

Fig. 1. Dated evolutionary tree of butterfly and moth relationships. The tree is derived from a maximum-likelihood analysis of 749,791 amino acid sites. Branch lengths and node ages are computed in a time-calibrated analysis of 198,050 amino acid sites and 16 fossil calibrations. Gray bars depict 95% credibility intervals of node ages. Asterisks indicate superfamilies that are nonmonophyletic in the tree. The color-coding of nodes indicates nonparametric bootstrap support values. Two of the 16 fossils were placed on outgroup branches; their placements are shown in *SI Appendix*, Fig. S4. Scale bar is in millions of years. MICROPT, Micropterigoidea; AGATH, Agathiphagoidea; HETEROBATH, Heterobathmioidea. Additional information on fossil calibrations is provided in Dataset S10 and *SI Appendix*, Supplementary Archive 8.

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