

Fig. S1. Character optimization of the total numbers of host plant orders on a phylogeny of the tussock moths subfamily Lymantriinae [25].

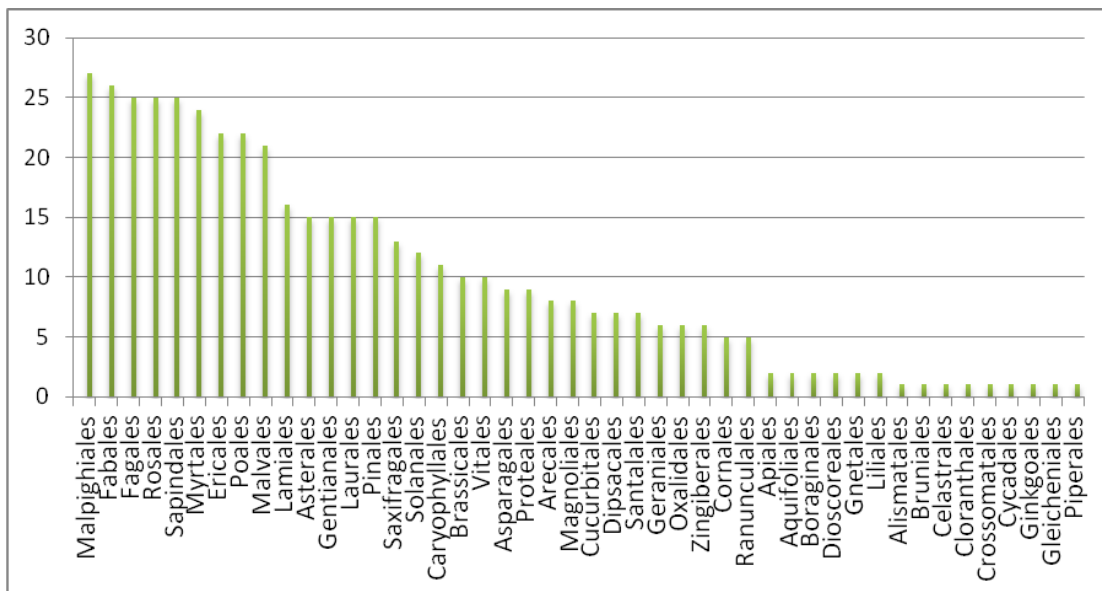
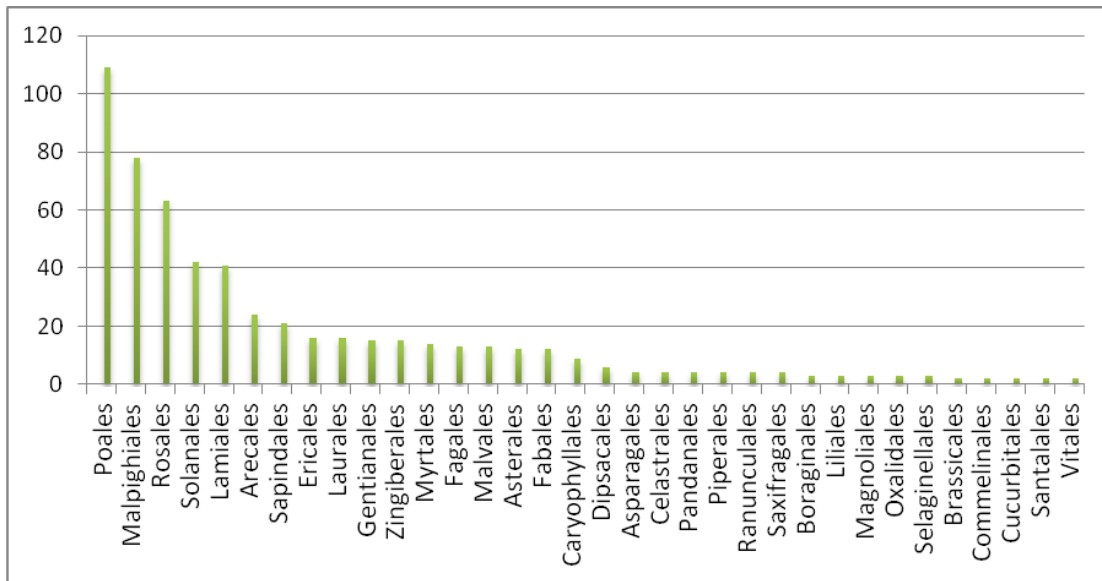


Fig. S2. Frequencies of use of different host orders by genus-level taxa in nymphalid butterflies (top figure, data from [8]) and in tussock moths (bottom figure). Note the different scales of the y-axes.

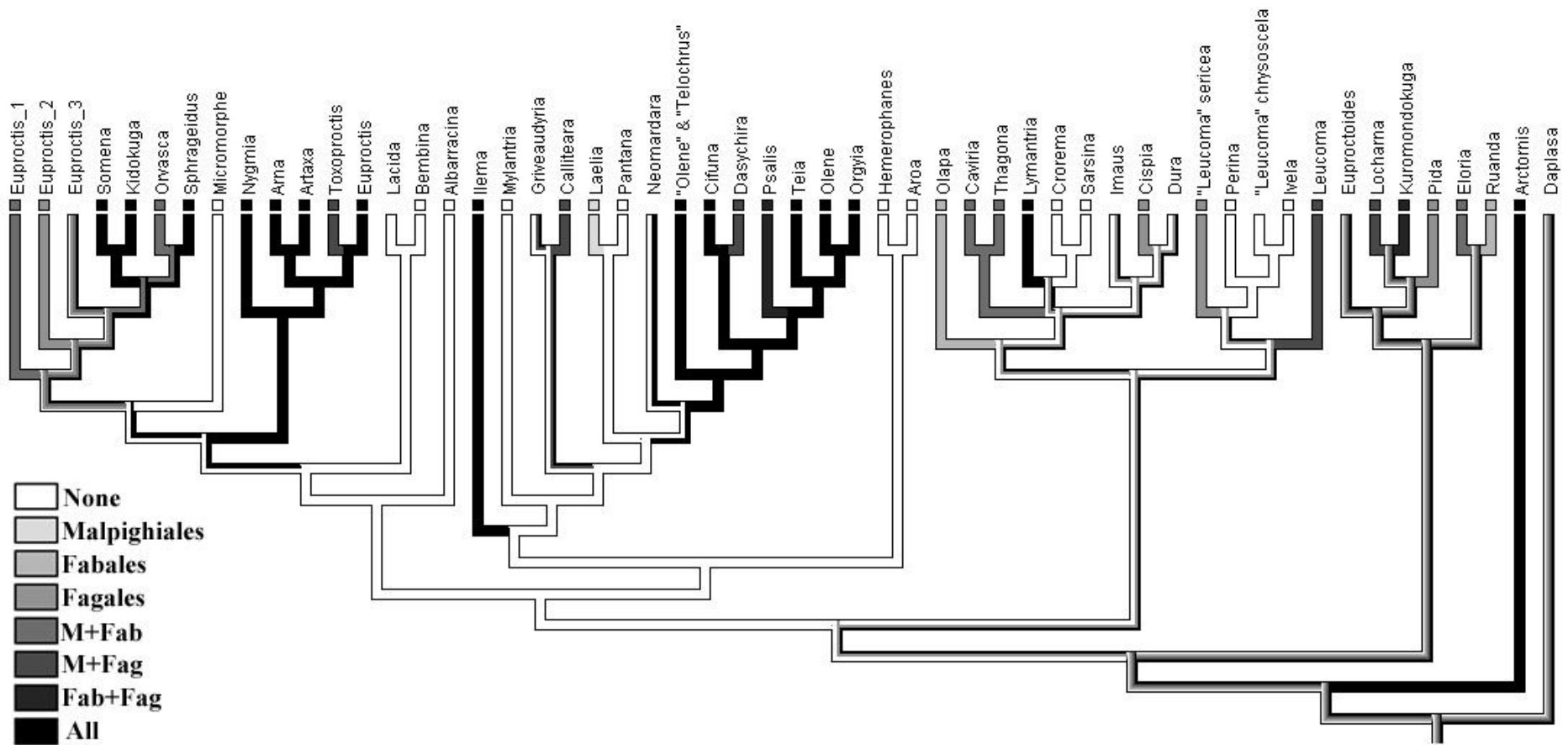


Fig. S3a. Character optimization of use of the three most common host orders, and combinations between them, by the tussock moths subfamily

Lymantriinae. Phylogeny from [25].

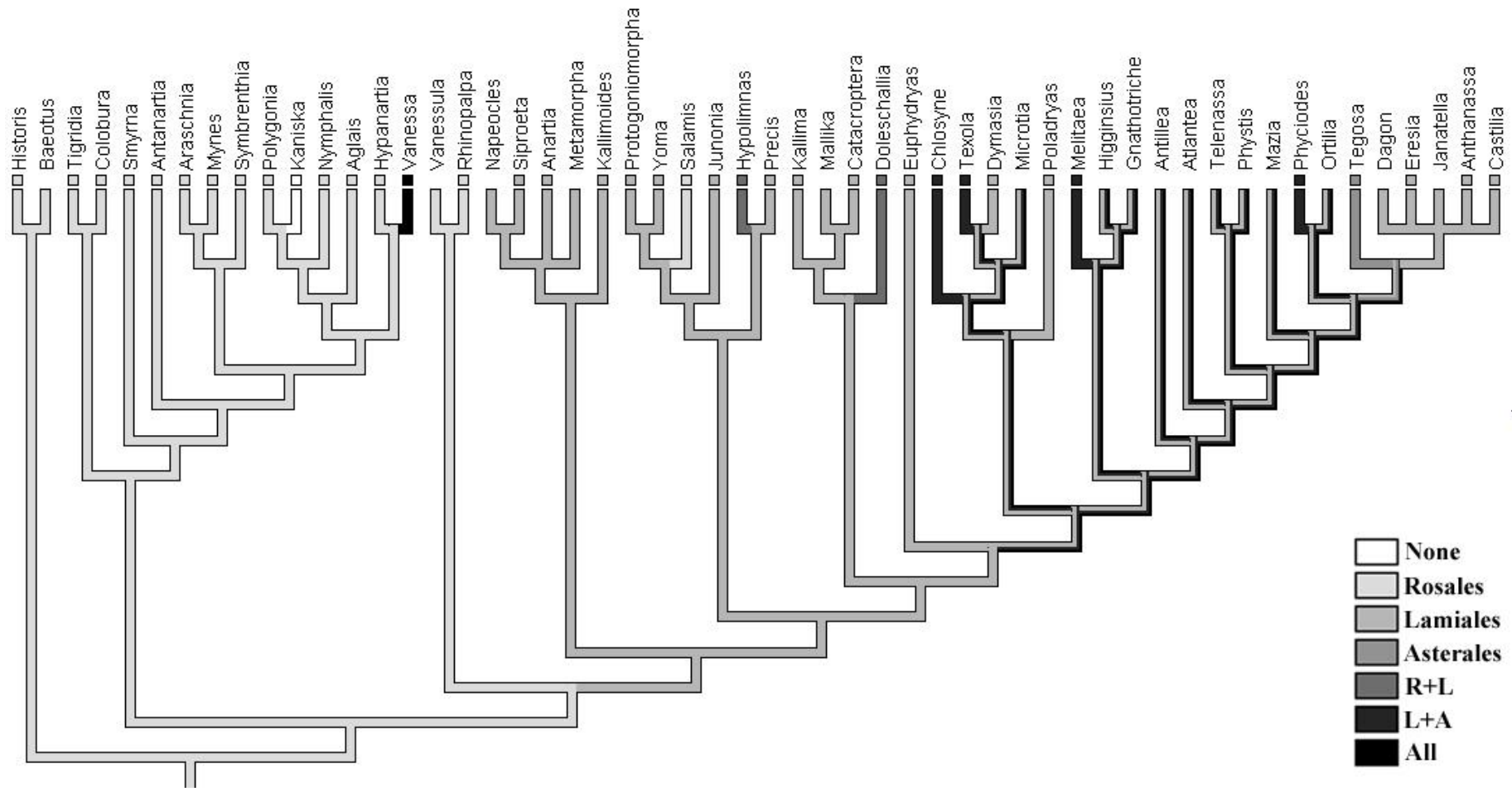


Fig. S3b. Character optimization of use of the three most common host orders, and combinations between them, by the butterfly subfamily Nymphalinae.

Phylogeny from [63] with modifications from [64]. Host data from [10].