



Kaempferia candida (Zingiberaceae): Curcuma in disguise



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Results of morphological studies supported by molecular analyses of chloroplast *psbA-trnH* and partial *petA-psbJ* DNA sequences indicate that *Kaempferia candida* cannot be maintained. The species has to be transferred to *Curcuma* and the name needs to be typified.



Figure 1. The original painting of *Kaempferia candida* from Plantae Asiaticae Rariores (1830) (reproduced with permission of Singapore Botanic Gardens) and the Wallich specimen, Wall. Cat. No. 6585, in K-W (reproduced with kind permission of the Trustees of the Royal Botanic Gardens, Kew).

MATERIAL, METHODS & RESULTS

Plant samples for molecular analysis - 42 accessions including 21 *Kaempferia* species, 9 *Curcuma* species and 10 species from the subfamily Zingiberoideae were included in the analysis (Table 1).

DNA extraction, Polymerase Chain Reaction (PCR), and DNA sequencing - The *psbA-trnH* and partial *petA-psbJ* spacer sequences of all *Kaempferia* species and selected Zingiberoideae species were obtained from a previous study by Techaprasan et al. (2006 and 2010). Genomic DNA of all *Curcuma* species, *Boesenbergia rotunda* and *Hedychium longicoriatum* was extracted from leaves using the CTAB method with minor modification (Doyle and Doyle 1987). The *psbA-trnH* and *petA-psbJ* regions of each sample were separately amplified and sequenced as described in Techaprasan et al. (2006).

Data analysis - Sequences of *psbA-trnH* and partial *petA-psbJ* spacers were aligned and edited using BioEdit version 7.0.5.2 (Hall 1999). Disregarding indels, nucleotide sequence divergence between pairs of taxa was calculated using a Kimura (1980) 2-parameter model. Maximum parsimony analysis was performed using Phylogenetic Analysis Using Parsimony (PAUP*) version 4.0 Beta 10 (Swofford 2004). Gaps were treated as missing data. The most parsimonious trees were obtained through a heuristic search with tree-bisection-reconnection (TBR) branch swapping option and 10,000 random sequence additions. The Bootstrap method (1,000 replicates) with heuristic search was also performed.

Results - After multiple sequence alignments, the lengths of the nucleotide sequences were 923 bp for *psbA-trnH* and 819 bp for partial *petA-psbJ* spacer. Based on the combined data, 1,742 bp in length were obtained, including 107 and 61 variable parsimoniously uninformative and informative sites, respectively. The pairwise nucleotide divergence of combined data within *Kaempferia*, *Curcuma* and across all investigated samples ranged between 0.00-1.61% (*K. parviflora* and *K. minuta* ined.), 0.00-0.96% (*C. parviflora* and *C. singularis*) and 0.00-2.53% (*K. minuta* ined. and *C. biloba*), respectively. The strict consensus tree of 5,589 most parsimonious trees from the combined data set generated 212 steps with consistency (CI), retention (RI), and homoplasy indices of 0.85, 0.88 and 0.15 respectively (Fig. 3). All *Kaempferia* species in Thailand clustered together in the same clade, except two accessions of *K. candida* which were nested within the *Curcuma* group with strong bootstrap support (93%). The *Curcuma* species were divided into two major groups; group I (*Curcuma* sp., *C. comosa*, *C. latifolia*, *C. rubrobracteata*, and *C. codonantha*) including *K. candida* and group II (*C. harmandii*, *C. rhodantha*, and *C. parviflora*) including *Stahlianthus* sp.

INTRODUCTION

Kaempferia candida Wall. (1830) is a peculiar ginger species described from a material consisting of an inflorescence with flowers only (Fig. 1). Wallich placed this taxon in the genus *Kaempferia*, plausibly based on the lack of anther spurs but presence of well-developed anther crest, inflorescence made of fertile bracts with no coma and unusually big flowers, which appear before the leaves, remotely resembling those of *K. rotunda*. Baker (1890), Schumann (1904) and Gagnepain (1908) with no new material on hand merely adapted the description from the protologue, but did not pay closer attention to this species, placing it unequivocally in *Kaempferia*, subg. *Protanthium* Horan.

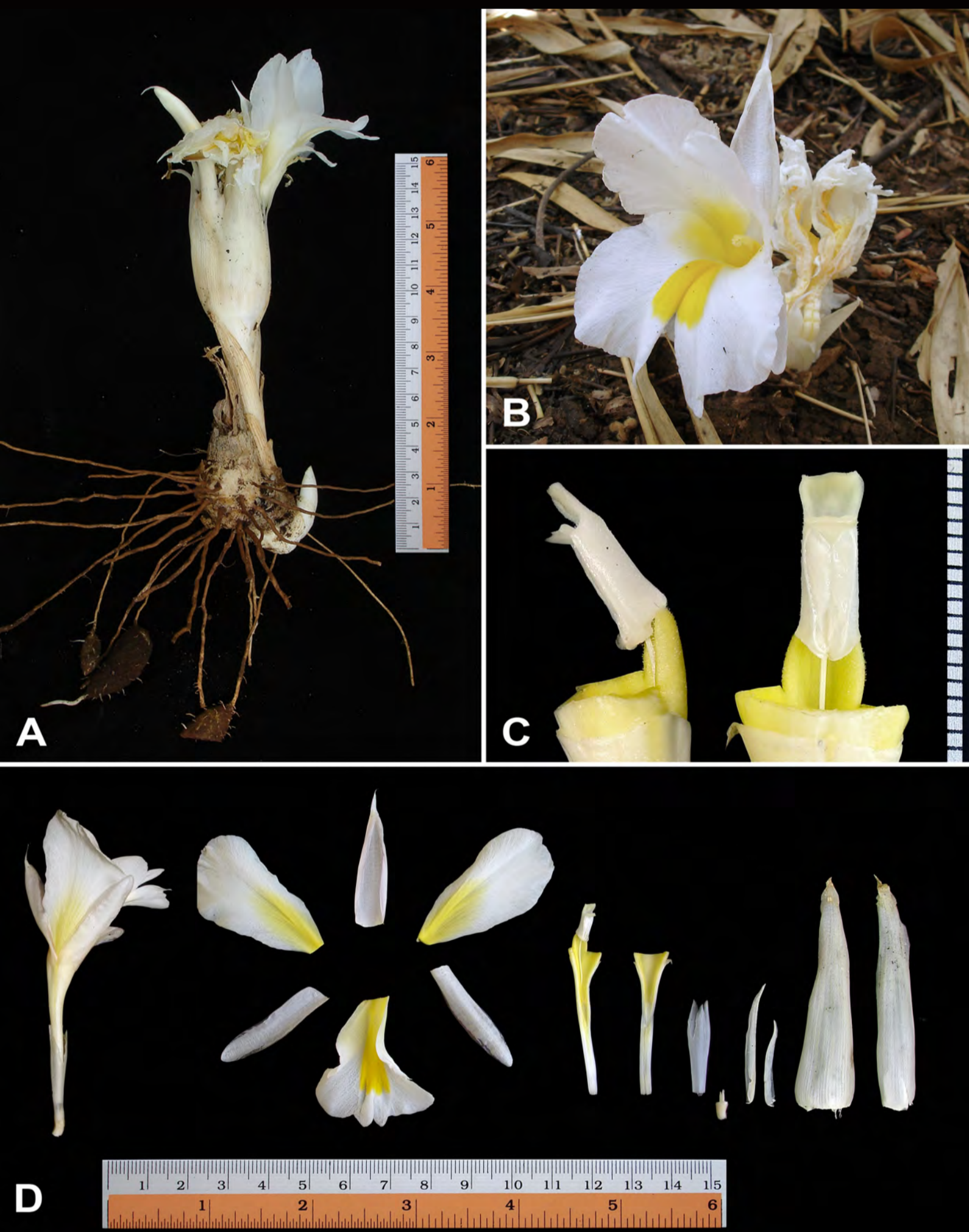
The new distributional record of this species by Jenittikul & Larsen (2000) from Kanchanaburi Province near the border with Myanmar and not far from its type locality (Amherst and Molmyne) included a detailed description, drawing and colour photographs. While the find was indeed a perfect match with Wallich's description and drawing, several morphological features of this unusual species raised our doubts about its generic placement in the genus *Kaempferia* (Fig. 2, Table 2.). All these characters suggest a possible close relationship with several members of *Curcuma*.

Techaprasan et al. (2010) studied 71 accessions of Thai *Kaempferia* and closely related taxa of Zingiberaceae using chloroplast *psbA-trnH* and partial *petA-psbJ* DNA sequences, and concluded that all *Kaempferia* species fall within the same group, except *K. candida*. *Curcuma* species were, however, not included in that study. The original description, type material, other herbarium material (including spirit) and recently collected living material of *K. candida* and *psbA-trnH* and partial *petA-psbJ* DNA sequences of several members of *Curcuma* and *Kaempferia* were therefore analysed in order to assess the generic placement of *K. candida*.

MORPHOLOGICAL & MOLECULAR EVIDENCE

Pairwise nucleotide divergence of the combined data in the *Curcuma* clade ranged between 0.00-0.96% which was lower than in *Kaempferia* (0.00-1.61%). Pairwise nucleotide divergence was particularly low (0.00-0.07%) in *Curcuma* group I (including *K. candida*), suggesting that cpDNA sequences of *psbA-trnH* and *petA-psbJ* in *Curcuma* group I have been conserved. In agreement with a previous study of *Kaempferia* using same markers (Techaprasan et al. 2010), all *Kaempferia* species were allocated to the same group, except *K. candida*. In addition, precociously flowering *Kaempferia* species, i.e., *K. rotunda*, *K. grandifolia*, *Kaempferia* sp. 1, *Kaempferia* sp. 2, and *Kaempferia* sp. 3, formed a well-supported group within *Kaempferia*. *Kaempferia candida* was strongly supported in *Curcuma* clade I (corresponding to the nominate subgenus *Curcuma*) with 93% bootstrap support. Therefore, based on molecular evidence of maternally inherited cpDNA *psbA-trnH* and partial *petA-psbJ* data, *K. candida* belongs in *Curcuma* (Fig. 3).

Morphological evidence listed in Table 2. also clearly supports inclusion of *Kaempferia candida* into *Curcuma*.



<i>Kaempferia</i>	<i>Kaempferia candida</i>	<i>Curcuma</i>
usually a very short or poorly developed pseudostem and a few leaves, which are often appressed to the ground	leafy shoot with a well-developed pseudostem and thin, prominently plicate laminae occasionally with a red patch on the midrib	leafy shoot with mostly well-developed pseudostem and thin, prominently plicate laminae occasionally with a red patch on the midrib
one flower per fertile bract	cincinnus of 4-6 flowers	cincinnus of 2-many flowers, rarely single flower
short bright yellow patches at the base of the labellum rarely seen in some precocious species, but never across the entire labellum	a deep yellow median band across the entire labellum	a deep yellow median band present in majority of <i>Curcuma</i> species
non versatile anther	versatile anther, the shape falls comfortably within <i>Curcuma</i>	versatile anther with large spectrum of morphological variability

Table 2. Morphological comparison of *Kaempferia candida* to the members of the genera *Kaempferia* and *Curcuma*. Shared characters are in bold.

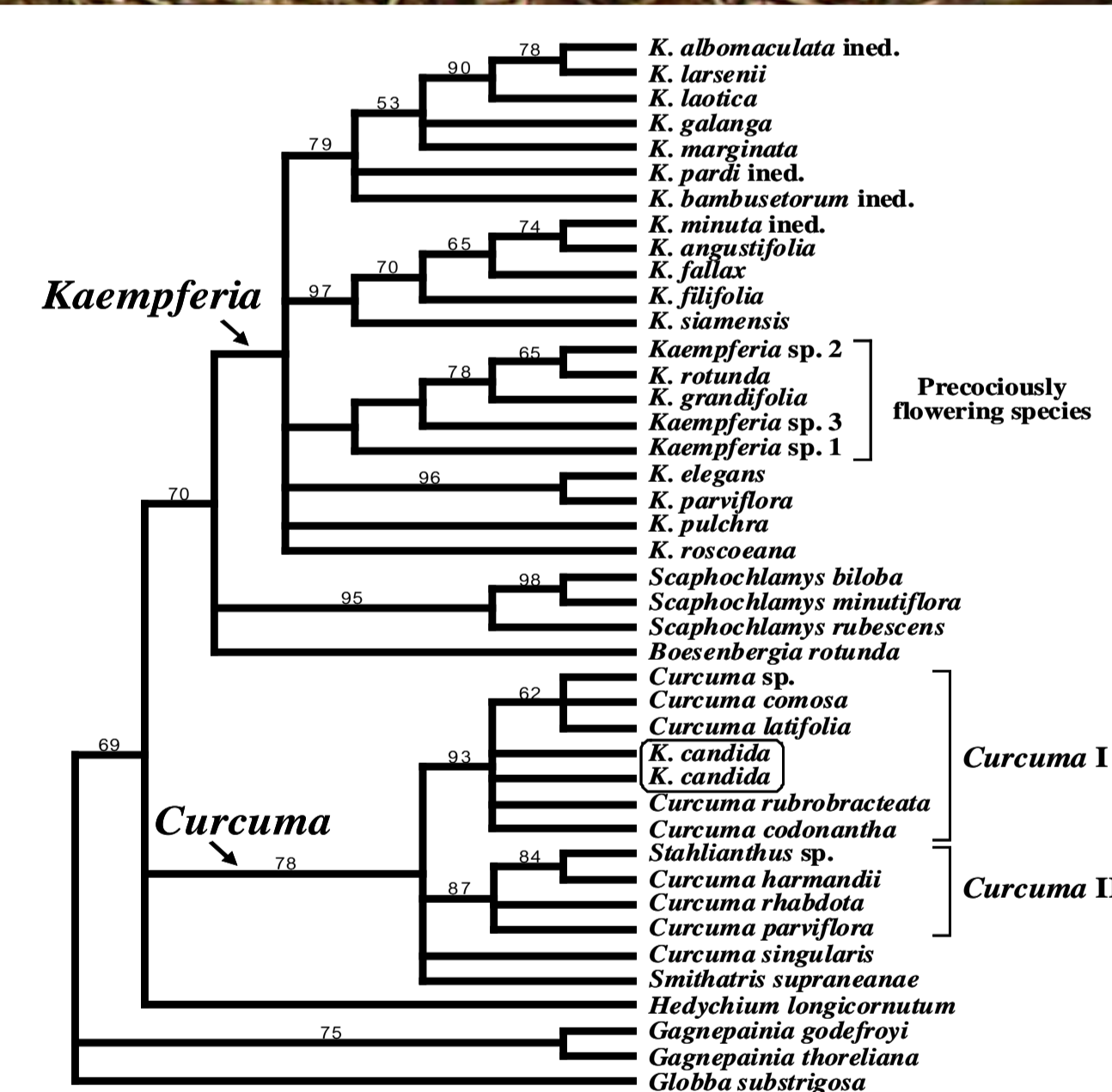


Figure 3. The strict consensus tree of 5,589 most parsimonious trees based on combined chloroplast *psbA-trnH* and partial *petA-psbJ* data generated 212 steps with consistency index (CI) of 0.85, 0.88, and 0.15, respectively. Numbers above branches indicate bootstrap values (>50%).

FORMAL TRANSFER & TYPIFICATION

Curcuma candida (Wall.) Techaprasan & Škorničková. comb. nov., in Nord. J. Bot. (in press)

Basionym: *Kaempferia candida* Wall. Pl. Asiat. Rar. I., part 3, 47, t. 56 (1830)

Typus: *Kaempferia candida*, Moalmyne, 1827, Wallich Cat. No. 6585 (K-W); [proposed lectotype]; [icon in] tab 56, in Wallich, Pl. Asiat. Rar. I., part 3, 1830 (proposed epitype).

While in the previous work Jenittikul & Larsen (2000) indicated that the Wallich specimen, Wall. Cat. No. 6585 at Kew is a holotype, it has to be acknowledged that Wallich did not designate a type specimen nor cite any herbarium material. In conformity with ICBN Art. 9.10., all duplicates of Wallich specimen, Wall. Cat. No. 6585 (Wallich, 1829-1832), as well as the excellent colour painting accompanying Wallich's original description (tab. 56), are considered to be part of the original material suitable for selection as lectotype. Leong-Škorničková et al. (2010) have explained that ideally the specimen and the drawing (if it exists) form material adequate for interpreting historical species names in Zingiberaceae. Therefore, we propose to designate the Wallich specimen, Wall. Cat. No. 6585 at K-W as the lectotype, supported by the colour drawing tab. 56 as its epitype (Fig. 1).

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WHAT NEXT?

Due to limited numbers of parsimoniously informative characters, evolutionary relationships within the *Curcuma* clade were unresolved. To determine the closest relative of *Curcuma candida* and to elucidate the evolutionary relationships and possible occurrences of hybridization within the *Curcuma* clade, more samples of *Curcuma* species, and more informative data from other DNA regions are required. *Stahlianthus* sp. and *Smithatris supraneeanae* were also nested within the *Curcuma* clade, a result which agrees with previous phylogenetic studies of Zingiberaceae and Zingibereae respectively using both nuclear and chloroplast DNA sequences (Kress et al. 2002, Ngamriabsakul et al. 2004). Work on a new infra-generic classification of the genus *Curcuma* and refinement of the position of *C. candida* is in progress by Závěská et al.

ACKNOWLEDGMENTS

We thank the curators of BK, BKF, L. K. SING and Suan Luang Rama IX herbaria for letting us examine specimens in their care, the Asian Zingiberaceae Information Centre at Singapore Botanic Gardens, Zingiberaceae Resource Centre at the Royal Botanic Garden Edinburgh (<http://elmer.rbge.org.uk/ZRC/>) for providing references, and the Trustees of the Royal Botanic Gardens, Kew and the Singapore Botanic Gardens for letting us reproduce images in Figure 1. We thank J.F. Veldkamp (L) for sending us digital images of several specimens. We would like to thank Dr. Thanya Jenittikul for providing numerous Zingiberaceae plant samples and accompanying us to the field, and to Miss Tidarat Puangpairote who also provided some of the samples. The first author is grateful to Dr. Sirawut Klinbunga for project advice. We also thank Dr. M. Newman (E) and Dr. N. Hind (K) for providing helpful comments on the manuscript. Funding by the Thailand Research Funds (TRF) and the National Center for Genetic Engineering and Biotechnology (BIOTEC) for Biodiversity Research and Training Program (BRT) [grant numbers BRT R251137 and R252111], National Parks Board (Singapore) and the Czech Science Foundation, GACR [grant numbers 521/09/0202 and P506/10/0623] is gratefully acknowledged.