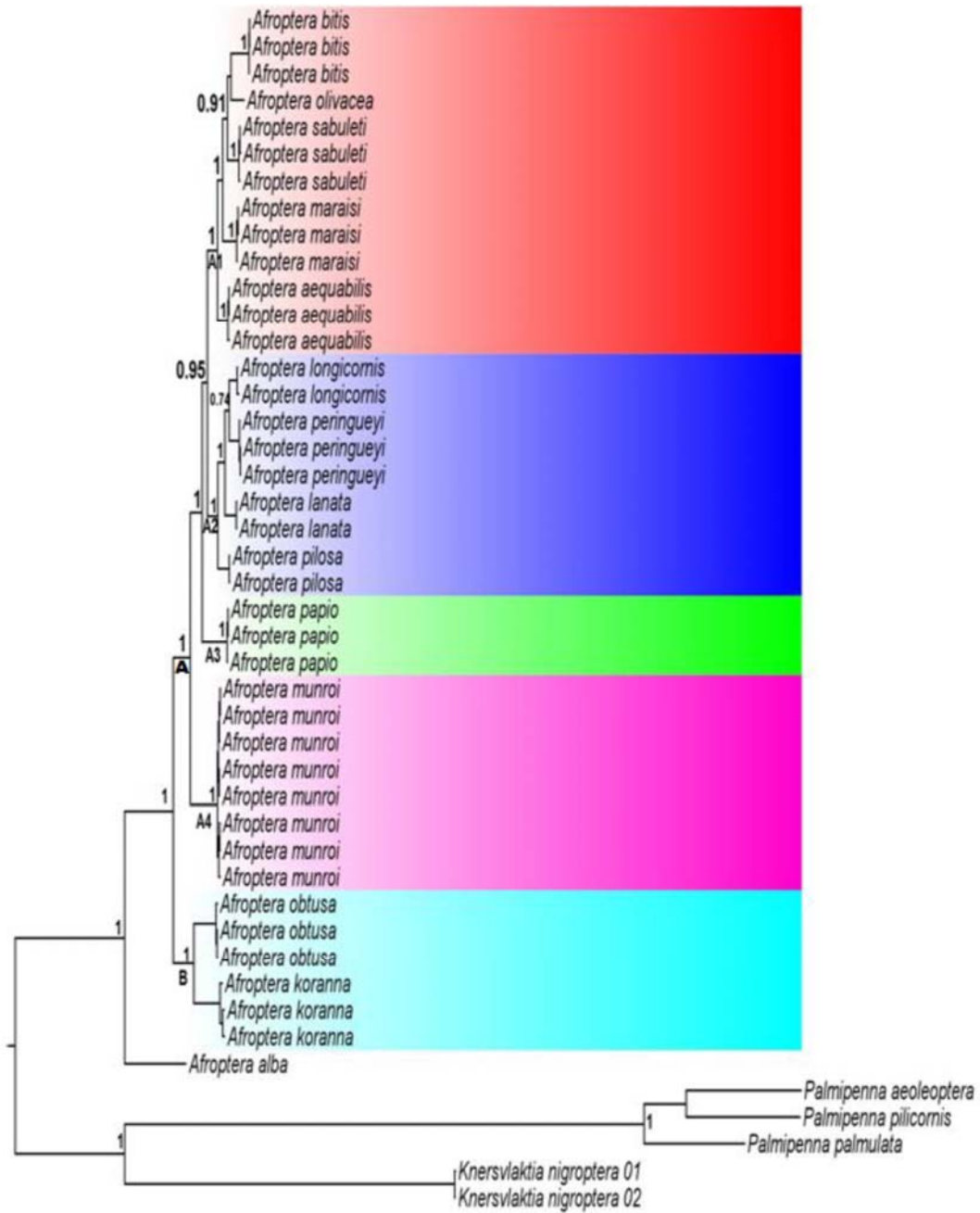**Fig S1.** Fifty percent majority rule consensus tree resulting from Bayesian analysis of the combined (COI, CAD, 16S, 28S and 18S) with PP, MP and MLB given, respectively. Dashes (-) on nodes indicate weak/no support. Letters below branches indicate the clade's name.
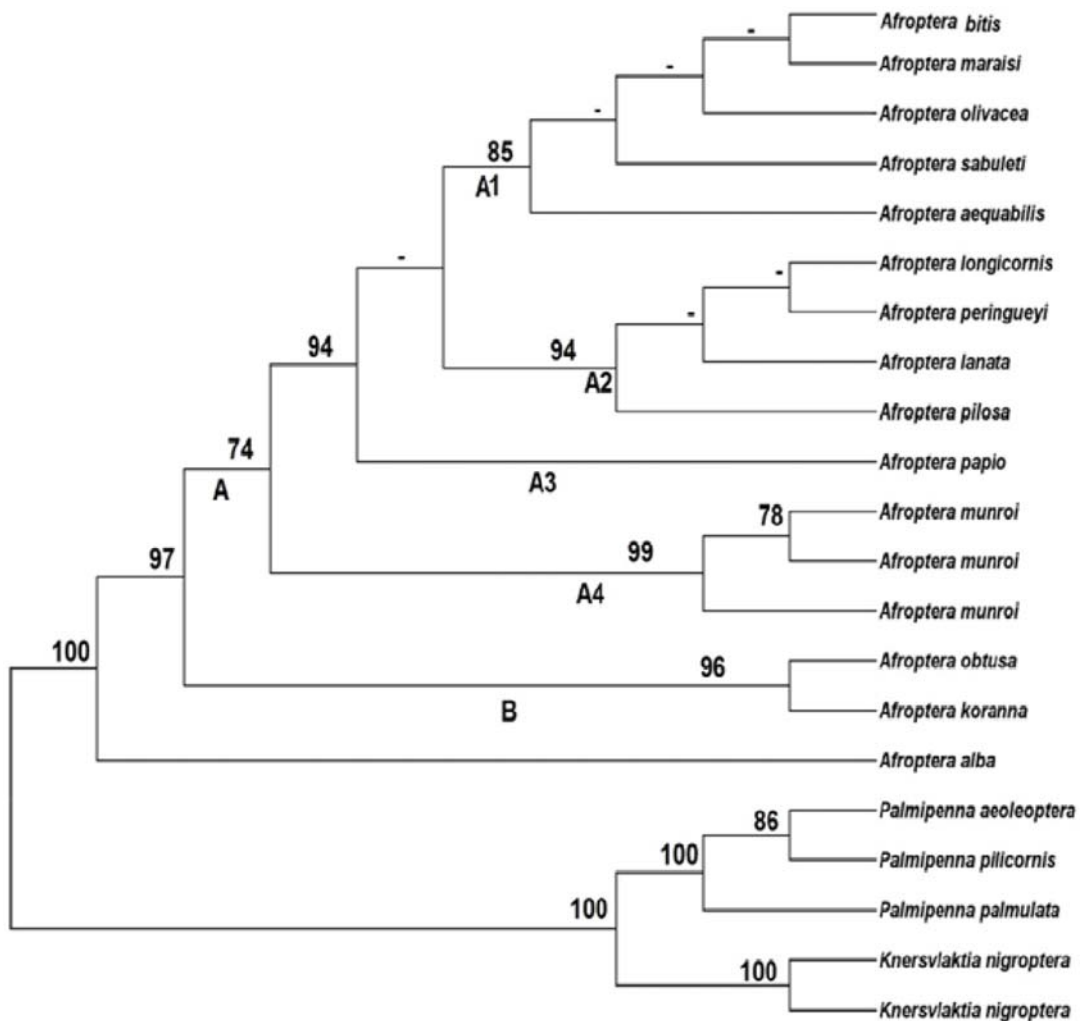
Fig S2. The single most parsimonious tree of the combined morphological/molecular concatenated dataset with bootstrap support values on each branch. Dashes (-) on branches indicate weak/no support.