SUPPLEMENTARY DATA

Captions

File S1: Accessions used in this study with GenBank numbers for each sequence.

File S2: Data matrix for TNT with details of loci and excluded positions.

File S3: Data matrix for RaxML (PHYLIP format).

Figure S1: Maximum likelihood tree with proportional branch lengths.

Figure S2: Maximum likelihood tree based on plastid DNA sequences with bootstrap support values.

Figure S3: Maximum likelihood tree based on nuclear DNA sequences with bootstrap support values.

Figure S4: Maximum likelihood tree for 175 taxa with bootstrap values.

Figure S5: Maximum likelihood tree for 49 taxa with bootstrap values.

Figure S6: Parsimony tree for 175 taxa with jackknife values.

Figure S7: Parsimony tree for 49 taxa with jackknife values.

Figure S8: Maximum likelihood tree with habit plotted.

Figure S9: Parsimony tree with habit plotted.

Figure S10: Maximum likelihood tree with presence of corm/pseudobulb plotted.

Figure S11: Parsimony tree with presence of corm/pseudobulb plotted.

Figure S12: Maximum likelihood tree with geography plotted.

Figure S13: Parsimony tree with geography plotted.

Figure S14: Maximum likelihood tree with pollinium orientation plotted.

Figure S15: Parsimony tree with pollinium orientation plotted.

Figure S16: Maximum likelihood tree with presence of pollinarium stipe plotted.

Figure S17: Parsimony tree with presence of pollinarium stipe plotted.

Figure S18: Maximum likelihood tree with early anther inflexion plotted.

Figure S19: Parsimony tree with early anther inflexion plotted.