





Aglaia fellii W.E.Cooper & Joyce (Meliaceae), a new species for Cape York Peninsula

W.E. Cooper, D.M. Crayn & E.M. Joyce

Australian Tropical Herbarium, James Cook University

Ludwig-Maximilians-Universität München

Corresponding author: wendy@williamtcooper.com.au

E.M. Joyce  <https://orcid.org/0000-0001-8291-8058>; D.M. Crayn  <https://orcid.org/0000-0001-6614-4216>.



© Copyright of this paper is retained by its authors, who, unless otherwise indicated, license its content under a CC BY 4.0 license

Abstract

Aglaia fellii W.E.Cooper & Joyce (Meliaceae) is described from restricted areas of rainforest on Cape York Peninsula, Queensland, Australia. Given the unusual morphological features of the species, including solitary flowers and fruits, a molecular phylogenetic analysis was conducted to confirm its placement within *Aglaia* prior to formal description. All Australian *Aglaia* species and eight Australian representatives of closely allied Meliaceae genera were sampled, and 353 nuclear loci were sequenced. Maximum likelihood analysis of these loci retrieved *A. fellii* as nested within *Aglaia*, most closely related to *A. cooperae* and *A. monticola*. This validates its assignment to *Aglaia*, making it the only *Aglaia* species with mostly solitary flowers (rarely 3- or 4-flowered) and solitary fruits. A full taxonomic description of *Aglaia fellii* and notes on its habitat are provided.

Cite this paper as: Cooper WE, Crayn DM & Joyce EM (2023). *Aglaia fellii* W.E.Cooper & Joyce (Meliaceae), a new species for Cape York Peninsula. *Australian Journal of Taxonomy* 16: 1–9. doi: <https://doi.org/10.54102/ajt.p8to6>

Introduction

In July 2018, botanist David Fell collected a specimen (DGF IRRS284 BRI) of an unknown Meliaceae at Steve Irwin Wildlife Reserve (SIWR), Cape York Peninsula, Queensland, Australia. Further material was later collected in a different area of SIWR and on Bramwell Station (c. 14 km to the east) in 2020. The specimens exhibit many characters typical of *Aglaia* Lour. (Meliaceae), a genus of 126 species in Indomalaysia, Australia and the Western Pacific (Pannell 2013; Joyce *et al.* 2023a), with twelve species occurring in Australia (Cooper & Forster 2021). *Aglaia* species are small to large trees, generally characterised by imparipinnate leaves (with a few trifoliolate or simple-leaved species), an indumentum of compound hairs (including stellate scales, peltate scales

and stellate hairs), and small flowers arranged in axillary panicles on which up to several hundred fruits are borne (Pannell 1992).

While the specimens are consistent with *Aglaia* in having an indumentum of peltate scales and compound leaves, they also exhibit characters unusual or previously unknown in the genus such as solitary, trimerous flowers, a small tree habit, and small trifoliolate leaves. We conducted a morphological assessment and molecular phylogenetic analysis to resolve the relationships of this novelty and inform an appropriate taxonomic status and generic placement. The results confirm the entity is distinct and phylogenetically nested within *Aglaia*, and we therefore describe it as *Aglaia fellii* W.E.Cooper & Joyce.

This paper was submitted on 21 October 2022 and published on 19 March 2023 (2023-03-19T01:59:53.626Z). It was reviewed by Caroline Pannell and an anonymous reviewer, and edited by Kevin Thiele. *Australian Journal of Taxonomy*. ISSN: 2653-4649 (Online).

Methods

Molecular analysis

Fifteen *Aglaiia* samples were obtained for this analysis, including three individuals from across the range of the putative novelty and one sample from each accepted Australian species (Table 1). To test the hypothesis of relationship to *Aglaiia*, Australian representatives of *Chisocheton*, *Prasoxylon*, *Dysoxylum*, *Epicharis* and *Didymocheton* (following the revised taxonomy of Holzmeyer *et al.* 2021) were also sampled. Together with *Aglaiia*, these genera have been placed within the 'GA clade' of Meliaceae (Koenen *et al.* 2015; Holzmeyer *et al.* 2021; Joyce *et al.* 2023b). *Vavaea amicornum* Benth. was used as the outgroup based on the phylogenetic results of Koenen *et al.* (2015). Leaf material was field-collected and dried on silica gel for all taxa except *Aglaiia brownii* Pannell, *Chisocheton longistipitatus* (F.M.Bailey) L.S.Sm., *Didymocheton mollis* (Miq.) Holzmeyer & Hauenschild and *Epicharis parasitica* (Osbeck) Mabb., for which herbarium material was used.

Genomic DNA was extracted from 40 mg of dried leaf material using the CTAB protocol of Doyle and Doyle (1987). The protocol was modified at the isopropanol precipitation step, with samples left to precipitate at -20°C over 24 hours. DNA was eluted to a final volume of 60 µl, and quality and quantity were ascertained using a NanoDrop 1000 Spectrophotometer (Thermo Fisher Scientific, Massachusetts, USA) and Quantus Fluorometer (Promega Corporation, Wisconsin, USA).

DNA samples were fragmented enzymatically and libraries were prepared using the NEBNext Ultra II FS Library Prep Kit (New England Biolabs, Ipswich, MA, USA), following the manufacturer's instructions with inserts of approximately 350 bp. Capture pools were 12–16 plex. Pooled libraries were enriched using the Angiosperms353 probe kit (Johnson *et al.* 2019) by hybridising at 65°C with the Arbor Biosciences MyBaits Expert Plant Angiosperms353 v1 bait set with V5 chemistry (Cat. # 308108.v5) following the manufacturer's instructions. Sequencing was performed on a NovaSeq 6000 (Illumina Inc., San Diego, USA) at the Australian Genome Research Facility (Melbourne) with v1.5 chemistry and 150bp paired-end reads.

Sequence reads for 23 samples were obtained. Trimmomatic (Bolger *et al.* 2014) was used to remove adapter sequences, poor quality base calls and poor quality reads with the settings: illuminaclip 2:30:10, leading 30, trailing 30, sliding window 4:2:30 and minimum length 36. Exon sequences were assembled using the HybPiper v2 pipeline for the amino acid translation of nucleotide data using BLASTx (Johnson *et al.* 2016). Trimmed reads were mapped against the Meliaceae subset of the mega target file of McLay *et al.* (2021). The HybPiper exon output was then processed through HybPhaser v2 (Nauheimer *et al.* 2021), to generate consensus sequences and identify single nucleotide polymor-

phisms (SNPs). Summary statistics for all samples and loci were generated, and the dataset was optimised by removing loci with >80% missing samples, <55% target sequence length recovery, and outlying heterozygosity (> 1.5x the inter-quartile range for heterozygosity). In the final dataset, an average of 334 loci were retrieved with a mean target recovery of 90.29%.

HybPhaser consensus sequences (i.e. sequences including ambiguity codes) were aligned using MAFFT with the -auto flag to automatically select alignment strategy (Katoh and Standley 2013). Sites with >75% missing data were removed from the alignment using the -clean option in Phyutility (Smith and Dunn 2008), and exon alignments concatenated with AMAS (Borowiec 2016). A maximum likelihood tree was estimated from the clean alignment in IQ-TREE, with the appropriate substitution model and partitioning scheme for the alignment chosen using ModelFinder Plus option -MFP+MERGE (Lanfear *et al.* 2012; Nguyen *et al.* 2015; Kalyaanamoorthy *et al.* 2017; Hoang *et al.* 2018). Support was estimated using 1000 ultrafast bootstrap replicates in IQ-TREE.

Morphological study

Morphology was assessed through examination of herbarium material from BRI and CNS, as well as field observations. All specimens cited were seen by WEC or EMJ. Measurements of floral parts and fruits are based on material preserved in 70% ethanol as well as fresh material from the field.

Results

Molecular Analysis

The concatenated alignment of 353 loci comprised 257557 bp and 18056 parsimony-informative sites with 7.32% gaps or ambiguities. IQ-TREE identified the best partition scheme and merged the alignment into 19 partitions (LnL = -832664.736, df=235), all of which were allocated an optimal substitution model with the ModelFinder function of IQ-TREE. After 102 tree search iterations IQ-TREE produced a consensus tree with a log-likelihood of -832640.20 (Figure 1).

All sampled *Aglaiia* species were retrieved as monophyletic with maximum support. Previous studies have indicated that *Aglaiia* may not be monophyletic—section *Neoaglaiia* does not group with the rest of the genus (Grudinski *et al.* 2014; Koenen *et al.* 2015)—but representatives of *Neoaglaiia* do not occur in Australia and so were not included in the present analysis. Our results support the monophyly of sections *Amoora* and *Aglaiia*. The topology of *Aglaiia* is also in broad agreement with previous phylogenetic studies on the genus, with *A. spectabilis*, *A. meridionalis* and *A. australiensis* retrieved as sister to the rest of the Australian species in section *Amoora*, and *A. silvestris* and *A. argentea* retrieved in the same clade of section *Aglaiia* (Grudinski *et al.* 2014). However, the relationships of *A. elaeagnoidea*, *A. brownii*, *A. sapindina*, *A. ferruginea* and *A. cooperae* differ from

Table 1. Samples included in the phylogenetic analysis of Australian *Aglaiia* and related species to test the generic assignment of *Aglaiia fellii*.

Species	Collector name & no.	Source	Herbarium accession	SRA accession
<i>Aglaiia argentea</i>	Cooper, W. WWC 2348	Silica	FHO 00123761K	SRR21798429
<i>Aglaiia australiensis</i>	Forster 27615	Silica	AQ 0607797	SRR21798428
<i>Aglaiia brownii</i>	Champion, I.G. 2158	Herbarium	CNS 148263	SRR21798417
<i>Aglaiia cooperae</i>	Cooper, W. WWC 2029	Silica	CNS 129530	SRR21798413
<i>Aglaiia elaeagnoidea</i>	Ford, A. 5776	Silica	CNS 134440	SRR21798412
<i>Aglaiia euryanthera</i>	Cooper, W. WWC 2780	Silica	CNS 151035	SRR21798411
<i>Aglaiia fellii</i>	Cooper, W. WWC 2716	Silica	CNS 152652	SRR21798408
<i>Aglaiia fellii</i>	Cooper, W. WWC 2764	Silica	CNS 152654	SRR21798410
<i>Aglaiia fellii</i>	Cooper, W. WWC 2769	Silica	CNS 152653	SRR21798409
<i>Aglaiia ferruginea</i>	Costion, C. 1328	Silica	CNS 131156	SRR21798407
<i>Aglaiia meridionalis</i>	Cooper, W. WWC 2780	Silica	FHO 00123764N	SRR21798427
<i>Aglaiia monticola</i>	Cooper, W. WWC 2378	Silica	CNS 144556	SRR21798426
<i>Aglaiia sapindina</i>	Cooper, W. WWC 2388	Silica	CNS 144561	SRR21798425
<i>Aglaiia silvestris</i>	Cooper, W. WWC 2342	Silica	FHO 00123760J	SRR21798424
<i>Aglaiia spectabilis</i>	Cooper, W. WWC 2354	Silica	FHO 00123763M	SRR21798423
<i>Chisocheton longistipitatus</i>	Ford, A. 4730	Herbarium	QRS 128685	SRR21798422
<i>Didymocheton gaudichaudianus</i>	Cooper, W. WWC 2347	Silica	FHO 00140604F	SRR21798421
<i>Didymocheton mollis</i>	Dowe, J.L. 1348	Herbarium	CNS 146676	SRR21798420
<i>Didymocheton rufus</i>	Cooper, W. WWC 2402	Silica	CNS 146421	SRR21798419
<i>Dysoxylum oppositifolium</i>	Cooper, W. WWC 2781	Silica	CNS 151036	SRR21798418
<i>Epicharis parasitica</i>	Costion, C. 2140	Herbarium	CNS134828	SRR21798416
<i>Prasoxylon alliaceum</i>	Costion, C. 3017	Silica	CNS 135374	SRR21798415
<i>Vavaea amicornum</i>	Cooper, W. WWC 2786	Silica	CNS 151039	SRR21798414

Grudinski *et al.* (2014). This is likely due to a difference in the amount of data used to reconstruct relationships; Grudinski *et al.* (2014) used one locus (ITS) and reported weak to moderate bootstrap support for most species relationships, while we used 334 loci and received maximum support for most relationships. A difference in sampling and in species concepts may also play a role in the differences in relationships. For example, *A. elaeagnoidea* has recently been recircumscribed by Joyce *et al.* (2023), and *A. monticola* was recently split from *A. brassii* by Cooper & Forster (2021). Future studies including comprehensive sampling with many loci should be conducted to corroborate the relationships retrieved in our analysis.

Discussion

Our analysis retrieved all samples of the putative novelty as a clade nested within *Aglaiia* section *Aglaiia*, most closely related to *A. monticola* and *A. cooperae* (relationships among these three are not resolved with support). Thus we describe the new taxon herein as *Aglaiia fellii* W.E.Cooper & Joyce. The addition of *Aglaiia fellii* brings the total number of *Aglaiia* species in Australia to 13 (Cooper & Forster 2021), of which six are endemic: *A. australiensis* Pannell, *A. cooperae* Pannell, *A. fellii*, *A. ferruginea* C.T.White & W.D.Francis, *A. meridionalis* Pannell and *A. monticola* W.E.Cooper & P.I.Forst. The description of *A. fellii* brings the total number of accepted species in *Aglaiia* to 127.

Aglaiia fellii is the only species of *Aglaiia* with solitary flowers and fruits (Pannell 1992). The number of petals in *A. fellii* is also noteworthy; although flowers with three petals are common in sections *Amoora* and *Neoaglaia*, the species of section *Aglaiia* usually have (4)5–6(7) petals (Pannell 1992). Genus-wide sampling of *Aglaiia* in future phylogenetic studies (including extra-Australian species) should be conducted to determine the closest relative of *A. fellii*, to infer its biogeographic history, and to investigate the evolution of its exceptional morphological traits.

Taxonomy

Aglaiia fellii W.E.Cooper & Joyce *sp. nov.*

Type: Australia, Queensland. Cook District: Steve Irwin Wildlife Reserve, 4 June 2022, *W. Cooper 2854* & *T. Hawkes* (holo: CNS 152656 [2 sheets CNS + spirit], iso: 6 sheets to BRI, CANB, K, L, MO, M).

Diagnosis. Similar to *Aglaiia cooperae* Pannell but differs in the trifoliolate leaves (v. 5–7 leaflets); leaflets obovate (v. elliptical); leaflets chartaceous (v. coriaceous); inflorescence to 7 mm long (v. 25–30 mm long); flower diameter c. 2 mm (v. 2.5–3 mm); petals glabrous (v. densely clothed in scales); staminal tube glabrous (v. clothed in scales); fruit obovoid and c. 15 mm long (v. subglobose and 17–25 mm long).

Small tree to c. 7 m high, trunk diameter at breast height to 30 cm; bark grey, tessellated, flaky; branches glabrous; twigs densely tuberculate; newer twigs, peti-



Figure 2. *Aglaia fellii* showing tessellated flaky bark. (Cooper 2854 & Hawkes, CNS). Photo W. Cooper.

Distribution & habitat. *Aglaia fellii* is endemic to rainforest patches on Steve Irwin Wildlife Reserve and Bramwell Station on Cape York Peninsula, north Queensland, where it is currently known to occur at three sites at

altitudes between 80–110 m. These forests are broadly consistent with Qld Regional Ecosystem 3.5.4 - Semi-deciduous notophyll vine forest on northern plateaus

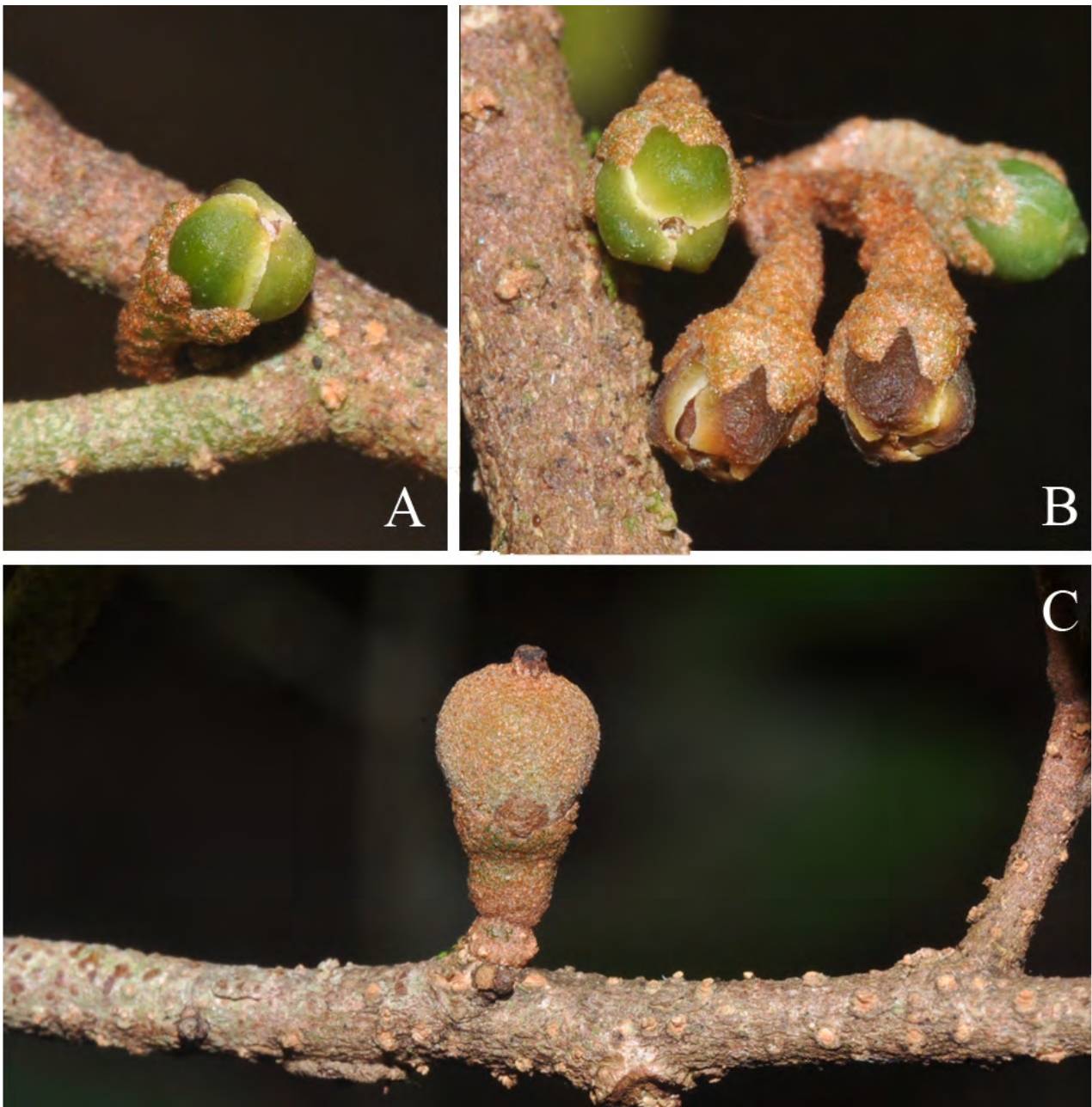


Figure 3. *Aglaia fellii* showing A. a typical solitary-flowered inflorescence (Cooper 2853 & Hawkes, CNS). B. a 4-flowered inflorescence with petals aging from green to brown (Cooper 2853 & Hawkes, CNS). C. immature fruit. (Cooper 2854 & Hawkes, CNS). Photos T. Hawkes.

on red earth soils on remnant lateritic surfaces (Queensland Herbarium 2021).

Aglaia fellii is an understorey tree that occurs beneath a closed canopy typically dominated by *Stenocarpus verticis* Foreman, *Welchiodendron longivalve* (F.Muell.) Peter G.Wilson & J.T.Waterh and *Dinosperma erythroccum* (F.Muell.)T.G.Hartley. Other co-occurring species include *Acacia fleckeri* Pedley, *Acacia polystachya* A.Cunn. ex Benth., *Aglaia elaeagnoidea* (A.Juss.) Benth., *Aidia racemosa* (Cav.) Tirveng., *Ailanthus tripyhsa* (Dennst.) Alston, *Arytera bifoliolata* S.T.Reynolds, *Brachychiton velutinosus* Kosterm., *Canarium australianum* F.Muell., *Celtis philippensis* Blanco, *Celtis timorensis* Span., *Cordia dichotoma*

G.Forst., *Denhamia peninsularis* J.J.Halford & Jessup, *Dimorphocalyx australiensis* C.T.White, *Drypetes deplanchei* (Brongn. & Gris) Merr., *Falcataria toona* (F.M.Bailey) Gill.K.Br., D.J.Murphy & Ladiges, *Garuga floribunda* Decne., *Gossia floribunda* (A.J.Scott) N.Snow & Guymmer, *Gyrocarpus americanus* Jacq., *Margaritaria dubium-traceyi* Airy Shaw & B.Hyland, *Medicosma riparia* (Proven) T.G.Hartley, *Meiogyne cylindriocarpa* (Burck) Heusden, *Miliusa traceyi* Jessup, *Mimusops elengi* L., *Rhodamnia australis* A.J.Scott and *Sersalisia sericea* (Aiton) R.Br.

Aglaia fellii is only known from within three well separated patches of rainforest on residual lateritic (or bauxitic)

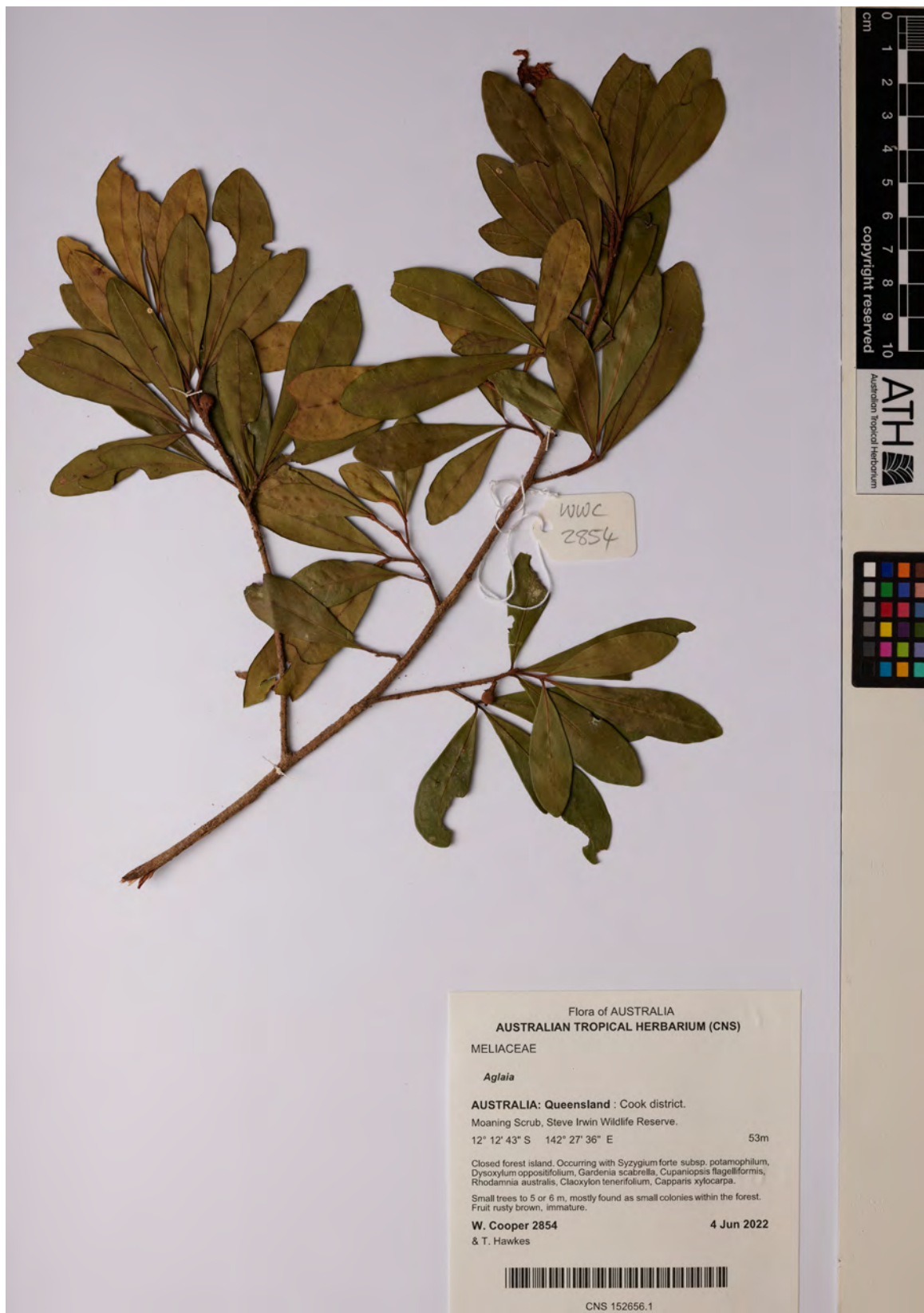


Figure 4. *Aglaia fellii* Type specimen (W.Cooper 2854 & Hawkes CNS).

low plateaus and rises with well-drained red earth soils. Similar patches are scattered between the Wenlock and Jackson rivers with another concentration between the Wenlock and Mission rivers (Stanton and Fell 2005) where the species may also occur.

Conservation status. *Aglaia fellii* is known from three small stands of 10–30 individuals each. Two of these stands are conserved in the private Steve Irwin Wildlife Reserve. The greatest threat to the rainforest habitat of *Aglaia fellii* is the impact of fire. One population occurs

close to the southern margin of a rainforest patch where past fire incursion is evident. Tropical cyclones cause catastrophic damage and accumulation of debris that increases the flammability of rainforests; the increased likelihood of such extreme stochastic weather events with climate change means that *A. fellii* populations are particularly sensitive to these sorts of events in the future.

Based on known locations, the extent of occurrence of *A. fellii* is estimated to be 78 km² and area of occupancy is 12 km² (calculated with GeoCat; Bachman *et al.* 2011). As such, *Aglaia fellii* is eligible for nomination as Endangered [EN B1ab(i, ii, iii, iv)+B2ab(i, ii, iii, iv)] according to Queensland's nomination procedure based on the IUCN Red List Categories and Criteria (IUCN 2012).

Etymology. The specific epithet honours David G. Fell (1962–), a botanist who has made outstanding contributions to knowledge of the flora of Cape York Peninsula, and who made the first collection of this taxon and recognised its novelty.

Notes. In many *Aglaia* species, male and female flowers cannot be easily distinguished morphologically (Pannell 1992:32). Floral segments of *A. fellii* seen by the first author, whether they be vestigial or functional (ovaries, stigmas, anthers and ovules) all appear similar and therefore the sexuality of *A. fellii* cannot be ascertained at present. All fruit observed have been solitary.

Aglaia fellii is most similar to *A. cooperae* Pannell and *A. monticola* W.E.Cooper & P.I.Forst., but is distinguished from both by its trifoliolate leaves and usually solitary flowers (or much-reduced inflorescences). Flowers of *A. fellii* and *A. cooperae* usually have three petals (rarely four) unlike other species in section *Aglaia* which always have five or six. These two species occur in disjunct areas on Cape York Peninsula and both are only known from small populations.

Disclosures

We have no conflicts of interest.

Acknowledgments

WEC is especially grateful to Tim Hawkes as well as Eda Addicott, David Fell, Rigel Jensen, Brian Venables and Frank Zich for their assistance in the field, and Frank Zich for helpful discussions. For hospitality at SIWR Suzie MacDonald and Talina O'Brien are sincerely thanked. Special thanks to Kate Berry from SIWR for permission to collect on their property, for without their congeniality this research might not have been possible. Permits to collect were issued by the Queensland Department of Environment and Science to the Australian Tropical Herbarium enabling staff or designated associates from this institution to collect herbarium samples. We would like to acknowledge the contribution of the Genomics for Australian Plants (GAP) Framework Initiative consortium in the generation of data for some samples used

in this publication. GAP is supported by funding from Bioplatforms Australia (enabled by NCRIS), the Ian Potter Foundation, Royal Botanic Gardens Foundation (Victoria), Royal Botanic Gardens Victoria, the Royal Botanic Gardens and Domain Trust, the Council of Heads of Australasian Herbaria, CSIRO, Centre for Australian National Biodiversity Research and the Department of Biodiversity, Conservation and Attractions, Western Australia. EMJ was funded by the Prinzessin Therese von Bayern Foundation during the course of this work.

References

- Bachman S, Moat J, Hill AW, De La Torre J, Scott B (2011). Supporting Red List threat assessments with GeoCAT: geospatial conservation assessment tool. *ZooKeys* **150**, 117–126. (Version BETA).
- Bolger AM, Lohse M, Usadel B (2014) Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* **30**, 2114–2120.
- Borowiec ML (2016) AMAS: a fast tool for alignment manipulation and computing of summary statistics. *PeerJ* **4**, e1660.
- Cooper WE, Forster PI (2021). *Aglaia monticola* W.E.Cooper & P.I.Forst. (Meliaceae), a new species for Queensland's Wet Tropics, *Austrobaileya* **11**, 80–86.
- Doyle J, Doyle JL (1987) Genomic plant DNA preparation from fresh tissue-CTAB method. *Phytochemical Bulletin* **19**, 11–15.
- Grudinski M, Wanntorp L, Pannell CM, Muellner AN (2014) West to east dispersal in a widespread animal - dispersed woody angiosperm genus (*Aglaia*, Meliaceae) across the Indo - Australian Archipelago. *Journal of Biogeography* **41**, 1149–1159.
- Hoang DT, Chernomor O, von Haeseler A, Minh BQ, Vinh LS (2018) UFBoot2: improving the ultrafast bootstrap approximation. *Molecular Biology and Evolution* **35**, 518–522.
- Holzmeyer L, Hauenschild F, Mabberley DJ, Muellner-Riehl AN (2021) Confirmed polyphyly, generic recircumscription and typification of *Dysoxylum* (Meliaceae), with revised disposition of currently accepted species. *TAXON* **70**, 1248–1272.
- IUCN (2012) IUCN Red List Categories and Criteria: Version 3.1. Second Edition. IUCN, Gland, Switzerland and Cambridge, UK. [Accessed Sept. 2022]
- Johnson MG, Gardner EM, Liu Y, Medina R, Goffinet B, Shaw AJ, Zerega NJC, Wickett NJ (2016) HybPiper: Extracting coding sequence and introns for phylogenetics from high-throughput sequencing reads using target enrichment. *Applications in Plant Sciences* **4**, 1600016.
- Johnson MG, Pokorny L, Dodsworth S, Botigué LR, Cowan RS, Devault A, Eiserhardt WL, Epitawalage N, Forest F, Kim JT, Leebens-Mack JH, Leitch IJ, Maurin O, Soltis DE,

- Soltis PS, Wong GK, Baker WJ, Wickett NJ (2019) A universal probe set for targeted sequencing of 353 nuclear genes from any flowering plant designed using k-medoids clustering. *Systematic Biology* **68**, 594–606.
- Joyce EM, Crayn DM, Rossetto M, Yap JYS, Pannell CM (2023a) Taxonomic recircumscriptions in the *Aglaia elaeagnoidea* complex (Meliaceae). *Blumea* **68**, 26–38.
- Joyce EM, Appelhans MS, Buerki S, Cheek M, de Vos JM, Pirani JR, Zuntini AR, Bachelier JB, Bayly MJ, Callmander MW, Devecchi MF, Pell SK, Groppo M, Lowry PP, Mitchell J, Siniscalchi CM, Munzinger J, Orel HK, Pannell CM, Nauheimer L, Sauquet H, Weeks A, Muellner-Riehl AN, Leitch IJ, Maurin O, Forest F, Nargar K, Thiele KR, Baker WJ, Crayn DM (2023b) Phylogenomic analyses of Sapindales support new family relationships, rapid Mid-Cretaceous Hothouse diversification, and heterogeneous histories of gene duplication. *Frontiers in Plant Science* **14**, 1063174.
- Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermini LS (2017) ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods* **14**, 587–589.
- Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* **30**, 772–780.
- Koenen EJM, Clarkson JJ, Pennington TD, Chatrou LW (2015) Recently evolved diversity and convergent radiations of rainforest mahoganies (Meliaceae) shed new light on the origins of rainforest hyperdiversity. *New Phytologist* **207**, 327–339.
- Lanfear R, Calcott B, Ho SYW, Guindon S (2012) PartitionFinder: combined selection of partitioning schemes and substitution models for phylogenetic analyses. *Molecular Biology and Evolution* **29**, 1695–1701.
- McLay TGB, Birch JL, Gunn BF, Ning W, Tate JA, Nauheimer L, Joyce EM, Simpson L, Schmidt-Lebuhn AN, Baker WJ, Forest F, Jackson CJ (2021) New targets acquired: Improving locus recovery from the Angiosperms353 probe set. *Applications in Plant Sciences* **9**, e11420.
- Nauheimer L, Weigner N, Joyce E, Crayn D, Clarke C, Nargar K (2021) HybPhaser: A workflow for the detection and phasing of hybrids in target capture data sets. *Applications in Plant Sciences* **9**, e11441.
- Nguyen L-T, Schmidt HA, von Haeseler A, Minh BQ (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution* **32**, 268–274.
- Pannell CM (1992) A taxonomic monograph of the genus *Aglaia* Lour. Royal Botanic Gardens, Kew: London.
- Pannell CM (2013) *Aglaia* (Meliaceae). In: Wilson AJG (ed.), Flora of Australia volume 26: 33–42. CSIRO Publishing: Melbourne.
- Queensland Herbarium (2021) Survey and Mapping of Pre-clearing Vegetation Communities and Regional Ecosystems of Queensland. Department of Science, Information Technology, Innovation and the Arts: Brisbane.
- Smith SA, Dunn CW (2008) Phyutility: a phyloinformatics tool for trees, alignments and molecular data. *Bioinformatics* **24**, 715–716.
- Stanton JP, Fell DG (2005) The Rainforests of Cape York Peninsula. Cooperative Research Centre for Tropical Rainforest Ecology and Management. Rainforest CRC: Cairns.



This paper was typeset using Prince

www.princexml.com