

Supplementary Material 5. Bayesian analysis of COI sequences via BEAST (enlarged version of Figure 2 over three pages; separated for ease of reading values of posterior probability). Specimen number and country of collection are given at tips (Suppl. Mat. 2). If primary species hypotheses lumped taxa, nominal species are listed in grey to the right. ESUs delimited by each method (section 3.2) are depicted via blocks (black, accepted ESUs; red, unaccepted splits; orange, unaccepted lumps), with putative species on the right (green). Putative species names are listed on the far right, with corresponding number in parentheses; species with changed generic assignments are in red font. Support values are posterior probabilities (PP); intraspecific support values were removed for legibility except where relevant (i.e., if there was conflict between delimited ESUs or prior species assignments). Inserts displayed on each page shows position within the tree.





