SUPPLEMENTARY FIG. S1. One of 17 equally parsimonious trees obtained from maximum parsimony analysis of the concatenated plastid dataset, with gaps ("indels") coded as binary presence/absence characters. Numbers above branches indicate maximum parsimony bootstrap proportions. Bars to the right indicate outgroup taxa and clades recovered.
SUPPLEMENTARY FIG. S2. Majority rule consensus topology obtained from one of three independent Bayesian inference (BI) analyses of the concatenated plastid dataset. Numbers above branches indicate BI posterior probabilities. Bars to the right indicate outgroup taxa and clades recovered.