THAI FOREST BULL., BOT. 54(2): 188–205. 2026.
DOI https://doi.org/10.20531/tfb.2026.54.2.16

A new species of *Neomicrocalamus* (Poaceae: Bambusoideae) from Thailand and the reduction of *Temochloa* indicated by morphological and molecular investigations

WATCHARA ARTHAN[1,2], SARAWOOD SUNGKAEW[2,3,4,*], KHOON MENG WONG[2,3,5], YI-HUA TONG[6,7], NIAN-HE XIA[6,7], WEI-LIM GOH[8], WEI LIM[8], PIYA PINYO[9], ARNUPAP JANLOY[3,10], TIPAJIN THAIPISUTIKUL[11], PORNSAWAN SUTTHINON[12], NATTHAPHONG CHITCHAK[12] & ATCHARA TEERAWATANANON[13]

ABSTRACT

Temochloa and *Neomicrocalamus* are closely related bamboo genera exhibiting a complex taxonomy and substantial morphological overlap. Their phylogenetic relationships and generic delimitation remain insufficiently resolved and are further complicated by intermediate morphological character states in the newly discovered species *N. patellaris* described in this study. Phylogenomic analyses were undertaken using plastome and 97 partial or complete nuclear gene regions. Results were combined with morphological reassessment of *Temochloa* and *Neomicrocalamus* to support the taxonomic subsumption of *Temochloa* under *Neomicrocalamus*. Inclusion of *N. patellaris* in the plastome and nuclear phylogenetic analyses yielded congruent, well supported, topologies and revealed intermixing of species between the two genera. *Neomicrocalamus patellaris* was recovered as sister to *T. liliana*, the type species of *Temochloa*. Phylogenetic reconstructions further showed that *Temochloa* is polyphyletic, with *T. elegans* nested within *Neomicrocalamus*. Shared characters of the two genera include a climbing or scrambling habit, a similar mid-culm branch complement, culm leaves lacking a distinct sheath–blade junction, needle-like blade tips, and modified pseudospikelets. Therefore, phylogenomic and morphological evidence support transferring *Temochloa* to *Neomicrocalamus* to achieve a monophyletic generic circumscription. Two species formerly recognized in *Temochloa*, *T. elegans* and *T. liliana*, are transferred to *Neomicrocalamus*, and *N. patellaris* is newly described.

KEYWORDS: Endemic; limestone; patella; Tenasserim; Western Forest Complex (WEFCOM).

Accepted for publication: 11 September 2026. Published online: 10 November 2026

INTRODUCTION

The limestone karst formations in the Western Forest Complex (WEFCOM) of western Thailand are renowned for their high biodiversity of animal and plant species (van de Bult & Greijmans, 2006; van de Bult & Steinmetz, 2006) due to the concurrence of transition zones of the Himalayan, Indo-Malesian, Indo-Chinese, and Indo-Burmese floristic regions (WCS Thailand Program, 2005; Clements *et al.*, 2006; Murray *et al.*, 2020; Kiew & Rahman, 2021). New

[1] Department of Pharmaceutical Botany, Faculty of Pharmacy, Mahidol University, 447 Si Ayutthaya Rd., Ratchathewi, Bangkok 10400, Thailand.

[2] Center of Excellence for Bamboos, Faculty of Forestry, Kasetsart University, Bangkok 10900, Thailand.

[3] Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok 10900, Thailand.

[4] Center for Advanced Studies in Tropical Natural Resources, Kasetsart University, Bangkok 10900, Thailand.

[5] Singapore Botanic Gardens, National Parks Board, 1 Cluny Road, 259569, Singapore.

[6] Laboratory of Plant Resources, Conservation and Sustainable Utilization/Guangdong Provincial Key Laboratory of Digital Botanical Garden, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou 510650, China.

[7] South China National Botanical Garden, Guangzhou 510650, China.

[8] Faculty of Science, Universiti Tunku Abdul Rahman, Jalan Universiti, Bandar Barat, 31900 Kampar, Perak, Malaysia.

[9] Department of National Parks, Wildlife and Plant Conservation, Bangkok 84000, Thailand.

[10] PTT Reforestation and Ecosystem Institute, 555 Vibhavadi Rangsit Road, Chatuchak, Bangkok 10900, Thailand.

[11] Faculty of Information and Communication Technology, Mahidol University, Nakhon Pathom, Thailand.

[12] Department of Botany, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand.

[13] Natural History Museum, National Science Museum, Technopolis, Pathum Thani 12120, Thailand.

* Corresponding author: fforsws@ku.ac.th

© 2026 Forest Herbarium

plant records and species have been frequently reported from limestone hills in the karst landscape of Thung Yai Naresuan in the Western Karst Complex, the largest limestone karst in Thailand (Smart, 2002; Middleton, 2010; Sirichamorn *et al.*, 2016; Rodda, 2020). This is particularly true for the endemicity of bamboos (Poaceae: Bambusoideae). Endemic bamboo species have been documented in limestone habitats across geographic regions (Dransfield, 2000; Haevermans *et al.*, 2020; Li & Stapleton, 2006). In this study, a suspected new taxon was discovered in the karst landscape of the WEFCOM at elevations of 850–1,095 m. It has a clambering habit, prominent patella (raised structure at node), culm leaf without obvious junction between the sheath and blade, and bracteate pseudospikelets. This combination of morphological characters corresponds closely to diagnostic features traditionally associated with the genera *Temochloa* S.Dransf. and *Neomicrocalamus* Keng f. (Keng, 1983; Stapleton, 1994; Dransfield, 2000; Li & Stapleton, 2006; Bamboo Phylogeny Group (BPG), 2012; Cai *et al.*, 2023, 2024; Cai & Xia, 2024). *Temochloa* and *Neomicrocalamus* have been regarded as two small genera of clambering bamboos (Poaceae: Bambusoideae: Bambuseae) restricted to limestone habitats (Keng, 1983; Dransfield, 2000; Li & Stapleton, 2006; Cai *et al.*, 2023, 2024).

When *Temochloa* was first established by Dransfield (2000), it was treated as a monotypic genus comprising only the type species *T. liliana* S.Dransf., which is endemic to Thailand. Subsequent taxonomic studies included two species in the genus (Cai *et al.*, 2023, 2024). This includes the recent addition of *T. elegans* N.H.Xia, You Y.Zhang, Z.Y.Cai & Y.H.Tong, and two varieties of *T. elegans*, from southwestern Guangxi, China, and northeastern Vietnam (Cai *et al.*, 2023, 2024; POWO, 2025). However, the 'Status' of *T. elegans* and its new variety *T. elegans* var. *glabra* N.H.Xia, Z.Y.Cai, You Y.Zhang & J.B.Ni are listed as 'Unchecked' in WFO (2025).

Neomicrocalamus is distributed in Bhutan, southwestern China, northeastern India, and Vietnam (Stapleton *et al.*, 1997; Li & Stapleton, 2006; Vorontsova *et al.*, 2016). Three species, *N. andropogonifolius* (Griff.) Stapleton, *N. dongvanensis* T.Q.Nguyen, and the type species of the genus, *N. prainii* (Gamble) Keng f., are currently accepted (POWO, 2026; WFO, 2026). The inclusion of *N. dongvanensis* in the genus has been questioned because it possesses erect culms (Nguyen, 1991; Stapleton *et al.*, 1997; Cai *et al.*, 2023).

Morphological similarities and phylogenetic evidence hinted close relationships between *Temochloa* and *Neomicrocalamus*. Cai *et al.* (2023, 2024) emphasized that *Temochloa* shares key diagnostic characters exclusively with *Neomicrocalamus*. The morphological affinity is based on similarities of both genera in the pseudospikelet structure, a clambering (climbing or scrambling) habit, the presence of a patella, culm leaves lacking a distinct junction between sheath and blade, the acicular (needle-like) blade tip, the shape of the primary branch bud and the geographic range. The sister relationship of the two genera was consistently strongly supported results from molecular phylogenetic analyses of plastome and nuclear sequence data (Baker *et al.*, 2022; Cai *et al.*, 2024; Liu *et al.*, 2024). However, phylogenomic analyses based on genome-wide single-nucleotide polymorphisms (SNPs), genome-wide single-copy nuclear genes and plastome showed discordant phylogenetic positions of *T. elegans* within the *Temochloa-Neomicrocalamus* complex, suggesting an evolutionarily entangled and still unresolved relationship between the two genera (Cai *et al.*, 2023).

Interestingly, the new species identified in this study exhibits morphological overlap between the two genera. It possesses an elliptic-ovate primary branch bud and a shallowly grooved culm leaf sheath, corresponding to the diagnostic features of *Temochloa* as circumscribed by Dransfield (2000) and Cai *et al.* (2024). Conversely, it also exhibits a cuspidate anther apex and occurs at elevations between 850 and 1,095 m, characters that broadly conform to *Neomicrocalamus* sensu Cai *et al.* (2024). Furthermore, morphological and phylogenetic affinities between the two genera have raised the question of whether *Temochloa* is congeneric with *Neomicrocalamus*.

Phylogenetic re-analysis, with additional data and taxa, has the potential to provide new taxonomic interpretations of *Temochloa* and to test its sister relationship with *Neomicrocalamus*. Combining phylogenetic analysis with an assessment of their overlapping morphological traits (including those of the new taxon), may help reconcile the recent phylogenetic classification with the morphology and could help to clarify the taxonomy of this lineage.

Here, we aimed to (1) re-evaluate the taxonomic status of *Temochloa* and (2) assess the taxonomic placement of the here described new taxon, *N. patellaris*. To achieve these objectives, we employ a phylogenetic framework based on both plastome and nuclear data (97 genes), together with morphological and geographic interpretation.

MATERIAL AND METHODS

Sampling design

The initial stage of this study was based on a detailed phylogenomic investigation of Bambusoideae in Thailand. For the analyses presented herein, the ingroup comprised species from the subtribe Bambusinae, including representatives of *Bambusa* Schreb., *Dendrocalamus* Nees, *Gigantochloa* Kurz ex Munro, *Melocalamus* Benth., *Neomicrocalamus*, and *Temochloa*, retrieved from GenBank. Two species of *Bonia* Balansa, *B. levigata* (L.C.Chia, H.L.Fung & Y.L.Yang) N.H.Xia and *B. saxatilis* (L.C.Chia, H.L.Fung & Y.L.Yang) N.H.Xia, were designated as outgroups following Cai *et al.* (2023). Additional genomic DNA was extracted from two samples, *Sungkaew et al. 1617* and *1668*, representing the new species *N. patellaris*. For the nuclear phylogenetic analyses, 10 ingroup accessions representing *Temochloa* and *Neomicrocalamus*, together with one outgroup accession (*B. levigata*), were included. Details of all samples analysed in this study are provided in Table 1.

DNA extraction, library preparation and sequencing

Total genomic DNA was extracted from silica dried plant material using a modified CTAB protocol (Doyle & Doyle, 1987). Library preparation and Illumina sequencing were conducted by NeoScience Sdn. Bhd., Malaysia. The quality of raw sequence reads of *Neomicrocalamus patellaris* was assessed using FastQC (Andrews, 2010). Reads were filtered and trimmed to remove adapter sequences and low-quality regions using Trimmomatic version 0.39 (Bolger *et al.*, 2014).

Plastid genome and nrDNA assembly and annotation

Plastome assemblies were generated from the cleaned reads using GetOrganelle version 1.7.7.1 (Jin *et al.*, 2020), with plastome sequences of *N. prainii* and *T. liliana* used as references. Six k-mers values (21, 45, 65, 85, 105, and 125) were applied in the GetOrganelle pipeline. Gaps between contigs in incomplete assemblies were filled by iterative extension between contig ends using clean reads until the contigs were successfully joined. Annotation of the newly assembled plastomes was performed using GeSeq (Tillich *et al.*, 2017) implemented in the MPI-MP CHLOROBOX platform (https://chlorobox.mpimp-golm.mpg.de/index.html). The annotated plastomes were subsequently checked for gene order, gene content, and the presence of premature stop codons by alignment with reference plastomes of *N. prainii* and *T. liliana* (Table 1) in Geneious Prime version 2023.0.4 (https://www.geneious.com). The two newly generated plastome sequences have been deposited in GenBank under accession numbers PX960082 for *Sungkaew et al. 1617* and PX970996 for *Sungkaew et al. 1668*.

To extract nuclear genes from the raw sequence data, peptide reference sequences generated by Cai *et al.* (2023) were used as target files. HybPiper version 2.2.0 (Johnson *et al.*, 2016) was employed to map reads from the two samples of the putative new species to the target peptide references, using DIAMOND to improve the efficiency of gene recovery. In addition, the "--cov_cutoff" parameter was adjusted from the default value of 8 to 4 to facilitate the assembly of nuclear genes from relatively low-depth sequencing data. Potential paralogous sequences and sequences containing internal stop codons were excluded from subsequent analyses. The resulting nuclear gene assemblies were further filtered to retain sequences with lengths of 200 bp or greater for downstream phylogenetic analyses.

Alignments and Phylogenetic Analyses

Whole plastome sequences and nuclear gene datasets were aligned using MAFFT version 7.526 (Katoh & Standley, 2013) with the local pairwise alignment algorithm and default parameters. Plastome alignments were visually inspected and manually adjusted, where necessary, in Geneious Prime version 2023.0.4 (http://www.geneious.com). Nuclear genes generated in this study were aligned individually with their corresponding homologous datasets from Cai *et al.* (2023).

Table 1. List of taxa and plastome and nuclear sequence accessions included in phylogenomic analyses and references.

Taxa	GenBank accession	Collector no.	Herbarium	Analyses		Reference
				Plastome	Nuclear	
Bambusa bambos	KJ870988	BI 1	BO	√	-	Wysocki *et al*., (2015)
Bonia levigata	OQ791229	NH050	IBSC	√	√	Cai *et al.*, (2023)
Bonia saxatilis	MK679779	12327	KUN	√	-	Liu *et al*., (2020)
Dendrocalamus strictus	NC050776	zmy018	KUN	√	-	Liu *et al*., (2020)
Gigantochloa albociliata	NC050765	Liujx15058	KUN	√	-	Liu *et al*., (2020)
Melocalamus yunnanensis	MK679790	Liujx15096	KUN	√	-	Liu *et al*., (2020)
Neomicrocalamus prainii	OQ791224	TYH2350 (NH095)	IBSC	√	√	Cai *et al*., (2023)
***Neomicrocalamus* sp**.	OQ791225	TYH2100 (NH098)	IBSC	√	√	Liu *et al*., (2020)
	OQ791227	CZY107 (NH152)	IBSC	√	√	Cai *et al.*, (2023)
	OQ791228	CZY 142 (NH178)	IBSC	√	√	Cai *et al.*, (*2023*)
Temochloa liliana (here *Neomicrocalamus lilianus*)	OQ791221	*Sungkaew s.n.* (NH234)	IBSC	√	√	Cai *et al.*, (2023)
Temochloa elegans (here *N. elegans*)	OQ791222	2018VNB018 (NH063)	IBSC	√	√	Cai *et al.*, (2023)
	OQ791223	2018VNB040 (NH065)	IBSC	√	√	Cai *et al.*, (2023)
	OQ791226	BH85 (NH114)	IBSC	√	√	Cai *et al.*, (2023)
Neomicrocalamus patellaris	ID2909274	*Sungkaew et al. 1617*	BKF	√	√	This study
	ID2904304	*Sungkaew et al. 1668*	BKF	√	√	This study

Maximum Likelihood (ML) and Bayesian Inference (BI) analyses of plastome sequences were conducted using RAxML version 8.2.12 (Stamatakis, 2014) and MrBayes version 3.2.7a (Ronquist *et al.*, 2012), respectively, via the CIPRES Science Gateway (https://www.phylo.org). For ML analyses, the GTRGAMMA nucleotide substitution model was applied with 1,000 bootstrap replicates. Prior to BI analyses, the best-fit nucleotide substitution model for the plastome alignment was determined as GTR+G+I model using jModelTest2 (Darriba *et al.*, 2012). Bayesian analyses were run for 10,000,000

generations, with trees sampled every 1,000 generations, and the first 25% of samples discarded as burn-in. Convergence, effective sample sizes, and posterior distributions were assessed using Tracer version 1.7.2 (Rambaut *et al.*, 2018). Resulting ML and BI trees were visualized using FigTree version 1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).

Phylogenetic analyses of nuclear genes were conducted using Maximum Likelihood methods implemented in IQ-TREE version 2.3.6 (Minh *et al.*, 2020) for 97 loci. Unrooted ML gene trees were combined to infer a species tree using ASTRAL-III (Zhang *et al.*, 2018), with 100 coalescent bootstrap replicates and other parameters set to default values. Because low-depth genome-skimming data were used, some effects of reduced nuclear gene sampling on topology and species-tree resolution are expected (Corl & Ellegren, 2013). To assess the influence of reduced gene sampling, the subset of nuclear genes recovered in this study was applied to the dataset of Cai *et al.* (2023), excluding *N. patellaris*, and analysed using the same ML and ASTRAL workflows to evaluate potential differences in topology within the *Neomicrocalamus–Temochloa* clade.

Morphological examination

Photographic documentation was used to complement field observations, facilitating the recording of natural habitats, growth habits, and additional morphological characters that may be ambiguous or difficult to assess from voucher specimens alone. Vegetative and reproductive parts of the focal taxon and related species were examined and compared with protologues and type and non-type specimens housed in the herbaria of the Bangkok Herbarium (BK), Forest Herbarium (BKF), Royal Botanic Gardens, Kew (K), Singapore Botanic Gardens (SING), and the collections of the Thailand Natural History Museum. Additional comparisons were made using online images of type specimens available from the herbarium of K (https://data.kew.org/), the Global Biodiversity Information Facility (GBIF, 2026), and JSTOR (https://plants.jstor.org/). To assess the conservation status of the new species, we applied the IUCN Red List Categories and Criteria (IUCN Standards and Petitions Committee, 2026), with calculations of Extent of Occurrence (EOO) and Area of Occupancy (AOO) performed using GeoCAT (Bachman *et al.*, 2011).

The base of a pseudospikelet is supplied with a prophyll and followed by one or more structures that have been interpreted either as glumes (Dransfield, 2000) or as bracts (Cai *et al.*, 2024). However, according to Wong (1995) and Cai *et al.* (2024), the terms bracts and glumes are sometimes considered indistinguishable structures in the case of iterauctant bamboo inflorescences, sometimes resulting in the use of differing terminology. To avoid ambiguity in the interpretation of the pseudospikelet in *Neomicrocalamus* (including species formerly treated under *Temochloa*), we follow Cai *et al.* (2024) in applying the term ‘bract’.

RESULTS

Basic features of the *Neomicrocalamus patellaris* plastome and nuclear genes

The sizes of two *N. patellaris* plastome sequences are 139,795 bp (*Sungkaew et al. 1617*) and 139,524 bp (*Sungkaew et al. 1618*). Each plastome exhibits a typical quadripartite structure comprising four regions: a large single-copy (LSC), a small single-copy (SSC), and two inverted repeats (IRs). The plastomes of *N. patellaris* accessions no.*1617* and no.*1668* contain 176 genes and have total GC contents of 54,232 bp and 54,287 bp, respectively. The alignment of 16 plastome sequences is 140,988 bp in length and includes 26,896 bp of gaps (1.2%) in the data matrix. Both *N. patellaris* samples yielded 97 complete and partial nuclear genes in common. Alignments of individual nuclear genes from 11 accessions produced data matrices ranging from 591 to 6,749 bp. Ns were inserted where gaps occurred in incomplete nuclear sequences extracted using HybPiper. Detailed information on plastome and nuclear sequences is provided in Table 2.

Phylogenetic analyses

Both the plastome tree and ASTRAL species tree based on nuclear genes agree that the new species forms a sister taxon to *Temochloa liliana* (here *N. lilianus*) with high support (Bootstrap support [BS]/Bayesian inference posterior probability [PP], 100/1; 98/0.85, respectively)(Figs. 1, 2), and that clade forms a sister clade to other *Neomicrocalamus* and *T. elegans* (here *N. elegans*) with high support in the plastome tree (100/1)(Fig. 1). In this study, the plastome tree supports a strong sister relationship

Table 2. Details of plastome and nuclear sequences of *Neomicrocalamus patellaris* W.Arthan, Teerawat & Sungkaew used in phylogenomic analyses of this study.

Species	Plastome sequence size range (bp)	LSC length (bp)	SSC length (bp)	IRs length (IRs)	GC content (%)	Nuclear sequence size range (bp)	Two paired-end NGS datasets (reads)	Total number of genes
N. patellaris (*Sungkaew et al. 1617*)	139,795	83,247	12,956	21,796	38.9%	390–6,606	41,692,580	176
N. patellaris (*Sungkaew et al. 1668*)	139,524	83,054	12,873	21,779	38.8%	429–6,552	40,061,910	176

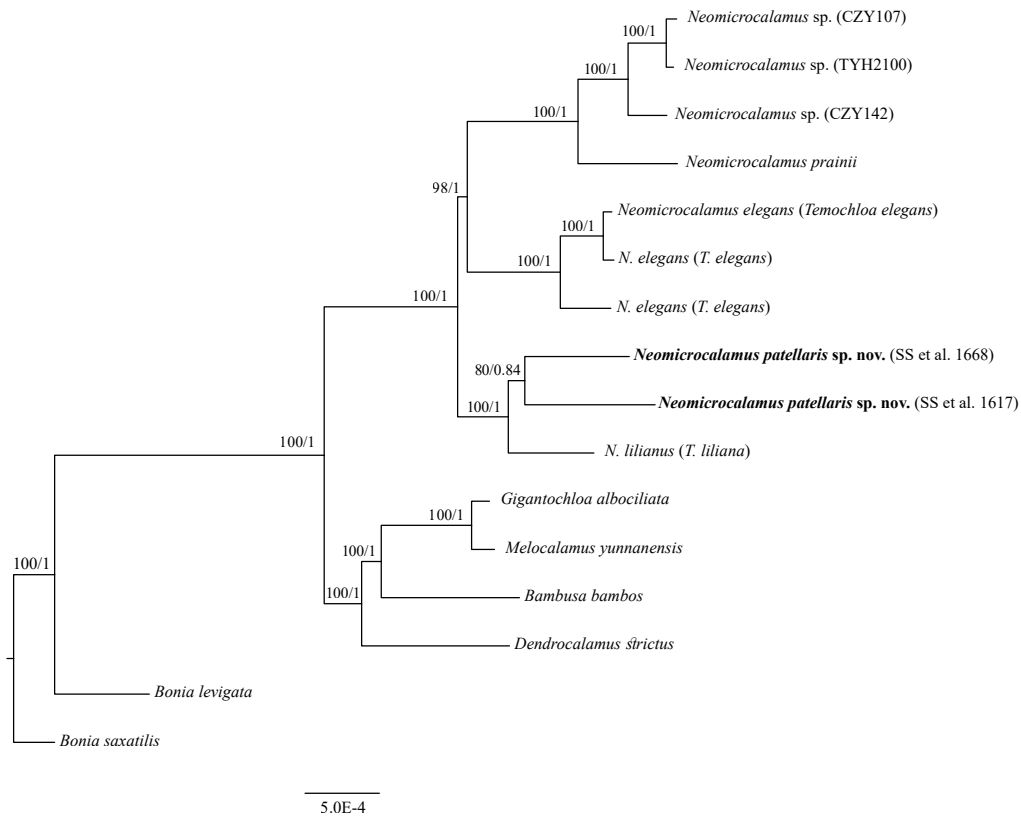


Figure 1. Maximum likelihood (ML) and Bayesian inference (BI) phylogenetic tree inferred from whole plastome sequences, including 16 accessions representing the genera *Bambusa*, *Dendrocalamus*, *Gigantochloa*, *Melocalamus*, *Neomicrocalamus* (including species formerly placed in *Temochloa*), and two *Bonia* species as outgroups.

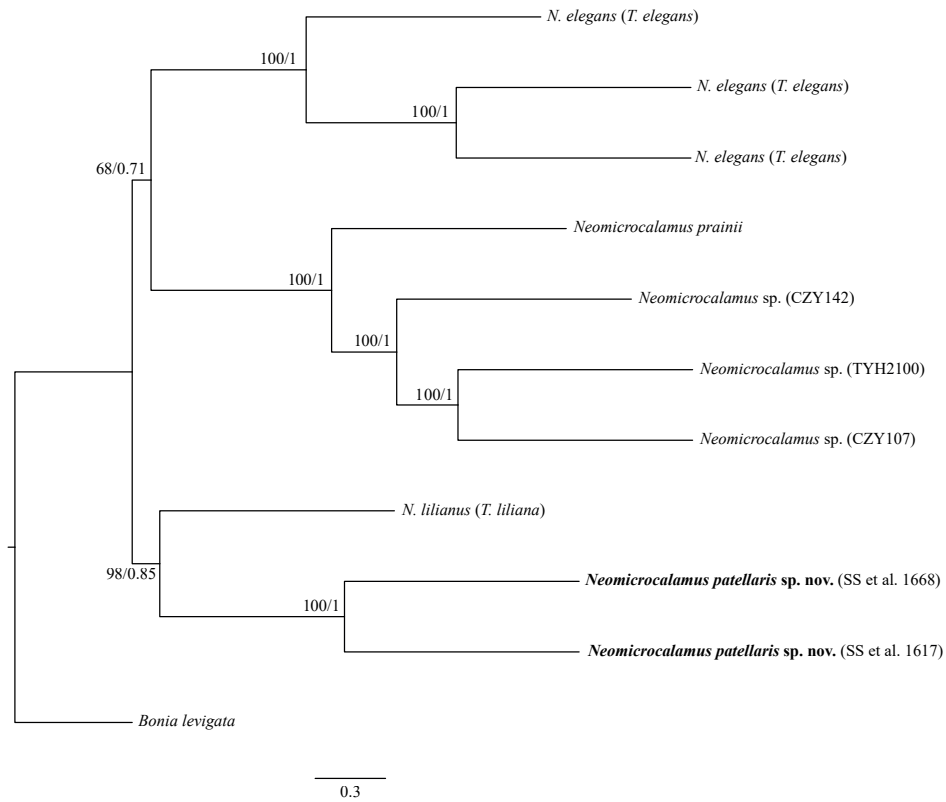


Figure 2. Nuclear phylogenetic tree produced ASTRAL-III analyses based on 97 nuclear orthologous genes from 11 accessions.

between other *Neomicrocalamus* and *T. elegans* (98/1, Fig. 1), but this relationship receives low BS and moderate but acceptable PP support (68/0.71, Fig. 2) in the ASTRAL nuclear species tree, as the threshold for local PP support ranges from 0.70 to 0.75 (Sayyari & Mirarab, 2016). Tests of the effect of using a smaller nuclear dataset indicated no changes in tree topology or in the phylogenetic relationship between *T. liliana* and *T. elegans* when the larger dataset of Cai *et al.* (2023) was compared with the smaller dataset used here, provided that the same methods and taxon sampling were applied (Fig. 3). In addition, the phylogenetic position of the new *Neomicrocalamus* species remained unchanged regardless of whether plastome or nuclear datasets were used in the analyses (Figs. 1, 2).

Comparative morphology of the three species

The new species, *Neomicrocalamus patellaris*, is distinguished from the two most morphologically similar species, formerly known as *Temochloa elegans* and *T. liliana* (transferred in this study to *N. elegans* and *N. lilianus*, respectively), in several vegetative and reproductive characters. *Neomicrocalamus patellaris* is characterized by a prominent patella, relatively long pseudospikelets, and stamens with a cuspidate anther apex. Detailed morphological comparisons are provided in Table 3 and Figs. 4 (B–K), 5. In addition, culm shoots of *N. lilianus* were re-collected from areas adjacent to its type locality to provide additional information for a comparison in culm leaf characteristics (Fig. 4A)

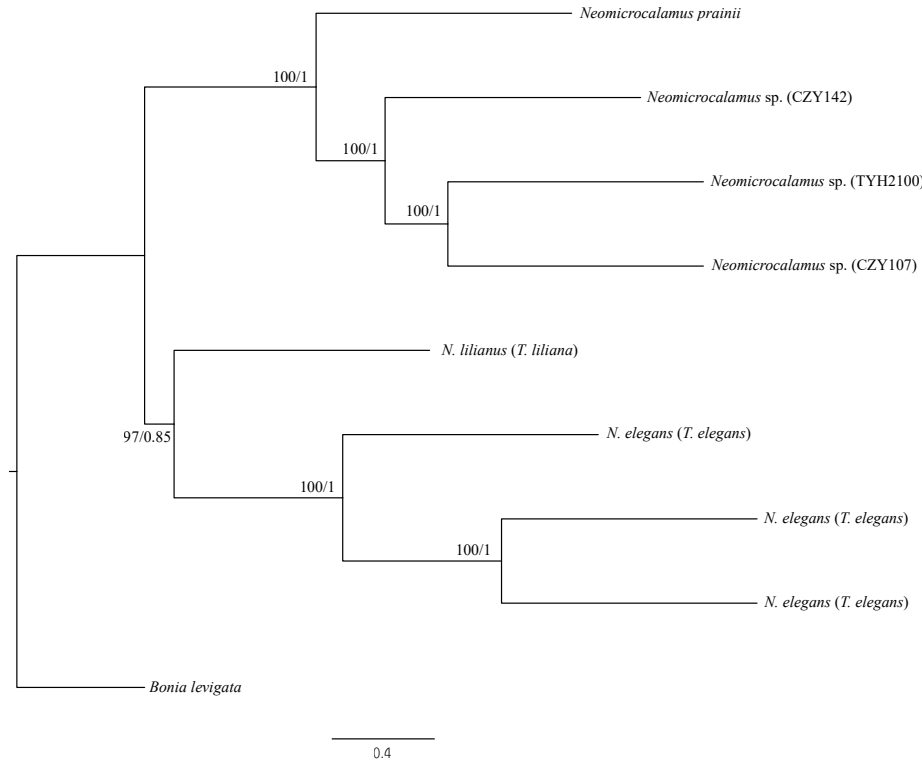


Figure 3. ASTRAL species tree inferred from 97 nuclear genes, based on nine taxa and excluding two accessions of *Neomicrocalamus patellaris* W.Arthan, Teerawat & Sungkaew. Support values at nodes are shown as bootstrap percentages/posterior probabilities (BP/PP).

that were incomplete in the protologue (Dransfield, 2000). Its culm leaves lack a distinct junction between the sheath and blade, with an acicular (needle-like) blade tip which is a diagnostic character of the genus *Neomicrocalamus* (Keng, 1983).

DISCUSSION

Phylogenetic relationships and taxonomic implications for *Neomicrocalamus* and *Temochloa*

The plastome and nuclear phylogenetic trees were broadly congruent and largely well supported. In both trees, when the new species, *Neomicrocalamus patellaris*, was included in the analyses, *Temochloa elegans* was consistently nested within the *Neomicrocalamus* clade rather than with *T. liliana*. The new species was instead most closely related to *T. liliana* (Figs. 1, 2). If *Temochloa* is retained as a genus, the position of *T. elegans* and *T. liliana* would make the genus polyphyletic, therefore the generic limits require re-evaluation to ensure monophyly. One solution would be to transfer *T. elegans* to *Neomicrocalamus*, thereby maintaining both genera as monophyletic. Alternatively, *Temochloa* could be treated as a synonym of *Neomicrocalamus*, which would also be taxonomically acceptable under the principle of nomenclatural priority (Turland *et al.*, 2025).

To evaluate whether synonymization of *Temochloa* and *Neomicrocalamus* is appropriate, morphological evidence is a key diagnostic criterion for defining generic boundaries. Although the genus *Temochloa* shows morphological similarity to *Neomicrocalamus*, such similarity has not, to date, been interpreted as sufficient to support their treatment as congeneric (Cai *et al.*, 2023, 2024). In the protologue of *Neomicrocalamus* by Keng (1983), with *N. prainii*

described as the type species, a needle-like culm leaf blade tip was identified as a diagnostic character of the genus. Another species, *N. andropogonifolius* (Griff.) Stapleton, was likewise circumscribed by this shared vegetative trait but can be distinguished from *N. prainii* by its raised nodes (Stapleton, 1994). The taxonomic status of *N. dongvanensis* T.Q.Nguyen, however, remains uncertain, as this species possesses erect culms that deviate from the typical morphology of the genus (Nguyen, 1991; Stapleton *et al.*, 1997; Cai *et al.*, 2023). Reproductive characters, including the number of glumes and florets, were previously used to compare *Neomicrocalamus* with putatively related genera such as *Racemobambos* Holttum (Stapleton, 1994). However, recent large-scale phylogenetic analyses have demonstrated that *Neomicrocalamus* and *Racemobambos* represent distinct evolutionary lineages (Liu *et al.*, 2024). Furthermore, Dransfield (2000) emphasized below-glume disarticulation, the presence of two glumes, and an elongated pseudospikelet stalk as key diagnostic characters of *Temochloa*, with the occurrence of a single floret serving to distinguish it from *Racemobambos*.

Because the morphological similarities of *Temochloa* and *Neomicrocalamus* have not been reconciled in previous studies, we re-examined a comprehensive set of vegetative and reproductive traits for the relevant taxa. Our results indicate that

Table 3. Morphological comparison of *Neomicrocalamus elegans* (N.H.Xia, You Y.Zhang, Z.Y.Cai & Y.H.Tong) W.Arthan, Teerawat & Sungkaew, *N. lilianus* (S.Dransf.) W.Arthan, Teerawat & Sungkaew, and *N. patellaris* W.Arthan, Teerawat & Sungkaew.

Characters	***N. lilianus*** (Dransfield, 2000; *Sungkaew et al. 1873*)	***N. elegans*** (Cai *et al.*, 2024)	***N. patellaris*** (*Sungkaew et al. 1617*, *1668*, *1669*, *1670*)
Internode diameter	1–2 mm	4–5 mm	5–10 mm
Patella at the culm node	inconspicuous	inconspicuous	prominent and deflexed
Culm leaf blade tip	acicular (needle-like)	acicular (needle-like)	acicular (needle-like)
Size of foliage leaves	4–7 × 0.5–0.9 cm	5–8 × 0.4–0.8 cm	(5.5–)9–13 × (0.8–)1.2–1.6 cm
Inflorescences	elongate, up to 4 cm long	not recorded	elongate, up to 60 cm long
Sheath subtending pseudospikelet	present	present	present
Pseudospikelet length	ca 1.5 cm	not recorded	2–3.5 cm
Pseudospikelet rachis	elongate	elongate	elongate
Prophylls	1, up to 5 mm long	1, 3–3.5 mm long	1, 5–7 mm long
Empty bracts	2	4–5	1
Fertile florets	1	2–4	2–3
Length of fertile florets	ca 7 mm long	7–9 mm long	8–12 mm long
Stamens	not seen	3.5–4.5 mm long	5–7(–9) mm long

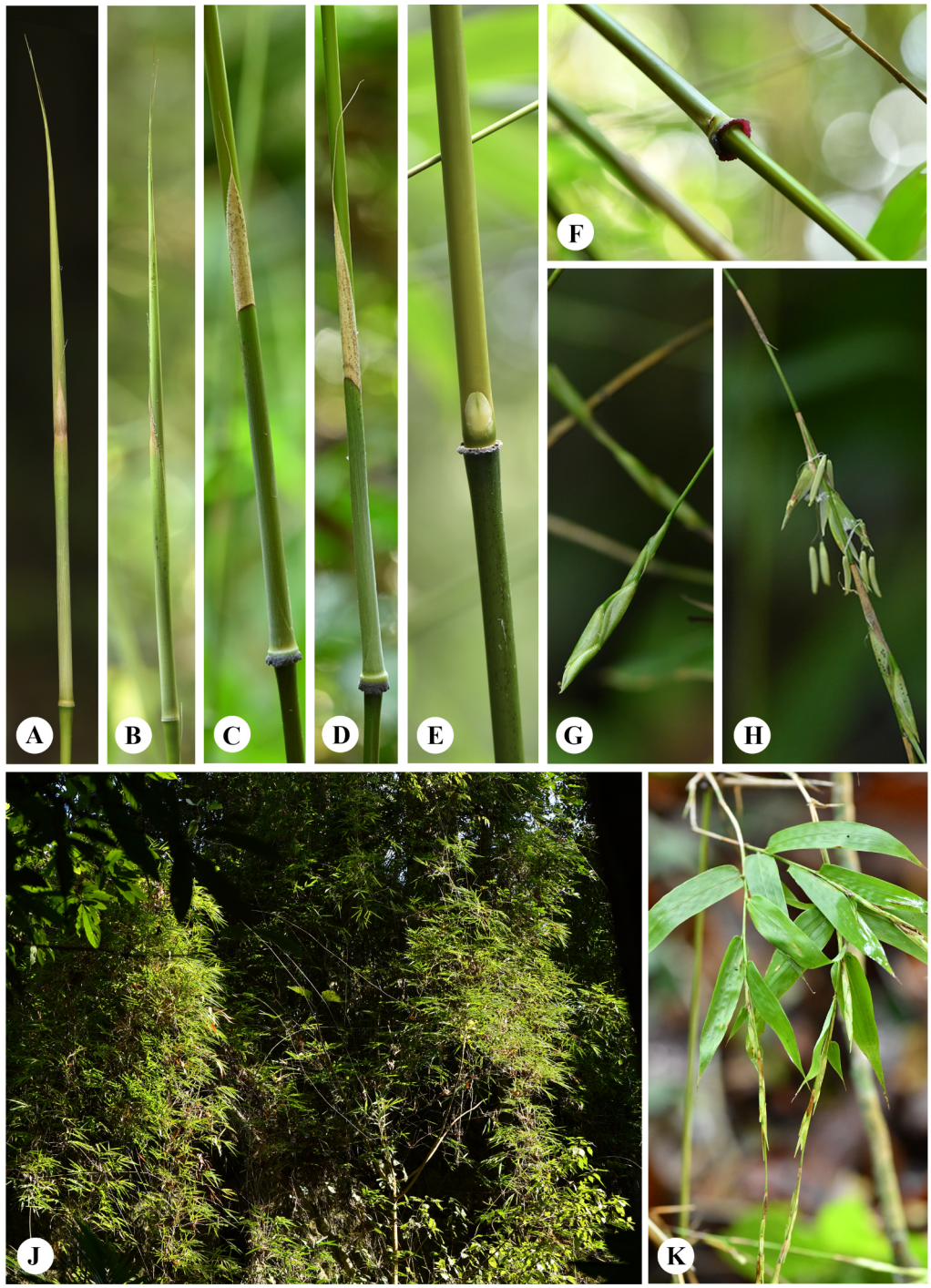


Figure 4. *Neomicrocalamus lilianus* (S.Dransf.) W.Arthan, Teerawat & Sungkaew. A. young shoot. *Neomicrocalamus patellaris* W.Arthan, Teerawat & Sungkaew. B. young shoot; C–D. young culms with culm leaves; E. elliptic-ovate primary branch bud at a culm node; F. patella at a young culm node; G. pseudospikelets; H. pseudospikelet with exserted stamens; J. habit; K. flowering branches. (photos A from *Sungkaew et al. 1873*; B–F, I from *Sungkaew et al. 1668*, G–H, K from *Sungkaew et al. 1617* by A. Teerawatananon).

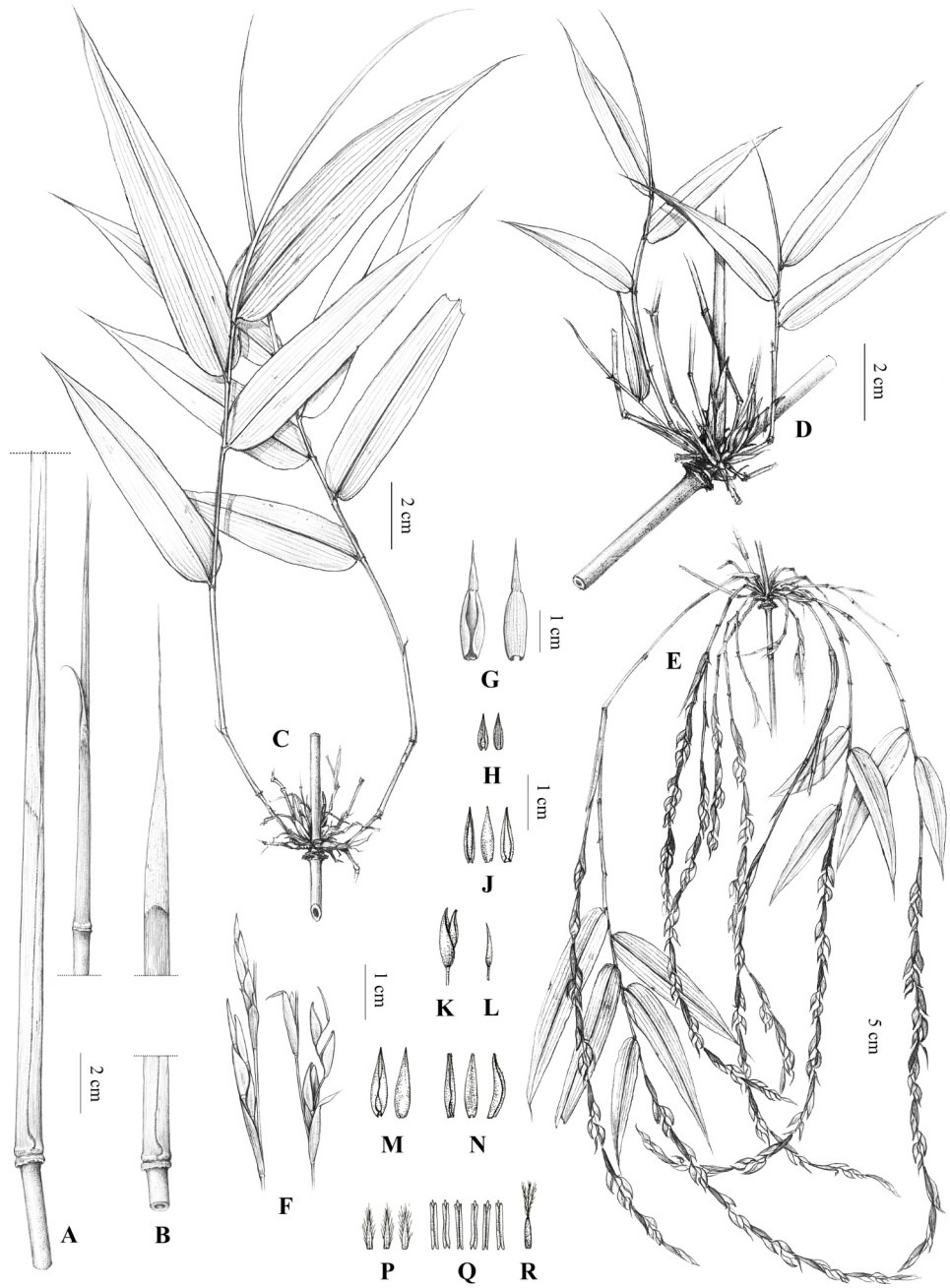


Figure 5. *Neomicrocalamus patellaris* W.Arthan, Teerawat & Sungkaew. A. portion of a young culm (left, showing a culm leaf) and a young shoot (right, showing culm leaves); B. below, a portion of a young culm, showing the basal part of a culm leaf and a node bearing a patella; above, an upper portion of a culm that had dried off earlier than the lower portion, showing the lack of a distinct junction between the sheath and blade and the acicular (needle-like) blade tip; C–D. branch complements and foliage leaves; E. portion of the main culm bearing flowering branches; F. pseudospikelets; G. sheaths in adaxial and abaxial views; H. prophylls in adaxial and abaxial views; J. bracts in adaxial and abaxial views; K. fertile floret; L. terminal vestigial floret; M. lemmas in adaxial and abaxial views; N. paleas in adaxial, abaxial, and lateral views; P. lodicules; Q. stamens; R. pistil. A–B from *Sungkaew et al. 1668*; C–R from *Sungkaew et al. 1617*. Drawn by P. Rayangkul.

the two genera form a morphologically natural group that shares several key characters, including an acicular (needle-like) culm leaf blade tip, an elongate rachis in the pseudospikelet, and the presence of a sheath subtending the pseudospikelet (Table 3). Our morphological observations are consistent with those of Cai *et al.* (2024), who noted the inactive nature of buds subtended by bracts within the pseudospikelet as an additional shared character, giving rise to a false semelauctant (determinate) inflorescence interpretation. Although Cai *et al.* (2024) suggested that bud shape and anther apex morphology distinguish *Temochloa* from *Neomicrocalamus*, we regard these characters as expressions of intra- and interspecific variation occurring in both genera. Consequently, we consider them to be of limited diagnostic value for generic delimitation in bamboos.

The inclusion of the new species, *Neomicrocalamus patellaris*, in the phylogenetic analyses broadens the morphological framework for generic delimitation. This taxon exhibits a clear combination of characters previously attributed to both *Temochloa* and *Neomicrocalamus*. Cai *et al.* (2024) proposed that a circular bud, a grooved culm leaf sheath, and an emarginate anther apex distinguish *Temochloa* from *Neomicrocalamus*, and consequently circumscribed *T. elegans* within *Temochloa*. However, the new species described here possesses both an elliptic-ovate primary branch bud and a cuspidate anther apex (Figs. 4, 5; Table 3), thereby directly undermining the diagnostic value of these characters. In addition, the number of florets per pseudospikelet is variable, indicating that this trait is labile and taxonomically unreliable at the generic level. Phylogenetically, the new species, *N. patellaris*, is consistently recovered as the sister species of *T. liliana* in both plastome- and nuclear-based analyses. Taken together, a comprehensive morphological reassessment and robust phylogenetic evidence demonstrate that the vegetative and reproductive characters previously used to separate *Temochloa* and *Neomicrocalamus* are insufficient for generic delimitation. We therefore formally revise the generic circumscription and place *Temochloa* in synonymy with *Neomicrocalamus*. Consequently, the new species is unambiguously treated as a member of *Neomicrocalamus* (see Taxonomic Implications).

Impact of interspecific hybridization, gene selection and taxon sampling on phylogenetic inference

Gene selection, the number of loci analysed, and taxon sampling can strongly influence species tree topology, particularly in studies involving introgressed lineages (Pollock *et al.*, 2010). Reports of plant hybridisation are rare in Thailand (Parnell *et al.*, 2013; Goh *et al.*, 2018) and more studies are required to assess the extent of hybridisation in different taxonomic groups. Incongruence among datasets and analyses can sometimes be explained by hybridisation however the incongruence here is more related to sampling than to the choice of gene. In the present study, although two additional accessions of the new species were included, the phylogenetic analyses were based on a reduced nuclear gene dataset. The results indicate a closer evolutionary relationship between the new species and *Temochloa liliana* than between the new species and *T. elegans*. The conflicting placements among taxa in published studies and the datasets compared here (full and reduced) may also indicate a more complex evolutionary history involving species of *Neomicrocalamus* and *T. elegans*, as suggested by the nuclear gene analyses, potentially shaped by interspecific hybridization. Taken together, differences in gene sampling, taxon representation, and the effects of reticulate evolution likely account for the inconsistent phylogenetic positions of *T. elegans* recovered across studies. According to Cai *et al.* (2024), the phylogenetic placement of *T. elegans* varies among different analyses. In their plastome-based phylogeny, *T. elegans* and *T. liliana* (the type species of *Temochloa*) form a grade, whereas the ASTRAL species tree inferred from nuclear data recovers them as monophyletic. Even if a reticulate evolutionary history involving *Temochloa* and *Neomicrocalamus* is inferred, such a pattern most plausibly explained by interspecific hybridization and does not invalidate the taxonomic re-evaluation proposed here. Rather, this evolutionary complexity further supports our conclusion that the characters previously used to distinguish the two ‘genera’ do not reflect independent evolutionary lineages. Their taxonomic unification is therefore justified and is additionally supported by comprehensive morphological evidence.

TAXONOMIC IMPLICATIONS

Our findings indicate that *Temochloa* and *Neomicrocalamus* cannot be clearly distinguished on the basis of either morphological or molecular characters. We therefore place *Temochloa* in synonymy with *Neomicrocalamus*, the latter having nomenclatural priority. An amended morphological description of *Neomicrocalamus* is provided here to reflect this broader generic circumscription. We also enumerate all taxa previously treated under *Temochloa* and provide their nomenclatural equivalents in *Neomicrocalamus*. Accepted names are shown in bold.

NEOMICROCALAMUS

Keng f., J. Bamboo Res. 2(2): 10. 1983. Type: *Neomicrocalamus prainii* (Gamble) Keng f. ≡ *Microcalamus* Gamble, J. Asiat. Soc. Bengal, Pt. 2, Nat. Hist. 59: 207. 1890, nom. illeg., non Franch., J. Bot. (Morot) 3: 282 (1889). ≡ *Temochloa* S.Dransf., Thai Forest Bull., Bot. 28: 179. 2000, **syn. nov.** Type: *Temochloa liliana* S.Dransf.

Clambering, unarmed bamboos. *Rhizomes* usually short-necked pachymorph. *Culms* unicaespitose, initially erect, later clambering, slender; internodes terete, smooth, not grooved, hollow to solid; nodes nearly level to more or less raised, with a persistent sheath-base collar, a girdle, or a patella; supranodal ridge usually inconspicuous or absent. *Primary branch buds* solitary, lanceolate to nearly circular with acuminate to obtuse apex, prophyll 2-keeled, initially closed at front. *Mid-culm branch* complements usually with many slender and subequal branches at each node, central primary branch sometimes dominant, reiterating and approaching the size of the culm. *Culm leaves* deciduous after branching, narrowly triangular, basally tough, apically papery and usually dried-off earlier; ligules inconspicuous or absent; auricles and fimbriae absent; blades persistent, erect, and tip long drawn-out (acicular or needle-like), continuous with the sheath, with no clear junction between sheath and blade. *Foliage leaves* broadly linear-lanceolate, 3–9 per branchlet, venation indistinct, apex acicular or long acuminate. *Inflorescences* iterauctant, terminal on leafy or leafless branches; comprising a sheath, a prophyll, and one to a few pseudospikelets. *Pseudospikelets* laterally compressed, bracts 1–5; rachilla internodes elongated above the upper bract; fertile florets 1–4(–6), with a terminal vestigial floret; lemmas glabrous or adaxial surface apically puberulent; paleae 2-keeled. *Lodicules* 3. *Stamens* 6; filaments free. *Ovary* ellipsoid or umbonate; stigmas 3. *Caryopses* ellipsoid.

A genus comprising six species and distributed in East Himalaya, India (Assam) China, Vietnam and Thailand. Two native species occur in Thailand.

Notes.— According to Dransfield (2000) and Li & Stapleton (2006), the term 'spikelet' is recognized as a basic flowering branch bearing glumes that do not subtend buds. In contrast, Wong (1995) and Cai *et al.* (2024) interpreted the basic flowering unit of *Neomicrocalamus* as a pseudospikelet rather than a true spikelet. A pseudospikelet is understood as a spikelet-bearing branch provided with one or more glumes, followed by bracts that subtend buds. Consequently, the structures positioned between the basal prophyll and the basic flowering branch in *Neomicrocalamus* may be interpreted either as bracts or as glumes. In iterauctant bamboo inflorescences, these structures are sometimes indistinguishable. To avoid ambiguity in the interpretation of the pseudospikelet in *Neomicrocalamus*, we follow Cai *et al.* (2024) in applying the term bract.

KEY TO THE SPECIES OF *NEOMICROCALAMUS* IN THAILAND

1. Nodes without a patella or with sheath scar prominent with a persistent sheath-base collar or absent; fertile floret 1 **1. N. liliana**

1. Nodes with a conspicuous patella; fertile floret 2 or 3 **2. N. patellaris**

1. Neomicrocalamus lilianus (S.Dransf.) W.Arthan, Teerawat & Sungkaew, **comb. nov.** ≡ *Temochloa liliana* S.Dransf. Thai Forest Bull., Bot. 28: 180, f.1, 2000. Type: Thailand, Phangnga, 24 Aug. 1967, *Shimizu, Fukuoka & Nalampoon 7904* (holotype **BKF** [BKF089574, photo seen]; isotypes **KYO**, **L**[L0105662, photo seen]). Fig. 4A.

Thailand.— PENINSULAR: Surat Thani; Khaosok, 23 Apr. 1990, *Pooma 419* (**BKF!**); Phanom district, 4 Oct. 2024, *Sungkaew et al. 1873* (**Thailand Natural History Museum**); ibid., 20 Feb. 2001, *Teerawatananon & Sungkaew 200201-1*; ibid., 16 July 2000, *Wong & Chamchumroon KWM2869* (**BKF!** [2 sheets], **K**); Phangnga, Thap Put, 24 Aug. 1967, *Shimizu et al. T7967* (**BKF!**).

Distribution.— Endemic to Thailand.

Ecology.— Restricted to the limestone hills of the peninsular region, in the slightly shaded limestone rockfaces of evergreen forest; at alt. 60–250 m.

2. Neomicrocalamus patellaris W.Arthan, Teerawat & Sungkaew, **sp. nov.** Type: Thailand. Tak, Umphang, alt. 825 m, 3 Apr. 2021, *Sungkaew, Teerawatananon & Pinyo 1617* (holotype **BKF!**; isotypes **BK!**, **BKF!**). Figs. 4B–K, 5.

Neomicrocalamus patellaris closely resembles *N. elegans* (formerly Temochloa elegans) and *N. lilianus* (formerly *T. liliana*) but can be readily distinguished from both species by the presence of a prominent patella at the culm node, a single bract, and comparatively longer pseudospikelets and stamens (Table 3).

Clambering, unarmed bamboos. *Rhizomes* short-necked pachymorph. *Culms* 5–7 m long; internodes dull green, 20–40(–60) cm long, 0.5–1 cm in diameter, glabrous; walls 2–3 mm thick; nodes slightly swollen, with a deflexed patella, patella up to 5 mm wide, pubescent to glabrous; supranodal ridges slightly prominent. *Primary branch buds* elliptic-ovate. *Culm leaves* initially green, later straw-colored, 10–20 cm long, symmetrical, glabrous, margins ciliate, base of outer margin sometimes with a tiny projection below the point of attachment; auricles absent, fimbriae absent; ligules absent; blades acicular to long acicular, usually curved, 2.5–9 cm long. *Foliage leaves* 3–7 per branchlet; auricles tiny, lobe-like, less than 1 mm high; ligules inconspicuous; blades (5.5–)9–13 × (0.8–)1.2–1.6 cm, adaxial glabrous, abaxial sparsely hairy along the veins to glabrous. *Inflorescences* up to 60 cm long. *Pseudo- spikelets* light green to green, 2–3.5 cm long; comprising 1 sheath, 1 prophyll, 1 bract, 2–3 fertile florets, and a terminal vestigial floret; sheaths 0.7–1.5 cm long, glabrous, usually with blades 1–5 mm long; basal prophylls 0.5–0.7 cm long, 2-keeled, glabrous; empty bracts chartaceous, 0.9–1 cm long, glabrous; rachilla internodes between the florets flat, 5–6 mm long, almost glabrous; fertile florets 0.8–1.2 cm long; lemmas folded, coriaceous, lanceolate, 0.8–1.2 cm long, almost glabrous; paleas 0.8–1.1 cm long, 2-keeled, apex truncate to slightly bifid, keels ciliate. *Lodicules* 3. *Stamens* 6, 5–7(–9) mm long; filaments free; anthers pale yellow to yellow, 0.5–0.9 mm long, apex cuspidate. *Caryopses* not seen.

Thailand.— Thailand. Tak, Umphang, alt. 1,085 m, 12 Jan. 2022, *Sungkaew et al. 1668* (**Thailand Natural History Museum**); ibid., alt. 1,095 m, 12 Jan. 2022, *Sungkaew et al. 1669* (**BK**, **BKF**, **Thailand Natural History Museum**); ibid., alt. 1,091 m, 12 Jan. 2022, *Sungkaew et al. 1670* (**BK**, **BKF**, **Thailand Natural History Museum**).

Distribution.— Endemic to Thailand.

Ecology.— Endemic to western Thailand, where it is currently known only from the Thung Yai Naresuan-East Wildlife Sanctuary. It occurs on limestone bedrock in dry evergreen forest and swamp forest.

Vernacular names.— Phai chanloi (ไผ่จันทร์ลอย) (Proposed here). The vernacular name is given in honour of Mr. Arnupap Janloy, who discovered this bamboo when he was a member of the Thailand Tiger Project.

Etymology.— The specific epithet is derived from the latin 'patella' meaning a small pan or dish referring to the appendage at the culm node that looks like a cup, a bowl or an umbrella.

Conservation status.— This species is currently known only from two locations of the Thung Yai Naresuan-East Wildlife Sanctuary in Umphang District of Tak Province, Western Thailand. A limited number of mature individuals have been identified, and their populations might be declining due to monocarpic flowering behavior and natural habitat succession. The species has an Extent of Occurrence (EOO) estimated to be less than 5,000 km² (specifically around 150 km²) and a restricted Area of Occupancy (AOO) of less than 500 km² (48 km²). As a result, we assess its conservation status as Endangered [EN B1ab(ii, v)+2ab(ii, v)].

New combinations in *Neomicrocalamus* outside Thailand

Neomicrocalamus elegans (N.H.Xia, You Y.Zhang, Z.Y.Cai & Y.H.Tong) W.Arthan, Teerawat & Sungkaew **comb. nov.**— *Temochloa elegans* N.H.Xia, You Y.Zhang, Z.Y.Cai & Y.H.Tong, PhytoKeys 246: 231, f. 1–2, 2024. Type: China, Guangxi, Jingxi, near Bandan Village, alt. 703 m, 10 June 2020, *N.H. Xia et al. BH85* (holotype **IBSC**).

Neomicrocalamus elegans var. glabra (N.H.Xia, Z.Y.Cai, You Y.Zhang, & J.B.Ni) W.Arthan, Teerawat & Sungkaew **comb. nov.**— *Temochloa elegans* var. *glabra* N.H.Xia, Z.Y.Cai, You Y.Zhang, & J.B.Ni, PhytoKeys 246: 235, 2024. Type: Vietnam, Ha Giang, Minh Ngoc Village, alt. 210 m, 24 May 2018, *N.H. Xia et al. 2018VNB040* (holotype **IBSC**; isotype **VNMN**).

ACKNOWLEDGEMENTS

This work was supported by (1) Kasetsart University Research and Development Institute, KURDI (FF(KU-SRIU)6.69); (2) a grant from the National Science Museum, Thailand (NSM), for the project "The Study on Species Diversity and Germplasm Collection of Bamboos genus *Bambusa* and genus *Schizostachyum* in Thailand"; (3) grants from the Kasetsart University Institute for Advanced Studies (KUIAS) and the Kasetsart University Center for Excellence Development Coordination (KUCOE) for the project "Brainstorming for the Application of DNA Sequence Data for Accurate and Precise Species Identification and Classification of the bamboo Genus *Schizostachyum* (Melocanninae-Bambuseae) and Related Genera in Thailand"; and (4) a Fundamental Fund (FF) research grant for the project "Studies of DNA Barcoding for Standardization of Accurate and Precise Species Identification of Economic Bamboos in the Subtribe Bambusinae in Thailand for Sustainable Applications". Molecular work was supported by the facilities provided by Universiti Tunku Abdul Rahman.

We would like to thank Dr. Zhou-Yu Cai for valuable suggestions and discussions on the taxonomy of this bamboo group. We are also grateful to the staff of all herbaria and the Department of National Parks, Wildlife and Plant Conservation (DNP) involved in this study for providing specimens and information. This research was conducted as part of the Flora of Thailand Project, organized by the Forest Herbarium of the DNP, the National Science Museum, Thailand (NSM), the Faculty of Forestry, Kasetsart University, and the Faculty of Pharmacy, Mahidol University.

We also thank the staff of the Khao Nang Rum Wildlife Research Station and the Tigers in Western Forest Complex Project for their assistance and for providing valuable information.

REFERENCES

Andrews, S. (2010). FastQC: a quality control tool for high throughput sequence data. http://www.bioinformatics.babraham.ac.uk/projects/fastqc. Accessed April 2026.

Bachman, S., Moat, J., Hill, A.W., de la Torre, J. & Scott, B. (2011). Supporting Red List threats assessment with GeoCAT: geospatial conservation assessment tool. ZooKeys 150: 117–126.

Baker, W.J., Bailey, P., Barber, V., Barker, A., Bellot, S., Bishop, D., Botigue, L.R., Brewer, G., Carruthers, T., Clarkson, J.J., Cook, J., Cowan, R.S., Dodsworth, S., Epitawalage, N., Francoso, E., Gallego, B., Johnson, M., Kim, J.T., Leempoel, K., Maurin, O., McGinnie, C., Pokorny, L., Roy, S., Stone, M., Toledo, E., Wickett, N.J., Zuntini, A.R., Eiserhardt, W.L., Kersey, P.J., Leitch, I.J. & Forest, F. (2022). A comprehensive phylogenomic platform for exploring the angiosperm tree of life. Systematic Biology 71: 301–319.

Bolger, A.M., Lohse, M. & Usadel, B. (2014). Trimmomatic: a flexible trimmer for Illuminasequence data. Bioinformatics 30: 2114–2120.

BPG (Bamboo Phylogeny Group). (2012). An updated tribal and subtribal classification of the bamboos (Poaceae: Bambusoideae). The Journal of the American Bamboo Society 24: 1–10. https://bamboo.org/_uploads/pdfs/BSCv25.pdf. Accessed April 2026.

Cai, Z.-Y., Niu Z.-Y., Zhang, Y.-Y., Tong, Y.-H., Vu, T.C., Goh, W.L., Sungkaew, S., Teerawatananon, A. & Xia, N.-H. (2023). Phylogenomic analyses reveal reticulate evolution between *Neomicrocalamus* and *Temochloa* (Poaceae: Bambusoideae). Frontiers in Plant Science 14: 1274337.

Cai, Z.-Y. & Xia, N.-H. (2024). A novel elucidation for synflorescences of Chinese bamboos. Plants 13: 29.

Cai, Z.-Y., Zhang, Y.-Y., Tong, Y.-H., Vu, T.C. & Xia, N.-H. (2024). *Temochloa* (Poaceae, Bambusoideae), a newly-recorded bamboo genus for China and Vietnam, with new taxa and a re-interpretation of flowering structures. PhytoKeys 246: 229–236.

Corl, A. & Ellegren, H. (2013). Sampling strategies for species trees: The effects on phylogenetic inference of the number of genes, number of individuals, and whether loci are mitochondrial, sex-linked, or autosomal. Molecular Phylogenetics and Evolution 67: 358–366.

Clements, R., Sodhi, N.S., Schilthuizen, M. & Ng, P.K.L. (2006). Limestone karsts of southeast Asia: Imperiled arks of biodiversity. BioScience 56: 733–742.

Darriba, D., Taboada, G.L., Doallo, R. & Posada, D. (2012). jModelTest2: more models, new heuristics and parallel computing. Nature Methods 9: 722.

Doyle, J.J. & Doyle, J.L. (1987). A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochemical Bulletin 19: 11–15.

Dransfield, S. (2000). *Temochloa*, a new bamboo genus (Poaceae-Bambusoideae) from Thailand. Thai Forest Bulletin (Botany) 28: 179–182.

Goh, W.L., Sungkaew, S., Teerawatananon, A., Ohrnberger, D., Xia, N.-H., Chan, K.S., How, Y.X. & Wong, K.M. (2018). The hybrid origin of Phai Liang, a bamboo of recent introduction into horticulture in Southeast Asia, and a new nothogenus, ×*Thyrsocalamus* (Bambuseae: Bambusinae). Phytotaxa 362: 271–281.

Haevermans, T., Mantuano, D., Zhou, M.-Y., Lamxay, V., Haevermans, A., Blanc, P. & Li, D.-Z. (2020). Discovery of the first succulent bamboo (Poaceae, Bambusoideae) in a new genus from Laos' karst areas, with a unique adaptation to seasonal drought. PhytoKeys 156: 125–137.

IUCN Standards and Petitions Committee. (2024). Guidelines for using the IUCN Red List categories and criteria. Version 16. Prepared by the Standards and Petitions Committee. http://www. iucnredlist. org/documents/RedListGuidelines.pdf. Accessed May 2026.

Jin, J.-J., Yu, W.-B., Yang, J.-B., Song, Y., dePamphilis, C.W., Yi, T.-S. & Li, D.-Z. (2020). GetOrganelles: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biology 21: 241.

Johnson, M.G., Gardner, E.M., Liu, Y., Medina, R., Goffinet, B., Shaw, A.J., Zerega, N.J.C. & Wickett, N.J. (2016). HybPiper. Extracting coding sequence and introns for phylogenetics from high-throughput sequencing reads using target enrichment. Applications in Plant Sciences 4: 1600016.

Katoh, K. & Standley, D.M. (2013). MAFFT Multiple alignment software version 7: Improvements in performance and usability. Molecular Biology and Evolution 30: 772–780.

Keng, P.C. (1983). A revision of the genera of bamboos from the world (IV). Journal of Bamboo Research 2: 1–17.

Kiew, R. & Rahman, R.A. (2021). Plant diversity assessment of karst limestone, a case study of Malaysi'as Batu Caves. Nature Conservation 44: 21–49.

Li, D.-Z. & Stapleton, C.M.A. (2006). *Neomicrocalamus*. In: C.Y. Wu, P.H. Raven & D.Y. Hong (eds), Flora of China 22: 57. Science Press, Beijing; Missouri Botanical Garden Press, St. Louis.

Liu, J.-X., Zhou, M.-Y., Yang, G.-Q., Zhang, Y.-X., Ma, P.-F., Guo, C., Vorontsova, M.S. & Li, D.-Z. (2020). ddRAD analyses reveal a credible phylogenetic relationship of the four main genera of *Bambusa-Dendrocalamus-Gigantochloa* complex (Poaceae: Bambusoideae). Molecular Phylogenetics and Evolution. 146: 106758.

Liu, J.-X., Guo, C., Ma, P.-F., Zhou, M.-Y., Luo, Y.-H., Zhu, G.-F., Xu, Z.-C., Milne, R.I., Vorontsova, M.S. & Li, D.-Z. (2024). The origin and morphological character evolution of the paleotropical woody bamboos. Journal of Integrative Plant Biology 66: 2,242–2,261.

Minh, B.Q., Schmidt, H.A., Chernomor, O., Schrempf, D., Woodhams, M.D., von Haeseler, A. & Lanfear, R. (2020). IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era. Molecular Biology and Evolution 37: 1,530–1,534.

Middleton, D.J. (2010). Three new species of *Wrightia* (Apocynaceae: Apocynoideae) from Thailand. Gardens' Bulletin Singapore 61: 369–378.

Murray, N.J., Keith, D.A., Tizard, R., Duncan, A., Htut, W.T., Hlaing, N., Oo, A.H., Ya, K.Z. & Grantham, H. (2020). Threatened ecosystems of Myanmar: An IUCN Red List of Ecosystem Assessment. Version 1.0. Wildlife Conservation Society. Yangon, Myanmar: Wildlife Conservation Society.

Nguyen, T.Q. (1991). A new genus and the new species of bamboos (Poaceae, Bambusoideae) from Vietnam. Botanicheskii Zhurnal (Moscow Leningard) 76: 874–880.

Parnell, J.A.N., Pedersen, H.Æ., Hodkinson, T.R., Balslev, H., Vanwelzen, P.C., Simpson, D., Middleton, D.J., Esser, H.-J., Pooma, R., Utteridge, T. & Staples, G. (2013). Hybrids and The Flora of Thailand. Thai Forest Bulletin (Botany) 41: 1–9.

Pollock, D.D., Zwickl, D.J., McGuire, J.A. & Hilis, D.M. (2010). Increased taxon sampling is advantageous for phylogenetic inference. Systematic Biology 51: 664–671.

POWO. (2026). Plants of the World Online. Facilitated by the Royal Botanic Gardens, Kew. https://powo.science.kew.org/. Accessed April 2026.

Rambaut, A., Drummond, A.J., Xie, D., Xie, D., Baele, G. & Suchard, M. (2018). Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. Systematic Biology 67: 901–904.

Rodda, M. (2020). Two new species and two new records of *Marsdenia* (Apocynaceae) from Thailand. Annales Botanici Fennici 57: 9–15.

Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D.L., Darling, A., Höhna, S., Larget, B., Liu, L., Suchard, M.A. & Huelsenbeck, J.P. (2012). MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice across a large model space. Systematic Biology 61: 539–542.

Sayyari, E. & Mirarab, S. (2016). Fast coalescent-based computation of local branch support from quartet frequencies. Molecular Biology and Evolution 33: 1654–1668.

Sirichamorn, Y., Balslev, H. & Mattapha, S. (2016). Two new species of *Callerya* Endl. (Leguminosae: Papilionoideae) from Thailand. Phytotaxa 263. 42–50.

Smart, D. (2002). Thungyai Naresuan Cave Survey Project. Final Report. Royal Forest Department, Bangkok.

Stamatakis, A. (2014). RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30: 1,312–1,313.

Stapleton, C.M.A. (1994). The bamboos of Nepal and Bhutan. part III: *Drepanostachyum*, *Himalayacalamus*, *Ampelocalamus*, *Neomicrocalamus* and *Chimonobambusa* (Gramineae: Poaceae, Bambusoideae). Edinburgh Journal of Botany 5: 301–330.

Stapleton, C.M.A, Li, D.-Z. & Xue, J.-R. (1997). A new combination in *Cephalostachyum* with notes on names in *Neomicrocalamus* (Gramineae: Bambusoideae). Kew Bulletin 52: 699–702.

Tillich, M., Lehwark, P., Pelllizer, T., Ulbricht-Jones, E.S., Fischer, A., Bock, R. & Greiner, S. (2017). GeSeq - versatile and accurate annotation of organelle genomes. Nucleic Acids Research 45: W6–W11.

Turland, N.J., Wiersema, J.H., Barrie, F.R., Gandhi, K.N., Gravendyck, J., Greuter, W., Hawksworth, D.L., Herendeen, P.S., Klopper, R.R., Knapp, S., Kusber, W.-H., Li, D.-Z., May, T.W., Monro, A.M., Prado, J., Price, M.J., Smith, G.F. & Zamora Señoret, J.C. (2025). International Code of Nomenclature for algae, fungi, and plants (Madrid Code). Regnum Vegetabile 162. University of Chicago Press, Chicago.

van de Bult, M. & Greijmans, M. (2006). Vegetation types and the deciduous-evergreen forest continuum along an elevation gradient in Mae Wong National Park, Western Thailand. The Natural History Bulletin of the Siam Society 54: 27–74.

van de Bult, M. & Steinmetz, R. (2006). Rare plants and new tree species distribution records from Thung Yai Naresuan Wildlife Sanctuary, Thailand. The Natural History Bulletin of the Siam Society 54: 81–88.

Vorontsova, M.S., Clark, L.G., Dransfield, J., Govaerts, R. & Baker, W.J. (2016). World checklist of bamboos and rattans. International Network of Bamboo and Rattan & the Board of Trustees of the Royal Botanic Gardens, Kew, London.

WCS Thailand Program. (2005). Western Forest Complex (WEFCOM). Bangkok: Wildlife Conservation Society Thailand. http://www.wcsthailand.org/english/wefcom. Accessed April 2026.

WFO. (2026). World Flora Online. Published on the Internet; http://www.worldfloraonline.org. Accessed April 2026.

Wong, K.M. (1995). The Bamboos of Peninsular Malaysia. Forest Research Institute, Malaysia.

Wysocki, W.P., Clark, L.G., Attigala, L., Ruiz-Sanchez, E. & Duvall, M.R. (2015). Evolution of the bamboos (Bambusoideae; Poaceae): A full plastome phylogenomic analysis. BMC Evolutionary Biology 15: 50.

Zhang, C., Rabiee, M., Sayyari, E. & Mirarab, S. (2018). ASTRAL-III: polynomial time species tree reconstruction from partially resolved gene trees. BMC Bioinformatics 19: 153.