**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 R package picante (*1*). 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 (*2*). MPD is the average distance separating all pairs of species on the phylogenetic tree (*3*). MNTD is the mean distance between each species and its closest relative (*3*). DSI is a Z-score of MPD or MNTD that measures specialization as a deviation from a random expectation (*4*).

To calculate these metrics, we used the calibrated phylogeny of seed plants from Smith and Brown (*5*) 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).

**Results**

The 1,316 herbivorous Lepidoptera sampled here on average feed on 1.7 plant families and 68.0% of them are monophagous. Among polyphagous species, *Emesis mandana* (Riodinidae) can feed on 22 different host plant families, making its diet the most diverse one reported in this study. At the family level, Lycaenidae and Riodinidae have the highest host plant richness based on the number and PD of host plant families, respectively. The average number of host plant families is 2.11 in Lycaenidae and 2.06 in Riodinidae; and the average PD is 419.3 in Lycaenidae and 443.4 in Riodinidae. On the other hand, Hesperiidae have the narrowest diet compared to other families with a mean host family number of 1.35 and mean PD of 362.6. To quantify host divergence, we used four measurements, including MPD, MNTD, and two DSI metrics. Compared to PD, these divergence metrics measure the average pairwise distance between hosts (MPD and MNTD) and compare it to a randomly generated null distribution (DSI metrics). The results are highly consistent when using different measurements and we found Papilionidae to have the highest average host plant divergence (mean MPD = 187.5, mean MNTD = 185.0, mean DSIMPD = -0.96, mean DSIMNTD = -1.03). Within each butterfly family, host divergence is often bimodally distributed, which is caused by the difference between monophagous and polyphagous species. When excluding monophagous species, Papilionidae still have the most divergent host range with a mean DSIMPD of -0.15 and mean DSIMNTD of -0.18. Here, the negative values of DSIMPD and DSIMNTD suggest that host plants are phylogenetically clustered (DSI<0) rather than randomly distributed (DSI 0). However, exceptions, though uncommon, are found in several species. There are 14 species demonstrating both high host plant richness (>5 families) and high divergence (MPD *p–*value >0.05 and MNTD *p–*value >0.05). Lycaenidae are overrepresented in these generalists with eight species included in the list. The wide breadth of host range is well known in some species such as *Hypolycaena phorbas* (Lycaenidae), *Zesius chrysomallus* (Lycaenidae), and *Pterourus glaucus* (Papilionidae), but reported for the first time in others. For example, *Shirozua jonasi* (Lycaenidae) can feed on 20 astonishingly diverse plants including conifers (Pinaceae, Cupressaceae), grasses (Poaceae), legumes (Fabaceae), and plants with toxic secondary compounds (Anacardiaceae, Caprifoliaceae).

**Figure caption**

**Fig. S# Host plant richness and divergence across butterfly families.** (a) Distribution of host plant richness measured by the number of host plant families. (b) Distribution of host plant richness measured by the phylogenetic distance (PD) of host plant families. (c) Distribution of host plant divergence measured by the mean pairwise distance (MPD, red) and the mean nearest taxon distance (MNTD, blue). (d) Distribution of host plant divergence measured by the distance-based speciation index (DSI) calculated from the normalized MPD (red) and MNTD (blue).

**Reference**

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