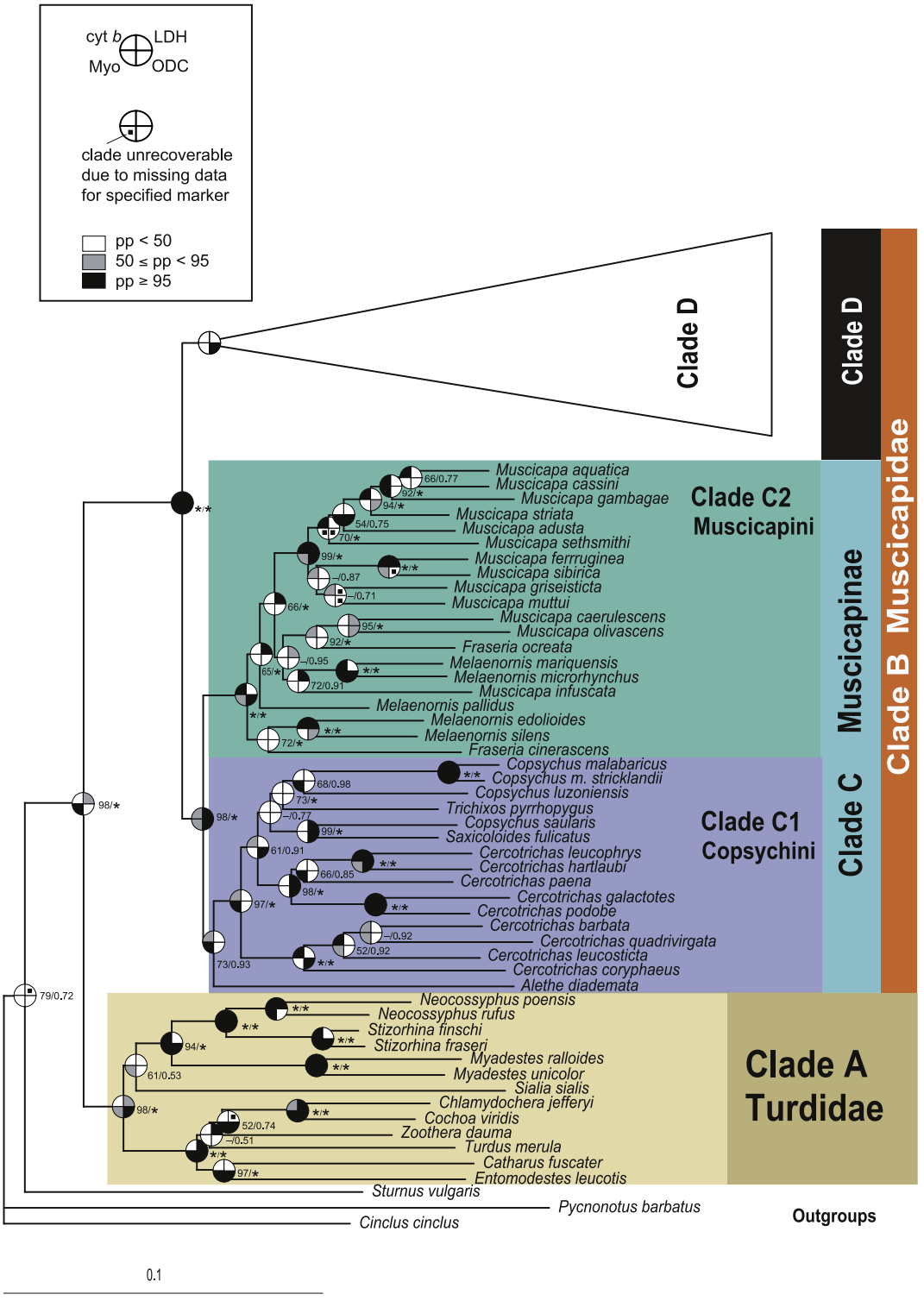

Fig. 1. Relationships of Muscicapidae and Turdidae based on Bayesian analysis of combined mitochondrial cytochrome *b*, and nuclear ODC, myoglobin and LDH intron sequences (3240 bp) divided into two partitions analyzed under the GTR + G + I model (cyt *b* and ODC), one partition analyzed under the GTR + G model (LDH) and one partition analyzed under the HKY + G model (myo). Maximum Likelihood bootstrap values and Bayesian posterior probabilities, respectively, are given for each clade. An asterisk denotes a bootstrap value of 100% or a posterior probability of 1.0. A '–' indicates that the node was not recovered by Maximum Likelihood analysis. The pie diagrams indicate support from individual gene trees. The names referring to the marked clades are the ones proposed here.

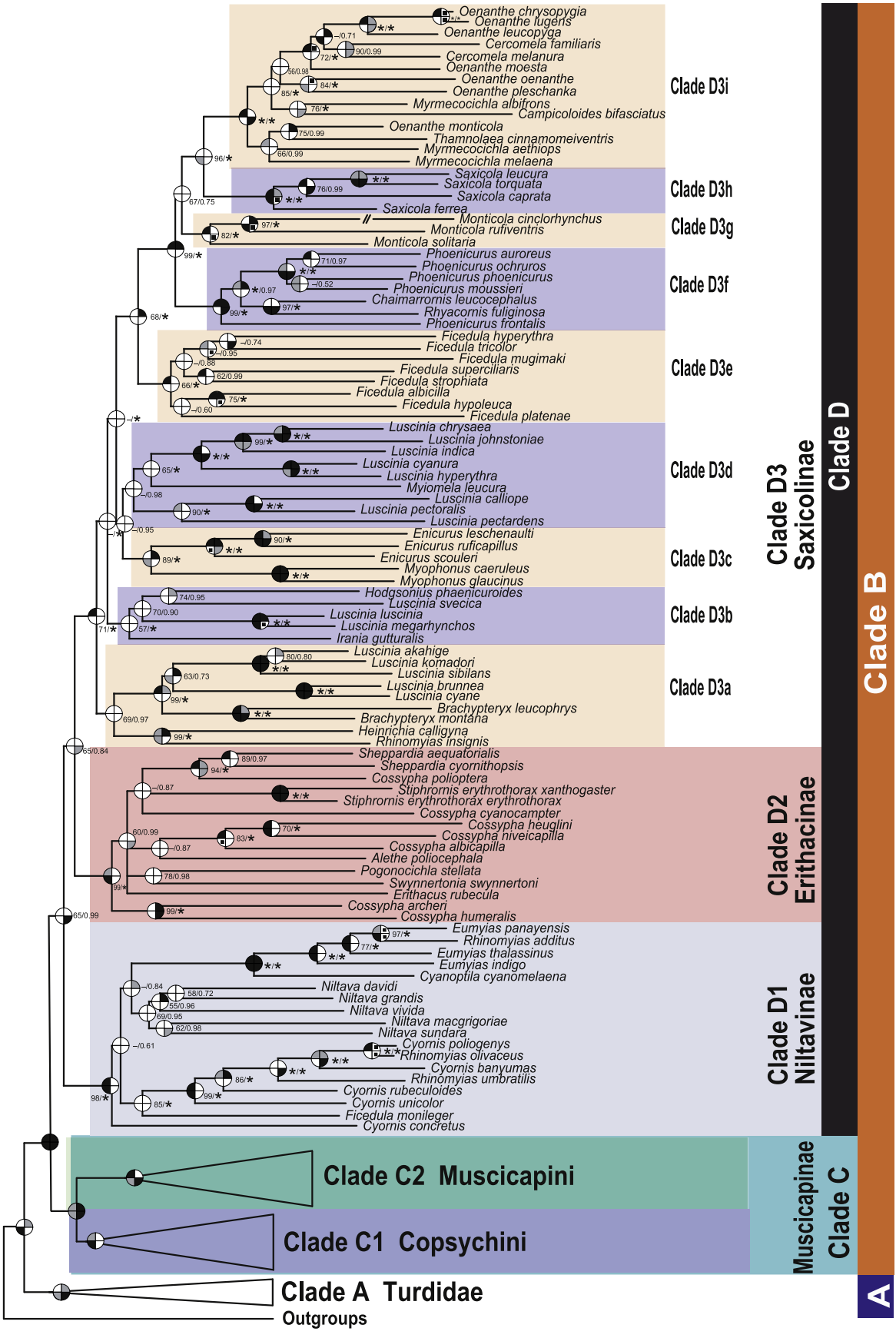

Fig. 1 (*continued*)