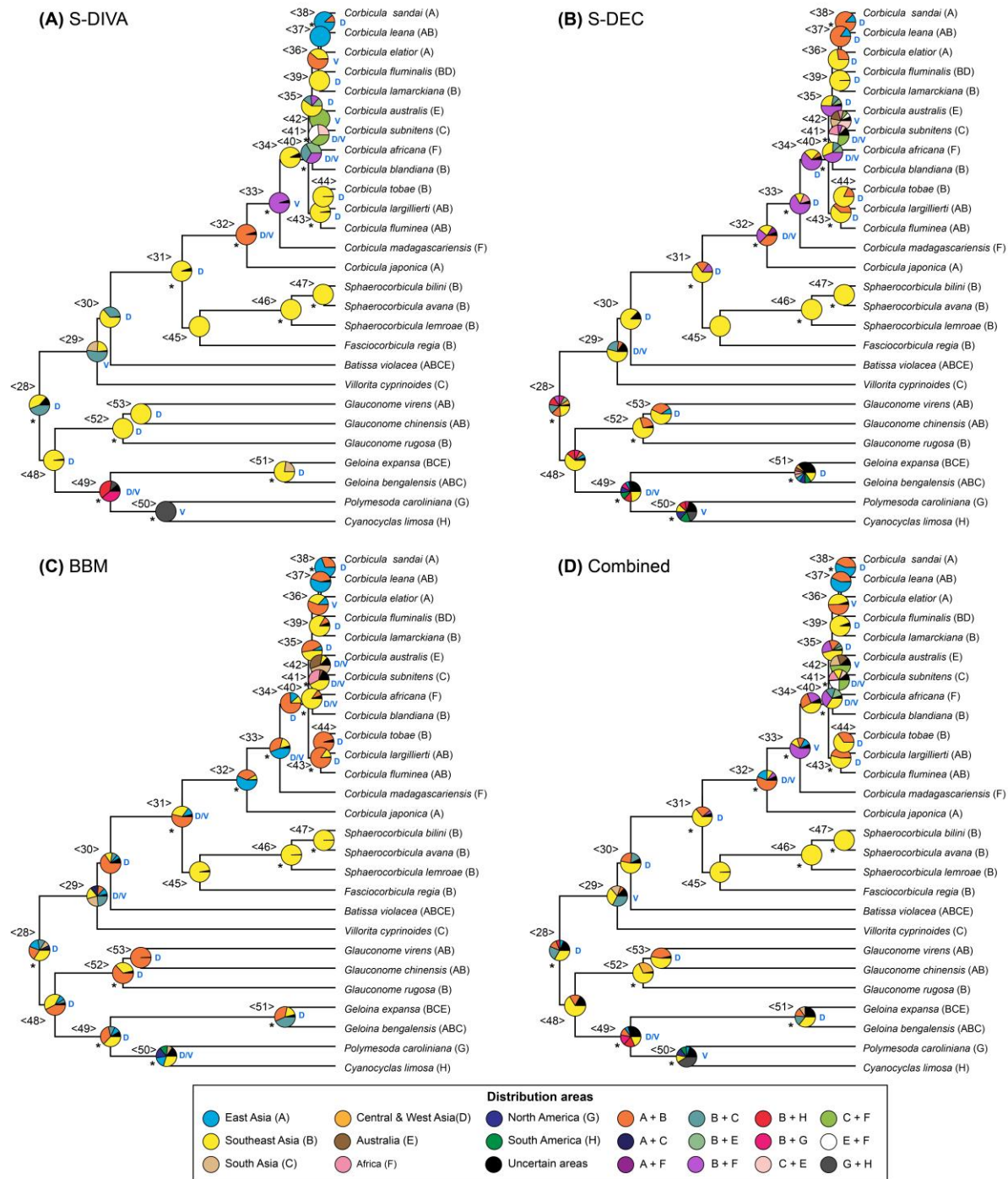




Supplementary Figure S1 Historical biogeographic events of the members in the family Cyrenidae and related taxa, inferred from three probabilistic algorithms: (A) Statistical Dispersal-Vicariance (S-DIVA), (B) Statistical Dispersal-Extinction-Cladogenesis (S-DEC), and (C) Bayesian Binary MCMC (BBM), and (D) the combined results of these analyses as implemented in RASP v4.2. Native distributions are shown in parentheses following taxon names. Node numbers of the internal node are shown near node. Pie charts at internal nodes indicate the probabilities of ancestral areas, while blue letters adjacent to nodes indicate inferred biogeographic events: dispersal (D) and vicariance (V). Phylogenetic trees are fossil-calibrated ultrametric trees generated in BEAST v2.6.1 based on a concatenated data set of COI, 16S rRNA, and 28S rRNA genes. Nodes with significant support (BPP ≥ 0.95) are marked with an asterisk (*).