

SI Results

Disparity analyses

Maximum pairwise disparity for pollination syndromes followed PD, with the “buzz-bee” syndrome containing the most disparate species pair ($R = 1$), followed by the “nectar-foraging vertebrate” syndrome ($R = 0.81$). When randomly subsampling syndromes to $n=17$ /syndrome, the “nectar-foraging-vertebrate” syndrome also came out as most disparate for R (Tab. S1a). Pairwise dissimilarities of regions were highest in Asia ($R = 1$; Fig. 3a, Tab. S2b), followed by South America ($R = 0.792$), Africa ($R = 0.75$) and Central America ($R = 0.674$). When randomly subsampling regions to the same number of species ($n = 42$ /region) Africa had the highest maximum disparity ($R = 0.83$), followed by Asia ($R = 0.79$) Central America ($R = 0.73$) and South America ($R = 0.7$, Tab. S2a).

Maximum disparity of tribes was positively correlated with species richness ($\rho = 0.87$, $p < 0.0001$; Sonerileae $R = 1$, Melastomateae $R = 0.75$, Miconieae $R = 0.67$), but not tribe age ($\rho = -0.027$, $p = 0.9$, Fig. S5a). When randomly subsampling to an equal number of species ($n = 8$ /tribe) we found similar results for maximum pairwise disparity (Sonerileae $R = 0.695$, Astronieae $R = 0.636$, Merianieae $R = 0.6$, Melastomateae $R = 0.591$, Fig. S5b).

Do pollinator shifts change selection regimes?

Shifts in phenotypic optima did not coincide with pollinator shifts (Fig. 4). Instead, we found one major shift in phenotypic optima in the evolutionary history of Melastomataceae (Fig. 4), along the branch separating the subfamilies Olisbeoideae and Kibessioideae (gray, Fig. 4) from subfamily Melastomatoideae (light cyan,). These optima relate to major changes in floral traits such as anther dehiscence, stamen arrangement and color contrasts independent of pollinator shifts. We recovered 10 additional, mostly singular shifts in phenotypic optima, of which only five correspond to species that shifted pollinators (out of 59, Fig. 4). The model assuming convergence was not preferred (Fig. S7a).

To determine whether the lack of shifts in phenotypic optima was a result of the comparatively small differentiation of shifted species when assessing the full Melastomataceae flower diversity (Fig. 2a), we reran the analyses on morphospaces calculated for each tribe with shifted species separately. Again, pollinator shifts did not coincide with shifts in phenotypic optima, except in tribe Pyxidanthae (two distinct “buzz-bee” and one “nectar-foraging vertebrate” optima, Fig. S6, S7, S7a).