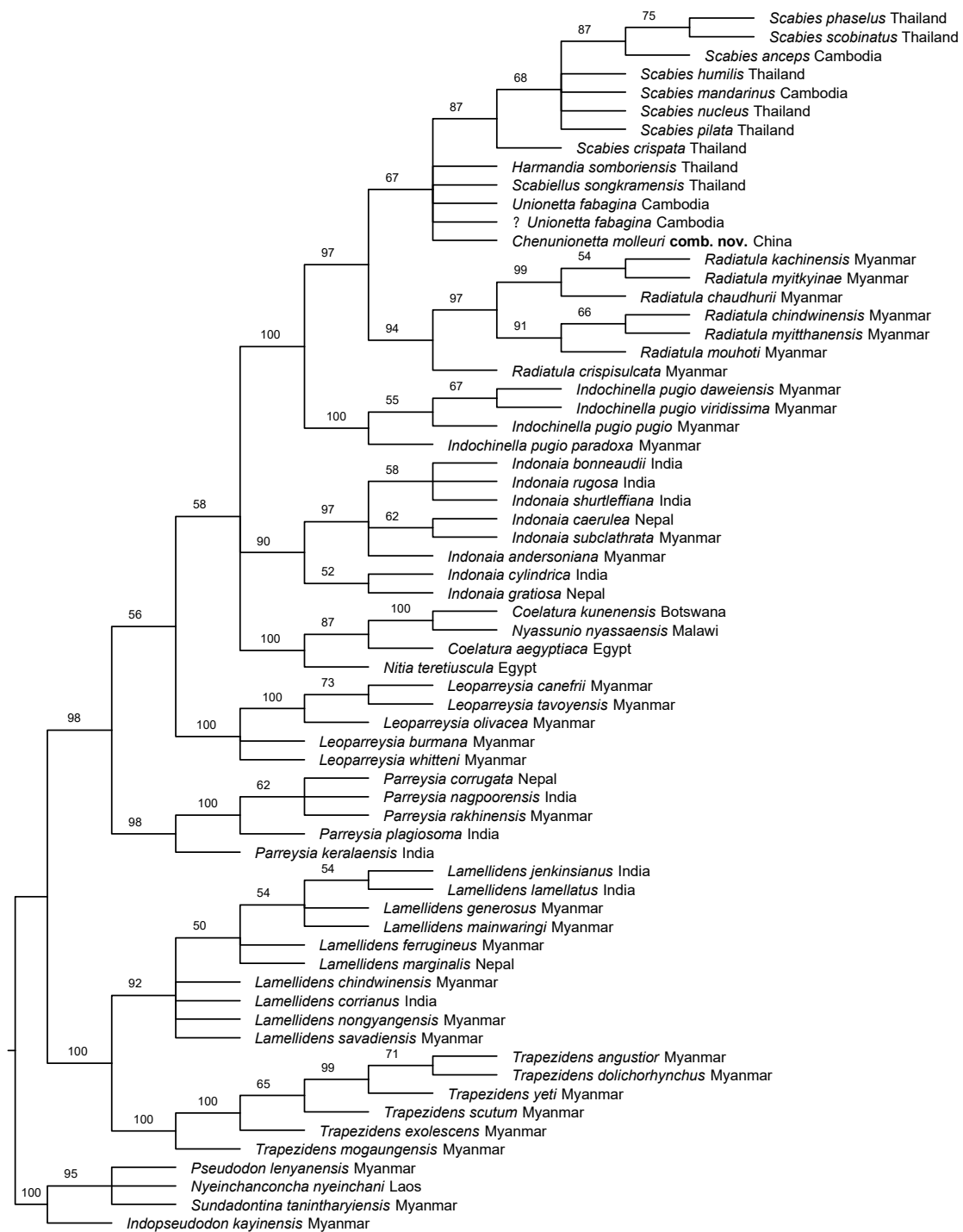




Supplementary Figure S4. Maximum parsimony phylogeny inferred from the concatenated three gene dataset (COI, 16S, and 28S). Bootstrap support values are indicated at nodes.