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Phanera godefroyi (Fabaceae: Cercidoideae), a newly recorded species for Thailand, based on morphological, palynological and molecular evidence

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ABSTRACT

Phanera godefroyi, previously only known from Cambodia, is recorded for Thailand. A full description of *Phanera godefroyi* is provided for the first time, based on fresh specimens with flowers and fruits, accompanied by colour photographs to assist identification, added are notes on its ecology, phenology, and taxonomy. Evidence from nuclear (ITS) and chloroplast data (*trnK*/*matK*, the *trnL* intron and *trnL–F* spacer) in our phylogenetic study suggests that the species is sister to *P. curtisii* and *P. scandens*. In addition, pollen morphology examined with Light and Scanning Electron Microscopes supports the recognition of the species by its typical combination of palynological characters, like the prolate spheroidal shape, colpi with granules, a distinctly thickened annulus around the endoaperture areas, and a rugulate ornamentation of the exine.

KEYWORDS: *Bauhinia*, Khao Ta Ngok, molecular phylogeny, pollen, Sa Kaeo

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INTRODUCTION

Phanera Lour., a formerly heterogeneous genus in the subfamily Cercidoideae, comprises 70–80 species, distributed in South Asia and Malesia. It was recently circumscribed by Sinou *et al.* (2009, 2020), Mackinder & Clark (2014), the Legume Phylogeny Working Group (LPWG, 2017) and Clark *et al.* (2017). According to Sinou *et al.*'s (2020) phylogeny-based circumscription, the typical morphological features of *Phanera* are a combination of emarginate or bilobed leaves, elongated hypanthia, and indehiscent or tardily dehiscent, laterally compressed, oblong fruits with distinctly funicled seeds.

The relationship amongst *Phanera*, *Bauhinia* Plum. ex L. and *Lasiobema* (Korth.) Miq. has long been debated due to their diverse morphological characters, such as variation in habit (shrubs, trees or woody climbers), leaf apices acute or bifid, calyx lobed or spathaceous, and stamen numbers ranging from 1–10. Based on molecular studies (Lai *et al.*, 1997, Bruneau *et al.*, 2001, 2008; Hao *et al.*, 2003; Sinou *et al.*, 2009 and Mackinder & Clark, 2014), *Phanera* is recognised as a distinct segregate genus from *Bauhinia s.str.* characterised from *Bauhinia s.str.* by being lianas or scandent shrubs (vs trees or shrubs in *Bauhinia s.str.*), calyx spitting into lobes (vs spathaceous) and 3 fertile stamens only (1, 3, 5 or 10 in *Bauhinia s.str.*). However, the paraphyletic genus *Lasiobema* was embedded in *Phanera*. Therefore, recently, Sinou *et al.* (2020) included *Lasiobema* in *Phanera* and broadened the generic concept of the latter genus. Species previously placed as *Lasiobema* are lianas with tendrils and three fertile stamens and, together with the other *Phanera* species, they form a uniform *Phanera s.str.*

According to earlier palynological studies (Larsen, 1974, as *Bauhinia*; Santos *et al.*, 2012, as *Bauhinia* and *Phanera*; Banks *et al.*, 2014; Bank & Lewis, 2018), the pollen of *Phanera* is heteromorphic, showing variation in exine ornamentation,

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aperture patterns and grain size. The pollen grains of the genus *Bauhinia s.l.* investigated from samples of Thailand and neighbouring countries can be classified into 15 pollen types based on the sexine structure (Larsen, 1974). A further refinement was provided by Banks *et al.* (2014), within *Phanera* (incl. *Lasiobema*). They also showed that the pollen morphological characters in *Phanera* and *Bauhinia s.str.* are diverse with a high degree of specialisation in surface ornamentation, wall structure and aperture type. Six distinct pollen types of the Asian *Phanera* species were recognised by Banks *et al.* (2014), who combined pollen morphology with the molecular phylogenetic framework derived from Sinou *et al.* (2009). The pollen types were classified using mainly by pollen shapes (prolate to subprolate, spheroidal and oblate), aperture type (tricolporate, syncolporate, triporate and tripororate), ornamentations (spinose, microperfoate, microreticulate–rugulate, psilate) and presence of granular aperture membranes.

In 2021, field investigations were conducted at Khao Ta Ngok limestone outcrop in Sa Kaeo Province (Thailand), near the Thai–Cambodian border. An unknown woody climber species, appearing to be a *Phanera*, was found. It had long inflorescences, a few remaining flowers and young fruits and was found amongst other species in the same genus, *P. bracteata* Benth. and *P. harmsiana* (Hosseus) Bandyop. & Ghoshal. Initially, the species was tentatively identified as *P. harmsiana* var. *media* (Craib) Bandyop. & Ghoshal, as it was a woody climber with elongated infructescences. In following years, more material was collected at the original site. A thorough investigation, including examination of literature and herbarium and digitalised specimens (see below), revealed that the species was not *P. harmsiana* var. *media*, but rather *P. godefroyi* (Gagnep.) Bandyop. & Anand Kumar, then considered to be endemic to Cambodia (Gagnepain, 1912; Larsen *et al.*, 1980; Bandyopadhyay & Kumar, 2024). Therefore, it is a newly recorded species for Thailand. We analysed the phylogenetic position of the new record based on nuclear (ITS) and chloroplast evidence (*trnK*/*matK*, the *trnL* intron and *trnL–F* spacer). Furthermore, we also provide the pollen morphological traits using Light Microscope (LM) and Scanning Electron Microscope (SEM).

MATERIAL AND METHODS

MOLECULAR WORK

Taxon sampling, DNA extraction, PCR amplification and sequencing

Four species in two genera were newly sampled for our analyses (Appendix 1), DNA was isolated from silica–dried leaf fragments using the standard CTAB method (Doyle & Doyle, 1987). In total 162 sequences (*trnK*/*matK*: 61; the *trnL* intron and *trnL–F* spacer: 60; ITS: 41), representing 14 accepted genera with 70 species of the subfamily Cercidoideae, were compiled from Genbank (https://www.ncbi.nlm.nih.gov/genbank/) for this study. Of these, 121 sequences (both ITS and *trnK*/*matK*) belonging to 21 accepted species of *Phanera* were included. *Cercis* species were selected as outgroup based on previous studies (Lai *et al.*, 1997; Bruneau *et al.*, 2001, 2008; Hao *et al.*, 2003; Sinou *et al.*, 2009, 2020; Gu *et al.*, 2024).

Four loci, the nuclear ribosomal internal transcribed spacer (ITS), and the chloroplast markers *trnK*/*matK*, the *trnL* intron and *trnL–F* spacer, were selected as representatives for the analyses. The nuclear ribosomal ITS regions (ITS1, ITS2, and 5.8S) were amplified using the primers ITS1 (forward) and ITS4 (reverse) (Taberlet *et al.*, 1991). For *trnK*/*matK*, we used the primers *trnK*-685F (forward) and *trnK*-2R (reverse) (Hu *et al.*, 2000). PCR amplifications were performed in 25 µL reaction volumes, which included 12.5 µL of 2x Phire Plant Direct PCR Master Mix (Thermo Scientific, Lithuania), 0.5–1 µL of bovine serum albumin (BSA), and 0.5–1 µL of DMSO and 0.9 µL of each primer, with the final volume adjustment with nuclease–free water (Thermo Scientific, Lithuania). One or two microlitres of DNA template were used for each reaction. The PCR cycling program for the ITS regions was set an initial denaturation step at 95°C for 3 mins, followed by 35 cycles of denaturation at 94°C for 30s, annealing at 59°C for 1 min, and extension at 72°C for 1.30 min with a final extension at 72°C for 7 mins, and those for the *trnK*/*matK* were 95°C for 3 min, followed by 35 cycles of 95°C for 30 s, 52°C for 40 s, and 72°C for 1 min and at 72°C for 5 min for a final extension. Following electrophoresis on 1.5% agarose gels and ethidium bromide staining, the amplified DNA fragments were

inspected. The PCR products underwent sequencing at Celemics Inc., Korea, via barcode–tagged sequencing, and at the Tsingke Company, Beijing, China, using Fast Next Generation Sequencing (FastNGS) technology. Newly generated sequences from this study and additional taxon sequences of the subfamily Cercidoideae obtained from GenBank are listed in Appendix 1.

Sequence alignment and phylogenetic analyses

Multiple alignments of each marker, ITS, *trnK*/*matK*, the *trnL* intron and *trnL–F* spacer, were independently aligned using MAFFT via XSEDE (7.505) via the CIPRES gateway V.3.3 (https://www.phylo.org; Miller *et al.* 2010). Per marker, an aligned matrix was then manually edited in Bioedit (Hall, 1999) before being amalgamated using Mesquite (Maddison & Maddison, 2011). The concatenated datasets of ITS, *trnK*/*matK*, the *trnL* intron and *trnL–F* spacer were phylogenetically analysed using Maximum-likelihood (ML), and Bayesian interference (BI) approaches. ML analysis was performed via RAxML–HPC2 on XSEDE version 8.2.12 (Stamatakis, 2014) on the CIPRES Gateway (Miller *et al.*, 2010) with 1,000 bootstrap replications per analysis. For BI analysis, best–fit evolutionary models calculated under the Bayesian information criterion (AIC) were GTR+I+G using jModelTest2 on XSEDE (Darriba *et al.*, 2012; Guindon and Gascuel, 2003). The analysis was then independently run using MrBayes on XSEDE (version 3.2.7a) (Ronquist *et al.*, 2012) via the CIPRES Gateway. Two simultaneous runs were performed each with four Markov Chain Monte Carlo (MCMC) chains, running for 10,000,000 generations with sampling every 1,000 generations. The initial 25% of the sampled data were discarded as burn–in prior to calculating a 50% majority–rule consensus tree. To check convergence, we inspected the effective sample size (ESS) values > 200 from the .P files using Tracer v.1.7.2 (Rambaut *et al.*, 2018). The 50% majority rule consensus tree based on the Bayesian analysis with branch lengths, posterior probability (PP) values cooperated with bootstrap values (BS) of the ML analysis, was visualised and annotated in FigTree version 1.4.4 (Rambaut & Drummond, 2012).

TAXONOMY

Morphology, identification and nomenclature

Taxonomic keys and descriptions from previous studies on the genus *Bauhinia s.l.* were consulted, specifically those by Larsen *et al.* (1980, 1984), and Hou *et al.* (1996). Herbarium specimens were checked in BK, BKF, CMU, KKU, PSU and QBG (acronyms follow Thiers, continuously updated). The generic delimitation followed Sinou *et al.* (2020). Careful comparison with digitised specimens of morphologically similar species was performed with online databases, namely Plants Of the World Online (https://powo.science.kew.org/), Leiden herbarium (https://bioportal.naturalis.nl/) and the Paris herbarium (https://science.mnhn.fr/institution/mnhn/collection/p/item/search/form?lang=en_US).

The morphological study was based on fresh materials. The flowers were dissected, photographed and measured under a Leica stereomicroscope with software apparatus Las 4.12.0. The terms used in the species description followed Beentje (2016).

PALYNOLOGICAL STUDY

Pollen material was acetolysed (Erdtman, 1960). For LM study, qualitative traits (e.g. polar and equatorial views, and exine ornamentation) were observed and photographed under a Leica microscope with software apparatus Las 4.12.0. At least 11 pollen grains were used for quantitative characteristics, namely pollen size, the length of the polar and equatorial axes and P/E ratio, mesocolpi and pores. For SEM analysis, acetolysed pollen was retained in 100% ethanol. The pollen material is then pipetted onto an aluminum foil to allow for air drying. Dried pollen grains were mounted onto metal stubs with a two–sided carbon adhesive tape followed by sputter–coating with gold using the Cressington 108auto sputter coater. SEM micrographs were viewed and photographed using a LEO 1450VP Scanning microscope at Faculty of Science, Khon Kaen University, Thailand. Pollen morphology terms in this study followed Erdtman (1969) and Hesse *et al.* (2009).

RESULTS AND DISCUSSION

PHYLOGENETIC ANALYSES

The phylogenetic trees obtained via ML and BI analyses yielded congruent topologies. Therefore, we present the tree that was generated based upon the BI analyses, with the corresponding ML bootstrap (BS) and posterior probability (PP) values indicated above the branches (Fig. 1). Generally, the tree is largely aligned with those from recent molecular phylogenetic studies by Sinou *et al.* (2009 & 2020) and Gu *et al.* (2024). Our phylogeny (Fig. 1) shows that *P. godefroyi* forms a well-supported clade with *P. curtisii* and *P. scandens* (L.) Lour. ex Raf. (BS: 81; PP: 0.96), well nested within the *Phanera* clade (Fig. 1). Apomorphic characters shared between *P. godefroyi* and its two sister species are elongated inflorescences with numerous small flowers, the presence of a floral disc and three fertile stamens. However, *P. godefroyi* is characterised by its bifid leaf only (vs mixed with entire to emarginate or bifid in *P. curtisii* and *P. scandens*), leaves having 8–12 veins arising from the base (vs 5–7 in *P. curtisii* and 7–9 in *P. scandens*), petals orbicular or ovate, 5–6 mm long (vs spathulate, 5–7 mm long in *P. curtisii* and obovate, 2–3 mm long in *P. scandens*), filaments 6–7 mm long (vs 4–5 mm long in *P. curtisii* and *P. scandens*) and absent staminodes (2 staminodes in *P. curtisii* and *P. scandens*).

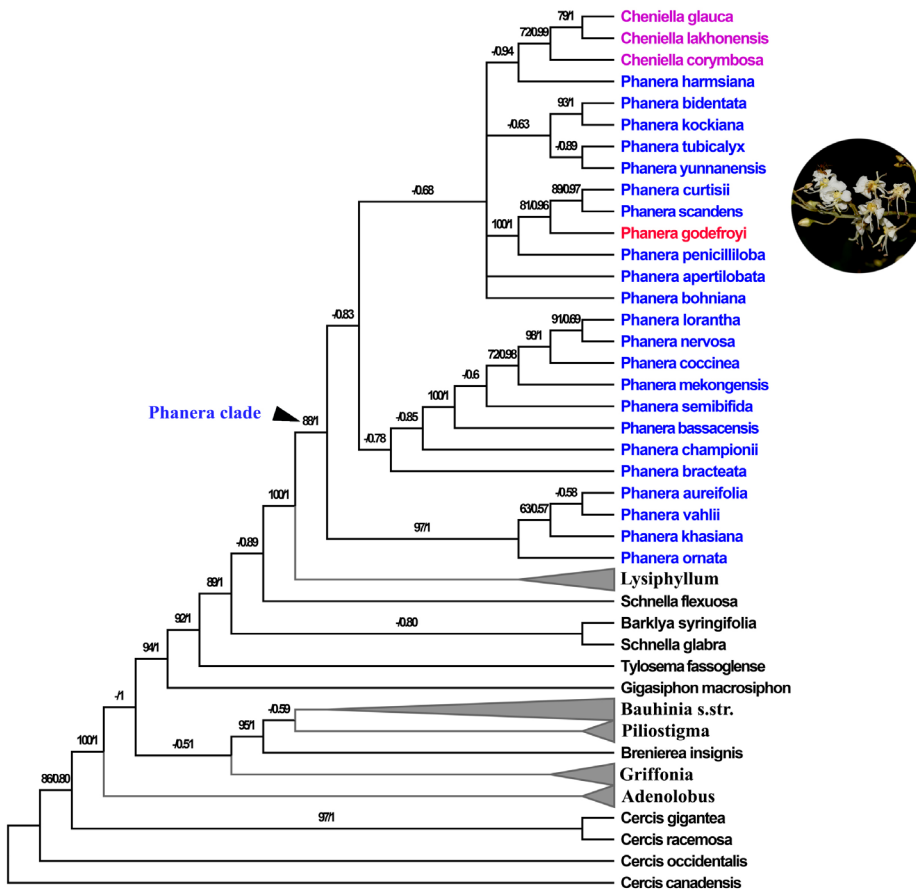

Figure 1. The 50 % majority–rule consensus tree of the concatenated dataset of three loci (*trnK*/*matK*, the *trnL* intron, *trnL–F* spacer and ITS) based on Bayesian Interference (BI) analysis, coinciding with the one based on Maximum Likelihood (ML) analysis. The newly recorded species, *Phanera godefroyi* (dark red), formed a sister to *P. curtisii* and *P. scandens*. Numbers above branches are the ML Bootstrap values (BS) and BI Posterior Probability (PP) values, respectively; values < 50 in ML and BI<0.50 are not shown. Flowers of *Phanera godefroyi* are shown (right).

According to our results, *P. harmsiana* is not part of *Phanera*, but sister to and perhaps part of the genus *Cheniella* R.Clark & Mackinder, which is in accordance with Sinou *et al.* (2020). A further discussion on the phylogenetic placement of *Phanera harmsiana* was provided by Gu *et al.* (2024).

TAXONOMY

Phanera godefroyi (Gagnep.) Bandyop. & Anand Kumar, Phytotaxa 642(4): 295. 2024.— *Bauhinia godefroyi* Gagnep., Notul. Syst. (Paris) 2: 278. 1912. Type: Cambodia, Mts de Pursat, 18 June 1875, *Godefroy 476* (lectotype **P** [P00798544!], first–step designated by Larsen *et al.* (1980), second–step designated by Bandyopadhyay & Anand Kumar (2024); isolectotypes **K** [K000760824!], **P** [P00798543!]). (Fig. 2).

Liana, ca 10 m long; tendrils opposite; young twigs puberulous. *Leaves* simple, bifid, spirally arranged, coriaceous; petioles 2–3.5 cm long, moderately puberulous; lamina ovate to orbicular, 9–11.5 by 4.5–5.5 cm, apically bifid to 1/4–1/5 of lamina length with a narrow sinus, lobes ovate, tip of lobes acute to rounded, margin entire, base cordate, 8–12-veined from base; upper surface glabrous; lower surface sparsely puberulous; stipules early caducous (not seen). *Inflorescences* axillary and terminal racemes, elongated, unbranched, slender, 10–18 cm long, axis moderately puberulous. *Infructescences* 23–37 cm long. *Pedicels* 13–15 mm long, densely puberulous; bracts lanceolate, ca 3 by 0.8 mm, apex acuminate, caducous, outer surface densely puberulous, inner surface glabrous; bracteoles inserted at middle or slightly higher of pedicel, opposite or subopposite, lanceolate, ca 1.5 by 0.2 mm, caducous, apex acuminate, outer surface puberulous, inner surface glabrous. *Buds* oval, 3–6 mm long, puberulous, apex acute. *Hypanthium* short, ca 2 mm long, puberulous. *Calyx* 5–lobed, splitting into 2 segments; lobes lanceolate, 4.5–5 by ca 2 mm, apex acute, margin puberulous, outer surface puberulous, inner surface glabrous. *Petals* 5, white, upper lobes slightly larger, orbicular or ovate, 5–6 by 5.5–6 mm, apex acute, margin undulate, crisped, outer surface densely silky along median veins, otherwise glabrous, claw of petals 0.5–1 mm long, flattened. *Fertile* stamens 3; filaments 6–7 mm long; anthers oblong, ca 2 by 1 mm, dehiscing by longitudinal slits, dorsifixed, white. *Staminodes* absent. *Floral disk* ca 1 mm high, yellow. *Ovary* glabrous, 6–8-ovuled; stipe ca 2 mm long; style short, 2.5–3 mm long, glabrous, emerging laterally from the disk; stigma capitate with a few hairs. *Pods* elliptic to obovate or slightly oblong, flattened, 3–6 by 1.5–2 cm, glossy, dehiscent, glabrous, 1–3-seeded. *Seeds* flattened, orbicular, 1–1.3 cm diam, hilum crescentic, glabrous, shiny, dark brown, thin-valved.

Thailand.— SOUTH–EASTERN: Sa Kaeo, Khlong Hat, Khao Ta Ngok, alt. 240 m, 29 July 2022 (flowers & fruits), *P. Phonsena 7537* (BKF!); ibid., 17 Sept. 2022 (fruits), *P. Phonsena 7540* (BKF!); ibid., 17 Sept. 2023 (flowers), *P. Phonsena 7544* (BKF!).

Distribution.— Cambodia (Pursat Province, type).

Habitat and Ecology.— On limestone outcrop in association with other species from the same genus, *P. bracteata*, *P. harmsiana* var. *harmsiana* and *P. curtisii*.

Phenology.— Flowering July to September, fruiting September to July.

Notes.— We report this species as a new record for Thailand, previously believed to be restricted to Cambodia. The species was initially described by Gagnepain (1912), within the genus *Bauhinia*, based on the collection *M. Godefroy 476*. In fact, the species is now rediscovered as no new collections were made during the 146 years since the type was collected. Our phylogenetic analyses support the transfer of the species to the genus *Phanera*, which is in agreement with Bandyopadhyay & Kumar (2024).

The fruit of *P. godefroyi* was not described in the original description by Gagnepain (1912) and also not in pertinent literature, such as Larsen *et al.* (1980).

PALYNOLOGY

Phanera godefroyi (Fig.3).

LM.— Pollen grains medium to large sized, 42.08–52.44 μm (polar axis), 37.73–50.26 μm (equatorial exis), isopolar, radially symmetric, tricolporate, rarely 4–colporate, prolate spheroidal (P/E x 100); mesocolpi convex, 32.36–38.40 μm long for 3–colporate pollen, 10.42–15.23 μm long

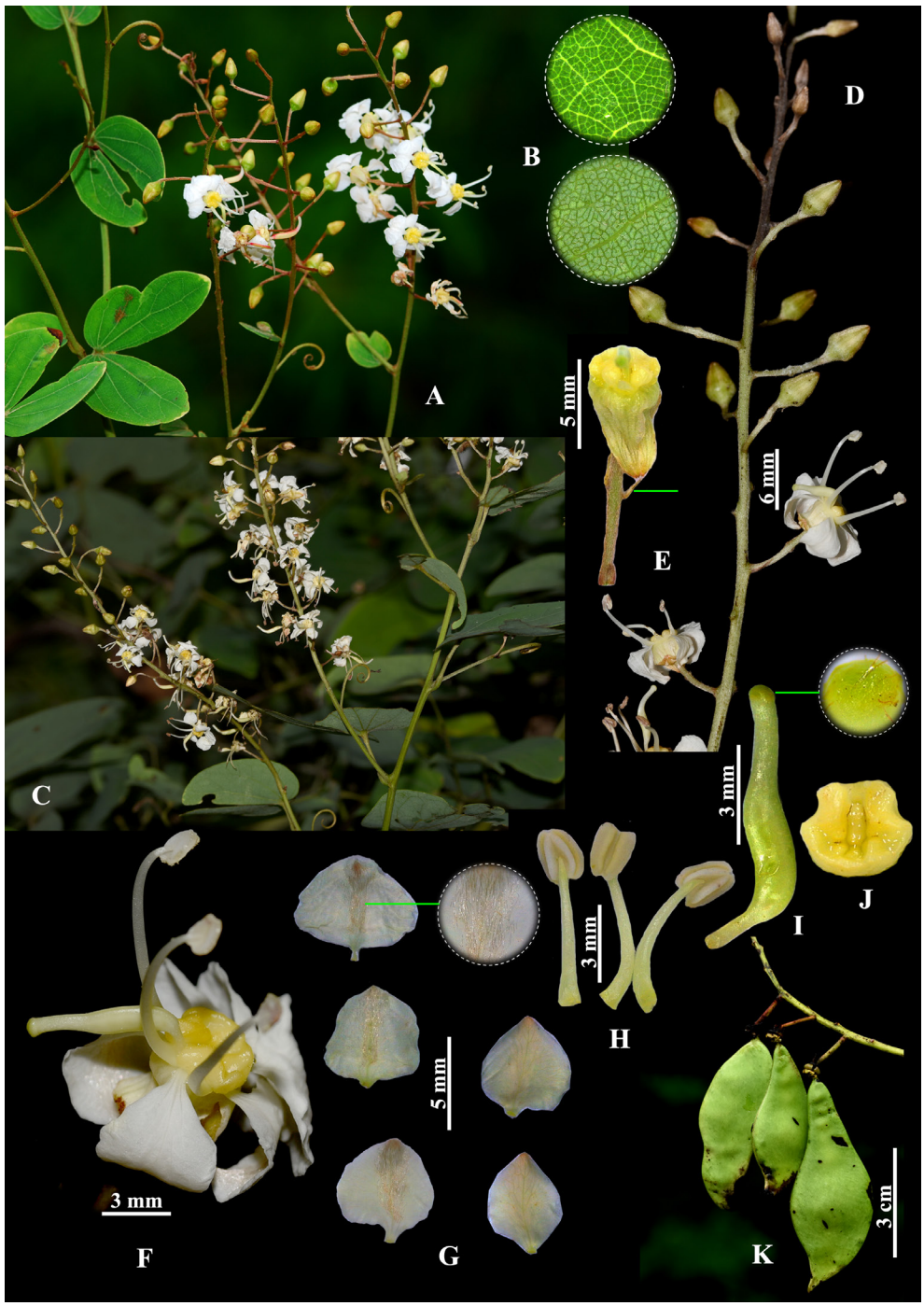

Figure 2. Photographs of *Phanera godefroyi* (Gagnep.) Bandyop. & Anand Kumar. A. Leaves and inflorescences; B. upper surface of leaf (upper) and lower surface of leaf (lower); C. Close up of inflorescences; D. Part of inflorescence; E. Calyx after anthesis (petals and stamens removed) showing bracteoles in a side view (green arrow); F. Close up of flower; G. Petals: outer surface with close up of hairs (left column;) and inner surface (right column); H. Fertile stamens; I. Ovary; J. Floral disc; K. Fruits. Photos by Phongsak Phonsena.

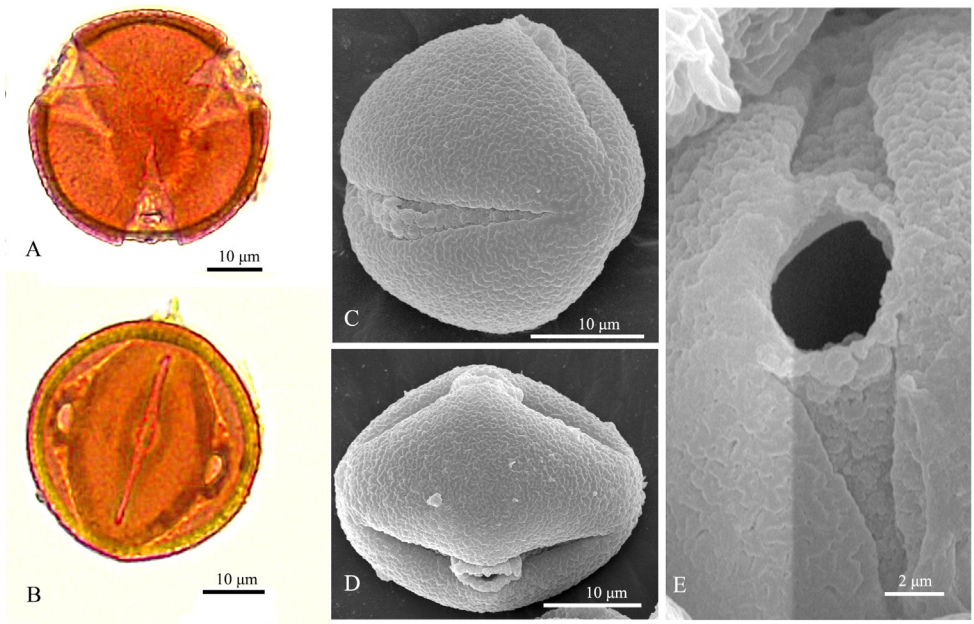

Figure 3. Pollen grains of *Phanera godefroyi* (Gagnep.) Bandyop. & Anand Kumar. A. Polar view (LM); B. Equatorial view (LM); C. Subpolar view showing the fusiform colpus (SEM); D. Equatorial view with an annulus around the endoaperture and rugulate exine in mesocolpi (SEM); E. Pore with a granular aperture membrane along the colpus (SEM). Photos by Boonsong Kongsook.

for 4–colporate ones; colpi 30.60–39.18 µm long, shallowly deep, fusiform; pori circular to semi–circular, 5.26–9.01 µm in diameter.

SEM.— Exine sculpture of mesocolpi rugulate; colpi granular, with a distinctly thickened annulus around the endoaperture areas.

The pollen of *Phanera godefroyi* belongs to the *curtisii* type (Larsen, 1974) or Group I of *Lasiobema* and Asian *Phanera* pollen group (Banks *et al.*, 2014). Within the group, *Phanera godefroyi* is distinct by its 3–colporate, rarely 4–colporate and distinct annulus.

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Appendix 1. List of species obtained from GenBank and newly generated sequences. The information of each species is provided as follows: collector and collection number (herbarium code), NCBI accession numbers of each marker *trnK/matK*, the *trnL* intron/*trnL–F* intergenic spacer and ITS respectively separated by colon, and country with relevant information. An en–dash (–) indicates missing data. An asterisk "*" represents newly sequenced in this study. The species name listed are based on POWO and the most update papers.

Adenolobus garipensis (E.Mey.) Torre & Hillc., *Leistuer et al. 246* (K), JN881352.1: *Leistuer et al. 246* (K), FJ801157.1: *Leistuer et al. 246* (K), KY306484.1, –; ***Adenolobus pechuelii*** (Kuntze) Korcz. & Hillc., *Oliver et al. 6527* (K), JN881353.1: *Oliver et al. 6527* (K) FJ801158.1: –, –, –; ***Barklya syringifolia*** F.Muell., *Weston 2449* (NSW), JN881354.1: *Weston 2449* (NSW), FJ801070.1: –, –, –; ***Barklya syringifolia***, –, –: –, –: –, AY258398.1, –; ***Bauhinia acreana*** Harms, *Nee 34983* (USF), JN881357.1: –, –: –, –, –; ***Bauhinia acuminata*** L., –, –: *Lawrence s.n.* (BH), KT461938.1: –, –, –; ***Bauhinia acuminata***, –, –: –, –: –, JX856405.1, –; ***Bauhinia apertilobata*** Merr. & F.P.Metcalf, *s.coll. SCBGP462_1* (–), KP094035.1: –, –: –, –, China, Dinghushan National Nature Reserve; ***Bauhinia apertilobata***, –, –: –, –: –, AY258398.1, –; ***Bauhinia bauhinioides*** (Mart.) J.F.Macbr., *Mereles 3862* (USF), JN881360.1: *Mereles 3862* (USF), FJ801107.1: –, –, –; ***Bauhinia × blakeana*** Dunn, *Fougere-Danezan 15* (MY), JN881361.1: *Fougere-Danezan 15* (MT), FJ801115.1: –, –, –; ***Bauhinia × blakeana***, –, –: –, –: –, AF387971.1, –; ***Bauhinia bohniana*** H.Y.Chen, –, –: *Douglas 766* (MEL), FJ801052.1: –, –, –; ***Bauhinia bohniana***, –, –: –, –: –, AY258403.1, –; ***Bauhinia brachycarpa*** Wall. ex Benth., *Douglas 766* (MEL), JN881433.1 –, –: –, –, –; ***Bauhinia brachycarpa***, –, –: –, GQ327972.1: –, –, –; ***Bauhinia brachycarpa***, –, –: –, –: –, FJ432276.1, –; ***Bauhinia brevicalyx*** Du Puy & R.Rabev., *Razafitsalama 945* (MO), JN881362.1: *Razafitsalama 945* (MO), FJ801136.1: –, –, –; ***Bauhinia cheilantha*** (Bong.) Steud., *s.coll. HUEFS43147* (–), MT370775.1: –, –: –, –, –; ***Bauhinia cheilantha***, –, –: –, –: *s.coll. FS3188* (–), DQ787410.1, –; ***Bauhinia lunarioides*** A.Gray ex S.Watson, *Rushforth KR0566* (K), JN881374.1: *Rushforth KR0566* (K), FJ801141.1: –, –, –; ***Bauhinia macranthera*** Benth. ex Hemsl., *Bridges 13138* (NY), JN881375.1: *Bridges 13138* (NY), FJ801063.1: –, –, –; ***Bauhinia macranthera***, –, –: –, –: *Schoenfeld & Fairey T72M64S* (UC), JN942381, –; ***Bauhinia mollis*** (Bong.) D.Dietr., *Kajita 94122909* (TUS), JN881377.1: *Kajita 94122909* (TUS), FJ801096.1: –, –, –; ***Bauhinia monandra*** Kurz, *Bruneau AB1385* (MT), JN881378.1: *Bruneau AB1385* (MT), FJ801127.1: –, –, –; ***Bauhinia monandra***, –, –: –, –: *Aramide 154* (LUH), KX057835.1, –; ***Bauhinia petersiana*** Bolle, *Fairchild Tropical Garden 86183* (–), JN881383.1, *Fairchild Tropical Garden 86183* (–), FJ801089.1, –, –, –; ***Bauhinia phoenicea*** B.Heyne ex Wight & Arn., *Klackenberg 364b* (K), JN881384.1: *Klackenberg 364b* (K), FJ801151.1: –, –, –; ***Bauhinia picta*** (Kunth) DC., *Devia 3205* (MO), JN881385.1: *Devia 3205* (NY), FJ801068.1: –, –, –; ***Bauhinia pottsii*** G.Don, *Herendeen 27-IV-99-9* (US), JN881388.1: *Herendeen 27-IV-99-9* (US); FJ801077.1: –, –, –; ***Bauhinia pulchella*** Benth., *Anderson 9373* (USF), JN881390.1: *Anderson 9373* (USF), FJ801097: –, –, –; ***Bauhinia purpurea*** L., *Redden 3736* (US), KX538425.1: –, –: –, –, –; ***Bauhinia purpurea***,–, –: *Wieringa 4179* (WAG), FJ801069: –, –, –;

Appendix 1. Continued.

Bauhinia purpurea, –, –: –, –: *s.coll. BP2* (–), JX856407.1, –; ***Bauhinia ramosissima*** Benth. ex Hemsl., *Stewart 9366* (USF), JN881393.1, *Stewart 9366* (USF), FJ801101, –, –, –; ***Bauhinia rufescens*** Lam., –, –: *Gillis 9498* (USF), FJ801082, –, –, –; ***Bauhinia rufescens***, –, –: –, –: *s.coll. 5124* (LUH), KX057837.1, Nigeria; ***Bauhinia ungulata*** L., *BioBot00200* (–), JQ587517.1: –, –: –, –, Costa Rica, Area de Conservacion Guanacaste, Sector Santa Rosa, Bosque San Emilio; ***Bauhinia ungulata***, –, –: *Araujo 1569* (HUEFS), FJ009873.1: *Araujo 1569* (HUEFS), FJ009818.1, –; ***Bauhinia variegata*** L., *Abbott 24907* (FLAS), GU135033.1: –, –: –, –, –; ***Bauhinia variegata***, –, –: *Hansen 5178* (USF), FJ801081.1: –, –, –; ***Bauhinia variegata***, –, –: –, –: –, AY258378.1, –; ***Brenierea insignis*** Humbert, *Du Puy M430* (K), JN881409.1: *Du Puy M430* (K), FJ801159.1: –, –, –; ***Cercis canadensis*** L., *Stevees s.n.* (MT), KX161997.1: –, –, –, –, –; ***Cercis canadensis***, –, –: *Nickerson St. Austin Texas 2108* (–), AF430768.1: –, –, USA; ***Cercis canadensis***, –, –: –, –, *s.coll. 980329* (–), JQ425127.1, USA, North Carolina State University; ***Cercis gigantea*** Cheng & Keng f., *Herendeen 1-V-2003-10* (US), JN881412.1: *Herendeen 1-V-2003-10* (US), FJ801164.1: –, –, –; ***Cercis occidentalis*** A. Gray, *Wojciechowski 873* (ASU), JN881413.1: *Wojciechowski 873* (ASU), FJ801156.1: –, –, –; ***Cercis racemosa*** Oliv., *Herendeen 1-V-2003-7* (US), AY386947.1: *Herendeen 1-V-2003-7* (US), FJ801160: –, –, –; ***Cercis racemosa***, –, –, –, *1980 Sino-American Botanical Expedition s.n.* (–), JN942390, –; ***Cheniella corymbosa*** (Roxb. ex DC.) R.Clark & Mackinder, *Fantz 3150* (FTG), JN881436.1: *Fantz 3150* (FTG), FJ801085.1: –, –, –; ***Cheniella glauca*** (Benth.) R.Clark & Mackinder, *Du HNK2335* (K), JN881440.1: –, –: –, –, –; ***Cheniella glauca***, –, –: *s.coll. Bau12* (BKF), MT498358.1: *s.coll. Bau12* (BKF), MT498358.1, Thailand; ***Cheniella lakhonensis*** (Gagnep.) R.Clark & Mackinder, *Mattapha s.n.* (BKF) PQ536961*–, –: *Mattapha s.n.* (BKF), PQ400067*, Thailand, Udon Thani, near Sampraow Campus in the south; ***Cheniella lakhonensis***, –, –: *s.coll. Bau16* (BKF), MT498359.1: –, –, Thailand; ***Cheniella tourannensis*** (Gagnep.) R.Clark & Mackinder, *Mengsong 145_9_8* (HITBC), HG004926.1: –, –: *Mengsong 145_9_8* (HITBC), HG004808.1, China, Yunnan; ***Gigasiphon macrosiphon*** (Harms) Brenan, *s.coll. ID1990-1508* (–), EU361953.1: –, –: –, –, –; ***Gigasiphon macrosiphon***, –, –: ID1990-1509 (K), FJ801108.1: –, –, –; ***Griffonia physocarpa*** Baill., *Van der Burgt 939* (K), JN881419.1: –, –: –, –, –; ***Griffonia physocarpa***, –, –: *Wieringa 4498* (WAG), FJ801166.1: –, –, –; ***Griffonia simplicifolia*** (Vahl ex DC.) Baill., *Daramola 546* (K), MN992866.1: –, –: –, –, –; ***Griffonia simplicifolia***, –, –: –, –: –, MH707248.2, –; ***Lysiphyllum binatum*** (Blanco) de Wit, *Hopkins 1729* (K), JN881424.1: *Hopkins 1729* (K), FJ801149.1: –, –, –; ***Lysiphyllum carronii*** (F.Muell.) Pedley, *Weston 2447* (NSW), JN881425.1: *Weston 2447* (NSW), FJ801054.1: –, –, –; ***Lysiphyllum carronii***, –, –: –, –: –, AY258401.1, –; ***Lysiphyllum cunninghamii*** (Benth.) de Wit, *Fairchild Tropical Garden 6805* (–), JN881426.1: F*airchild Tropical Garden 6805* (–), FJ801083.1: –, –, –; ***Lysiphyllum gilvum*** (F.M.Bailey) Pedley, *Weston 2446* (NSW), JN881427.1: *Weston 2446* (NSW), FJ801057.1: –, –, –; ***Lysiphyllum gilvum***, –, –: –, –: –, AY258401.1, –; ***Lysiphyllum hookeri*** (F.Muell.) Pedley, *Weston 2445* (NSW), JN881428.1: *Weston 2445* (NSW), FJ801059.1: –, –, –; ***Lysiphyllum winitii*** (Craib) de Wit, *s.coll. 2125* (K), JN881430.1: *s.coll. 2125* (K), FJ801152.1: –, –, –; ***Lysiphyllum winitii***, –, –: –, –: –, AY258402.1, –; ***Phanera aureifolia*** (K.Larsen & S.S.Larsen) Bandyop., Ghoshal & M.K.Pathak, *Herendeen 30-IV-99-2* (US), JN881431.1: –, –: –, –, –; ***Phanera aureifolia***, –, –: *s.coll. Bau09* (BKF), MT498356.1: *s.coll. Bau09* (BKF), MT515379.1, Thailand; ***Phanera bassacensis*** (Pierre ex Gagnep.) de Wit, –, –: *s.coll. BauPB* (BKF), MT498352.1: *s.coll. BauPB* (BKF), MT515375.1, Thailand; ***Phanera bidentata*** (Jack) Benth., *Stone 12643* (K), JN881432.1: *Stone 12643* (K), FJ801143.1: –, –, –; ***Phanera bracteata*** Benth., *Toyama et al. 930* (JPN), AB925116.1: –, –: –, –, Cambodia, Kampong Thom; ***Phanera bracteata*** Benth., –, –: *s.coll. Bau18* (BKF), MT498354.1: *s.coll. Bau18* (BKF), MT515377.1, Thailand; ***Phanera championii*** Benth., *SCBGP204_1* (–), KP093598.1: *SCBGP204_1* (–), –: –, –, –; ***Phanera championii***, –, –: –, –: *S.N. 975* (–), MG730636.1, –; ***Phanera coccinea*** Lour., *Du HNK3076* (K), JN881435.1–: –: –, –, –; ***Phanera coccinea***, –, –: *s.coll. BauPCSM* (–), MT498351.1: *s.coll. BauPCSM* (–), MT515374.1, Laos; ***Phanera curtisii*** (Prain) Bandyop. & Ghoshal, *Mattapha s.n.* (BKF) PQ550805*–, –: *Mattapha s.n.* (BKF), PQ400068*, Thailand, Loei, Kunming Mueang Loei; ***Phanera godefroyi*** (Gagnep.) Bandyop. & Anand Kumar, *Phonsena 7537* (BKF), PQ641244*: –, –: *Phonsena 7537* (BKF), PQ427445*, Thailand, Sa Kaeo, Khlong Hat, Khao Ta Ngok; ***Phanera harmsiana*** (Hosseus) Bandyop. & Ghoshal, –, –: *s.coll. Bau02* (–), MT498353.1: *s.coll. Bau02* (–), MT515376.1, Thailand; ***Phanera khasiana*** (Baker) Thoth., –, –: *Sugong WS-1940* (MO), KT461972.1: –, –, –; ***Phanera khasiana***, –, –: –, –: –, AY258381.1, –; ***Phanera kockiana*** (Korth.) Benth., *s.coll. KR1756* (–), MG816812.1: –, –: –, –, Indonesia, Jambi, Bukit Duabelas National Park; ***Phanera kockiana***, –, –: *s.coll. BauBK* (BKF), MT498355.1: *s.coll. BauBK* (BKF), MT515378.1, Thailand; ***Phanera mekongensis*** Mattapha, Suddee & Duangjai, –, –: *s.coll. BauWC* (BKF), MT498350.1: *s.coll. BauWC* (BKF), MT515373.1, Thailand, Bueng Kan, Phuwua Wildlife Sanctuary; ***Phanera nervosa*** Benth., *Mengsong 145_5_4* (HITBC), HG004910.1: –, –: –, –, China, Yunnan, Mengsong; ***Phanera nervosa***, –, –: –, –: –, AY258399.1, –; ***Phanera ornata*** (Kurz) Thoth., *Larsen 45006* (K), KT461982.1: –, –: –, –, –; ***Phanera ornata***, –, –: *Du et al. HNK3122/CS40* (MT), KT461960.1: –, –, –; ***Phanera penicilliloba*** (Pierre ex Gagnep.) Sinou & Bruneau, *Larsen et al. 31900* (K), JN881422.1: *Larsen et al. 31900* (K), FJ801138.1: –, –, –; ***Phanera saigonensis*** (Pierre ex Gagnep.) Mackinder & R.Clark, *Fougere-Danezan 16* (MT), JN881396.1: *Fougere-Danezan 16* (MT), FJ801114.1: –, –, –; ***Phanera scandens*** (L.) Lour. ex Raf., *Larsen 4505* (–), JN881423.1: –,–: –, –, –; ***Phanera scandens***, –, –: *s.coll. Bau14* (BKF), MT498357.1: –, –, Thailand; ***Phanera scandens***, –, –: –, –: –, AY258408.1, –; ***Phanera semibifida*** (Roxb.) Benth., *s.coll. KR1340* (–), MG816802.1: –, –: –, –, Indonesia, Jambi, Bukit Duabelas National Park; ***Phanera semibifida***, –, –: *s.coll. AS026* (–), KU853204.1: –, –, –; ***Phanera semibifida***, –, –: –, –: *s.coll. 102* (–), OL579732.1, Indonesia, West Sumatra; ***Phanera tubicalyx*** (Craib) Bandyop. & Ghoshal, *Tragoolsri s.n.* (BKF), PQ550806*: –, –: –, –, Thailand, Krabi, Mueang district, Saithai subdistrict, Ao Nammao village; ***Phanera vahlii*** (Wight & Arn.) Benth., *Gillis 6882* (FTG), JN881452.1: –, –: –, –, –; ***Phanera vahlii***, –, –: *Gillis 7882* (FTG), FJ801090.1: –, –, –; ***Phanera yunnanensis*** (Franch.) *Wunderlin, Hart s.n.* (FTG), JN881453.1: –, –: –, –, –; ***Phanera yunnanensis***, –, –: *Hart s.n.* (USF), FJ801084.1: –, AF286360.1, –; ***Piliostigma reticulatum*** (DC.) Hochst., –, –: *s.coll. 426* (LUH), KX268205.1: *s.coll. 426* (LUH), KX057894.1, ***Nigeria; Piliostigma thonningii*** (Schumach.) Milne-Redh., –, –: –, –: Mwaura & Mbale, *NMK EA 13630* (–), –, Kenya; ***Piliostigma thonningii***, –, –: *s.coll. 5181* (LUH), KX268206.1: –, –, Nigeria; ***Schnella flexuosa*** (Moric.) Walp., *Lewis 1866* (K), JN881438.1: *Lewis 1866* (K), FJ801150.1: –, –, –; ***Schnella glabra*** (Jacq.) Dugand, *Redden 1038* (US), JN881439.1: –, –: –, –, –; ***Schnella glabra***, –, –: *Redden 1040* (US), FJ801116.1: –, –, –; ***Schnella glabra***, –, –:–, –: –, AY258409.1, –; ***Tylosema fassoglense*** (Kotschy ex Schweinf.) Torre & Hillc., *s.coll. 79-393* (FTG), JN881458.1: –, –: –, –, –; ***Tylosema fassoglense***, –, –: *Herendeen 21-XII-97-6* (US), KF794201.1: –, –, –; ***Tylosema fassoglense***, –, –: –, –: –, AY258393.1, –;.