

Supplementary file 5 – The majority-rule tree resulting from Bayesian inference analysis based on the pruned dataset containing only taxa having data for all three DNA regions.

Numbers on branches show posterior probabilities (PP) and ultrafast bootstrap support (UFBS). Dashes indicate branches that received less than 50% support. Sectional placement of taxa is indicated by abbreviations: ACR (*Acrochaene*), BEC (*Beccariana*), BIF (*Biflorae*), BIS (*Biseta*), BLE (*Blepharistes*), BRA (*Brachyantha*), BSC (*Brachystachyae*), CIR (*Cirrhopetaloides*), CIRR (*Cirrhopetalum*), DES (*Desmosanthes*), EMA (*Emarginatae*), EPH (*Ephippium*), EPI (*Epicrianthes*), EUB (*Eublepharon*), HIR (*Hirtula*), ION (*Ione*), LEM (*Lemniscata*), LEO (*Leopardinae*), MNP (*Monanthaparva*), OXY (*Oxysepala*), PHY (*Physometra*), PLU (*Plumata*), RAC (*Racemosae*), REP (*Repantia*), RHY (*Rhytionanthos*), SES (*Sestochilus*), and STA (*Stachysanthes*).

