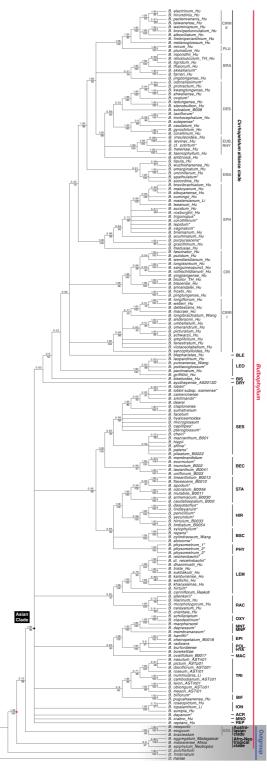
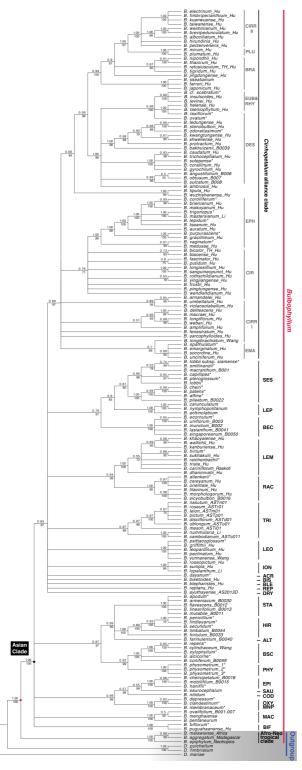
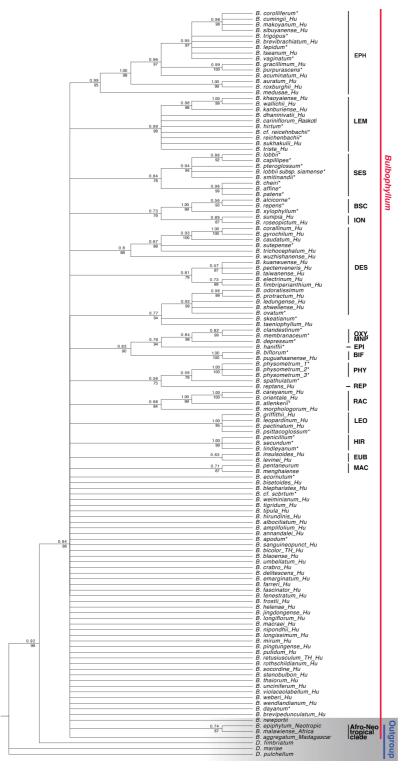
$Supplementary\ file\ 6-Phylogenetic\ trees\ based\ on\ single-maker\ datasets.$ 



Supplementary file 6.1. The majority-rule tree resulting from Bayesian inference analysis based on ITS sequence data. 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), ADL (Adelopetalum), BEC (Beccariana), BIF (Biflorae), BIS (Biseta), BLE (Blepharistes), BRA (Brachyantha), BSC (Brachystachyae), CIR (Cirrhopetaloides), CIRR (Cirrphopetalum), DES (Desmosanthes), DRY (Drymoda), EMA (Emarginatae), EPH (Ephippium), EPI (Epicrianthes), EUB (Eublepharon), HIR (Hirtula), HYA (Hyalosema), ION (Ione), LEM (Lemniscata), LEO (Leopardinae), MAC (Macrocaulia), MNO (Monomeria), MNP (Monanthaparva), MNT (Monanthes), OXY (Oxysepala), PHY (Physometra), PLU (Plumata), POL (Polymeres), RAC (Racemosae), REP (Repantia), RHY (Rhytionanthos), SES (Sestochilus), STA (Stachysanthes), and TRI (Trias)



Supplementary file 6.2. The majority-rule tree resulting from Bayesian inference analysis based on *mat*K sequence data. 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*), ALT (*Altisceptrum*), BEC (*Beccariana*), BIF (*Biflorae*), BIS (*Biseta*), BLE (*Blepharistes*), BRA (*Brachyantha*), BSC (*Brachystachyae*), CIR (*Cirrhopetaloides*), CIRR (*Cirrphopetalum*), COD (*Codonosiphon*), DES (*Desmosanthes*), DRY (*Drymoda*), EMA (*Emarginatae*), EPH (*Ephippium*), EPI (*Epicrianthes*), EUB (*Eublepharon*), HIR (*Hirtula*), ION (*Ione*), LEM (*Lemniscata*), LEO (*Leopardinae*), LEP (*Lepidorhiza*), MAC (*Macrocaulia*), MNP (*Monanthaparva*), OXY (*Oxysepala*), PHY (*Physometra*), PLU (*Plumata*), RAC (*Racemosae*), REP (*Repantia*), RHY (*Rhytionanthos*), SES (*Sestochilus*), SAU (*Saurocephalum*), STA (*Stachysanthes*), and TRI (*Trias*).



Supplementary file 6.3. The majority-rule tree resulting from Bayesian inference analysis based on psbA-trnH sequence data. 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: BIF (Biflorae), BSC (Brachystachyae), DES (Desmosanthes), EPH (Ephippium), EPI (Epicrianthes), EUB (Eublepharon), HIR (Hirtula), ION (Ione), LEM (Lemniscata), LEO (Leopardinae), MAC (Macrocaulia), MNP (Monanthaparva), OXY (Oxysepala), PHY (Physometra), RAC (Racemosae), REP (Repantia), and SES (Sestochilus).