



**Figure 3.** A rate-smoothed tree with the topology and branch lengths (GTR +  $\Gamma$  + I) from a Bayesian analysis of a combined data set of mitochondrial cytochrome *b* and 12S and nuclear myoglobin intron 2 sequences. The depth of the tree was estimated at 10.97% (i.e., 21.94% sequence divergence across the root) in a separate analysis that used the cytochrome *b* data only in a maximum likelihood enforced clock with no outgroups, and mid-point rooting. Species in bold have Himalayan distributions as in Figure 2. Scale bar indicates inferred amount of evolution along a branch; dashed lines indicate inferred sequence divergence at 4% intervals.