



Fig. 2. Trees based on the independent markers Cytochrome *b* (1038 bp) and myoglobin intron II (717 bp), analyzed separately by Bayesian inference under the GTR +  $\Gamma$  + I and HKY models, respectively. Posterior probabilities ( $\geq 50\%$ ; 141,000 trees) and parsimony bootstrap support are indicated above and below, respectively, the nodes.