



Figure S3. Phylogram inferred by maximum likelihood (ML) analysis of *rbcL* sequence data (1278 bp). Support values are listed as bootstrap for ML analyses and Bayesian posterior probabilities respectively. Asterisks denote nodes that are strongly supported (bootstrap values  $\geq 98$ , posterior probabilities = 1.0) in all analyses. Support values are not indicated for all nodes (i.e., bootstrap values  $\leq 50$ , posterior probabilities  $\leq 0.65$ , or between closely related species). Scale bar refers to substitutions per site.