

SUPPLEMENTARY FIGURE 1. A chronogram with node numbers based on a fifty percent majority rule consensus tree of a Bayesian Markov chain Monte Carlo (MCMC) analysis of a combined data set of mitochondrial (12S, cytochrome b) and nuclear (ODC, myoglobin) DNA sequences. Breeding region for each taxon, as delimited in Figure 1b, is given after each taxon name. Horizontal bars at nodes represents the length of the highest posterior density (HPD) 95% intervals of node ages derived by integrating over r8s analyses of 500 trees randomly sampled from an original MCMC sample of 20,000 trees. Detailed information on posterior node probabilities and ancestral area reconstructions at each node can be found in Supplementary Table 1.