



Fig. 1. Combined molecular phylogenetic tree for Diptera. Partitioned ML analysis of combined taxon sets of tier 1 and tier 2 FLYTREE data samples ($-\ln L = 344155.6169$) calculated in RAXML. Circles indicate bootstrap support $>80\%$ (black/bp = 95–100%, gray/bp = 88–94%, white/bp = 80–88%). Nodes with improved bootstrap values resulting from postanalysis pruning of unstable taxa are marked by stars (black/bp = 95–100%, gray/bp = 88–94%, white/bp = 80–88%). Colored squares on terminal branches indicate the presence, in at least one species of a family, of ecological traits as shown to lower left. The number of origins of each trait was estimated with reference to the phylogeny, the distribution of each trait among genera within a family, and the known biology of the organisms.

thermore, a paraphyletic relationship of phorids and syrphids would support the hypothesis that their shared special mode of extraembryonic development (dorsal amnion closure) (26) evolved in the stem lineage of Cyclorrhapha and preceded the origin of the schizophoran amnioserosa.

To test this hypothesis, we used a relatively recent phylogenomic marker: small, noncoding, regulatory micro-RNAs (miRNAs). miRNAs exhibit a striking phylogenetic pattern of conservation across the metazoan tree of life, suggesting the accumulation and maintenance of miRNA families throughout organismal evolution