



Figure S2. Phylogram inferred by maximum likelihood (ML) analysis of *psbA* sequence data (778 bp). Support values are listed as bootstrap for ML analyses and Bayesian posterior probabilities respectively. Asterisks denote nodes that are strongly supported (bootstrap values ≥ 98 , posterior probabilities = 1.0) in all analyses. Support values are not indicated for all nodes (i.e., bootstrap values ≤ 50 , posterior probabilities ≤ 0.65 , or between closely related species). Scale bar refers to substitutions per site.