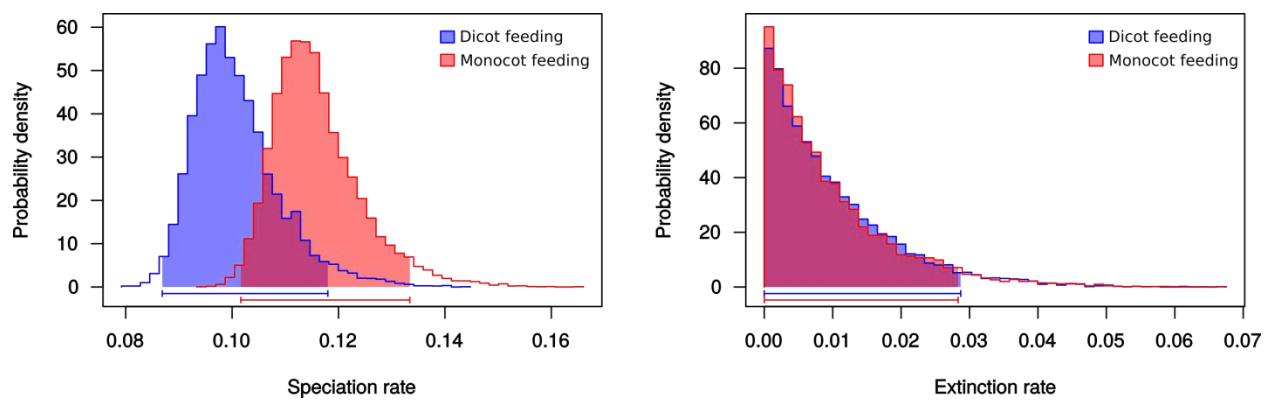
Best Constant Rate Model = pureBirth; AIC = -183.987

Best Rate Variable Model = yule2rate; AIC = -398.01

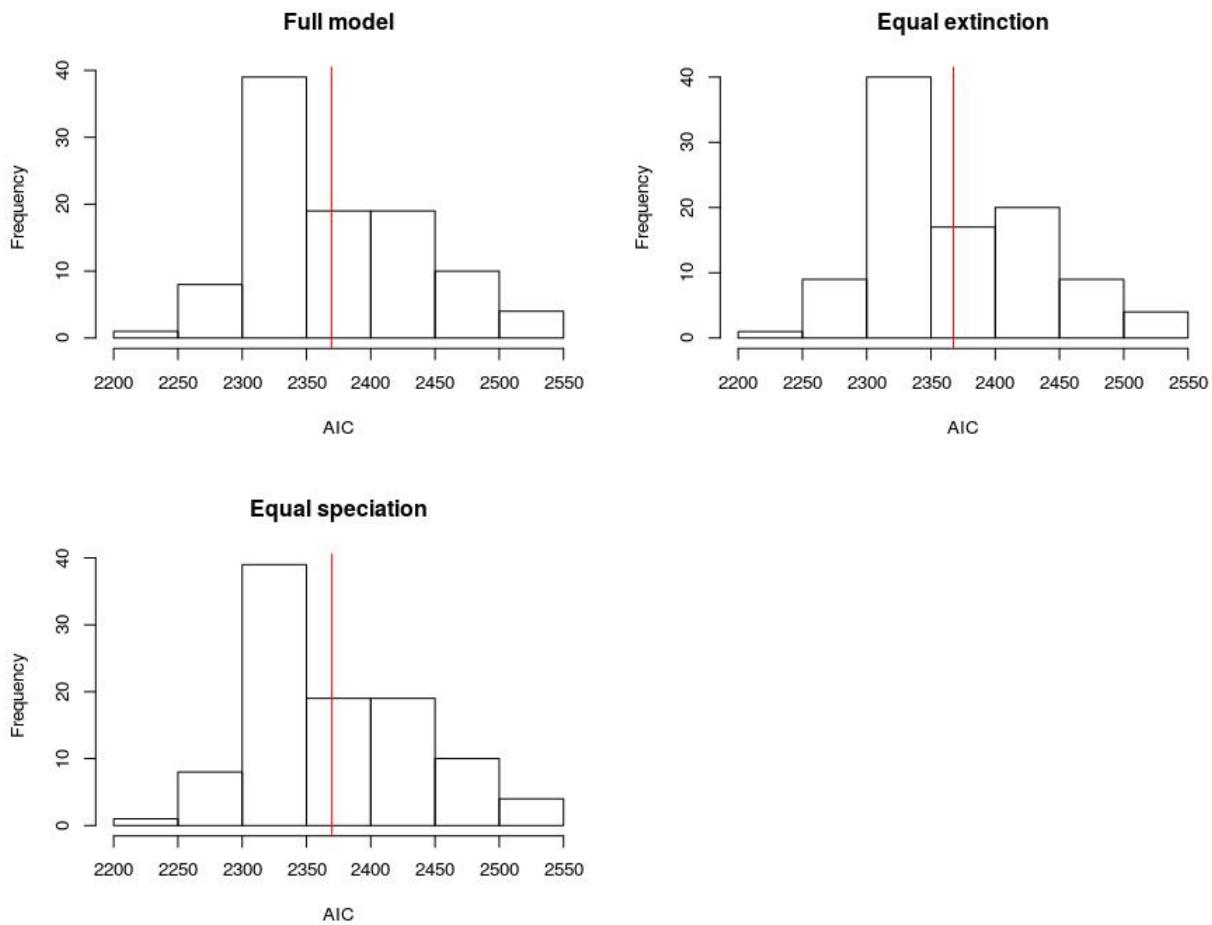
The test statistic delta AIC = 214.023



**Figure S2:** 95% credibility shift configurations with the configuration frequencies (mentioned on the top of each tree) summarized from the BAMM analysis. Size of the circles at the nodes correspond to the marginal probability of the shifts at the positions.



**Figure S3:** The posterior distribution of the speciation and extinction rates of dicot- and monocot- feeding lineages from BiSSE analysis. Lines below each distribution are 95% confidence intervals.



**Figure S4:** Graphs showing the relative positions of AIC (Akaike information criteria) values from the BiSSE analysis of the time tree on the distribution of the AIC values from 100 posterior trees from the dating analysis. All analyses were performed for equal sampling frequency (290/3941) for both character states.

**Table S2:** Exploring the effect of hidden state on the diversification rate estimation. Null model on the HiSSE framework allows trait independent change in diversification rate. The rate changes as a function of an unobserved hidden trait. Null model on the BiSSE framework allows equal rates across the states and no hidden character. In trait dependent BiSSE model, either the diversification rate changes with the trait or one of the trait may associate with a hidden state. Comparison of these shows that the model where an unobserved hidden state is associated with monocot feeding lineages gets the lowest AIC value. AIC = Akaike information criteria; logLik = log-likelihood.

	logLik	AIC	ΔAIC
null HiSSE	-859.8965	1729.793	0
full HiSSE	-848.3926	1736.785	6.992
null BiSSE	-944.5391	1897.078	167.285
BiSSE (trait dependent)	-943.8176	1899.635	169.842
BiSSE (hidden state associated with monocot feeding)	-869.1325	1758.265	28.472

## Appendix S1: Data References

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