Figure S7. Results of traditional *dN/dS* estimates for the COI gene using the alternative (mitochondrial gene-based) topology from Fig. S1, with branches colored based on *dN/dS* ratios. Branch lengths are based on all mitochondrial protein-coding genes, optimized on this topology in PAUP* under a GTRΓI model. Estimates of *dN/dS* are from codon model-based analyses conducted HyPhy (See Supplementary Methods).