**Methods**

*Quantification of host plant richness and divergence*

For each butterfly species that feed on seed plants, we quantified the host plant richness and divergence using six different phylogenetic metrics implemented in the package picante (*1*). Particularly, the taxon sampling of Espeland (*2*) is designed to represent the tribe-level diversity across Lepidoptera. In order to better reflect the breadth of the diet of within each tribe, we consolidated the host plant information from [ref butterflynet] to include at least one species per genus for each tribe. To quantify the host plant richness, the raw number of host plant families and Faith's PD are used. To quantify the host plant divergence, the mean pairwise distance (MPD), the mean nearest taxon distance (MNTD), and the distance-based speciation index (DSI) are used. Here, PD is the sum of phylogenetic branch lengths (*3*). MPD is the average distance separating all pairs of species on the phylogenetic tree (*4*). MNTD is the mean distance between each species and its closest relative (*4*). DSI is a Z-score of MPD or MNTD that measures specialization as a deviation from a random expectation (*5*).

To calculate these metrics, we used the calibrated phylogeny of seed plants from Smith and Brown (*6*) as reference. We pruned the tree to include two species per plant family whose divergence time represent the crown group age for each family. This exercise enabled the calculation of pairwise distance based measures such as MPD, MNTD, and DSI for monophagous butterflies that feed on only one plant family. Finally, the function *pd*, *ses.mpd*, and *ses.mntd* were used to calculate these phylogenetic metrics using 1000 replicates in picante. The R script is available on GitHub (https://github.com/lmcai/BNet-PD-analysis).

Reference:

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