



Figure S1. All phylogenetic hypotheses generated in this study. Trees in the same row have the same selection of terminals (any one marker (at least one mitochondrial), any two markers, and any three markers). Trees in the same column were analyzed under the same optimality criterion, alignment, and cost scheme. The left column contains trees analyzed in RAxML under maximum likelihood and a partitioned model, in the middle column are trees analyzed in MrBayes using the same alignment as in RAxML, and in the right column are trees analyzed in POY using dynamic homology for length-variable markers and a cost scheme in which transitions, transversions, and gaps cost 1. The top middle tree (B) has taxonomic point of interest noted in red.