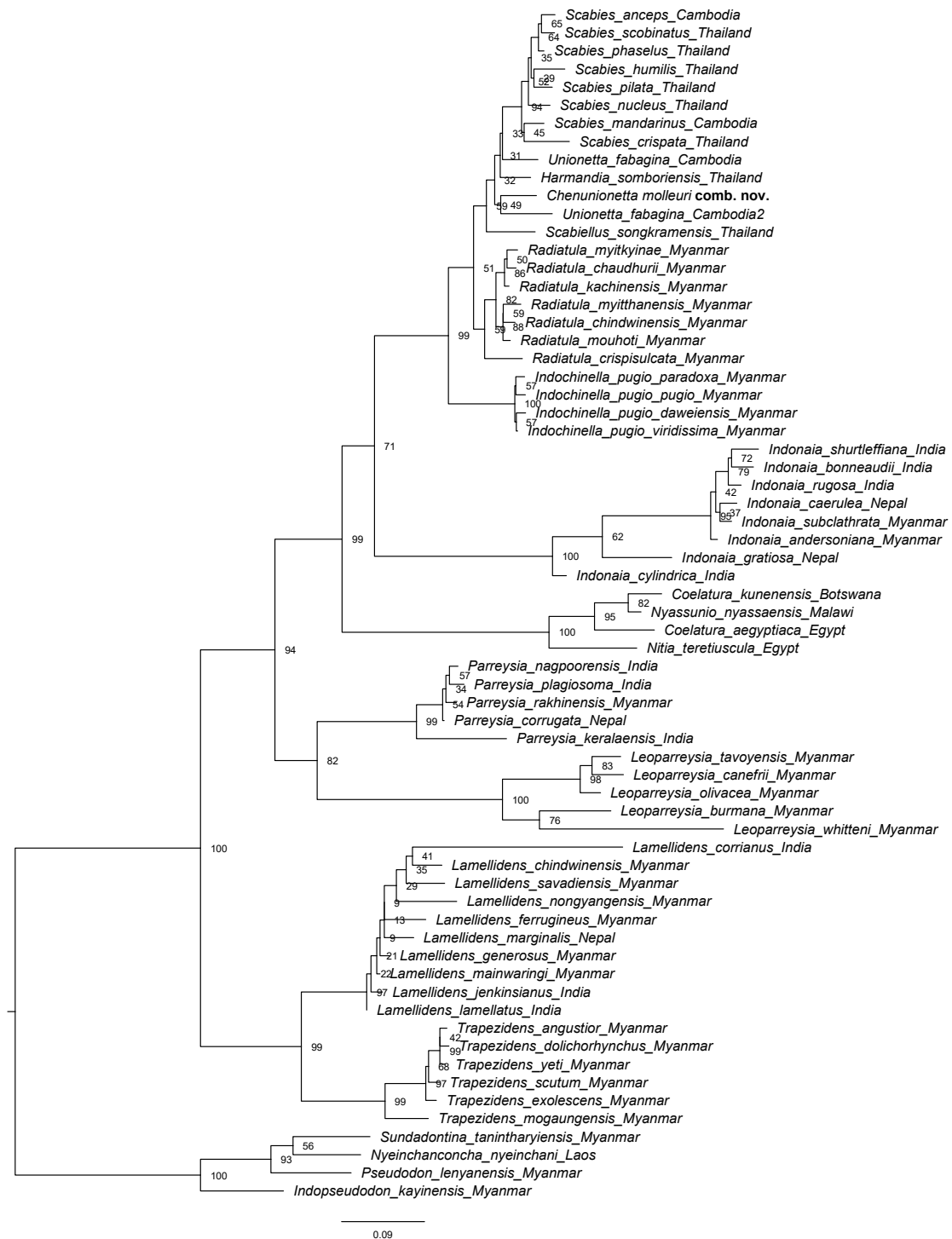




Supplementary Figure S2. Maximum likelihood phylogeny inferred from the concatenated three gene dataset (COI, 16S, and 28S). Bootstrap support values are indicated at nodes.