

DNA barcoding for identification of water-onion (*Crinum thaianum*), an endangered species in Thailand

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Received 22 Jan 2024, Accepted 8 May 2025

Available online 15 Jun 2025

ABSTRACT: *Crinum thaianum*, also known as water-onion, has been widely used as an ornamental plant in fish tanks and aquariums, an indicator of water quality in natural water sources, and a component in some skincare products. Unfortunately, it is now listed as an endangered species because of the ongoing reduction in its natural area due to habitat destruction, a result of flood protection measures and illegal harvesting for exportation and domestic consumption. This study reported for the first time the use of DNA barcoding, a molecular technique for species-specific identification of this endangered species. Four DNA barcoding regions in six water-onion samples were studied, i.e., the chloroplast-encoded maturase K (*matK*), ribulose-bisphosphate carboxylase large subunit (*rbcL*) and transfer RNA-histidine (*trnH*)-photosystem II protein D1 (*psbA*) intergenic spacer, and the nuclear-encoded the internal transcribed spacer of ribosomal DNA (ITS of *rDNA*). The six water-onion samples were collected from different locations and 13 other *Crinum* species. The results showed a high genetic similarity among the six water-onion samples. Four nucleotide substitutions were identified in two different regions (*trnH-psbA* and ITS) in the 6 water-onion samples. Although all 4 regions could be used to distinguish the species from each other, the ITS of *rDNA* region gave the best result for *Crinum* species discrimination, based on the bootstrap value of the phylogenetic tree and the optimum genetic distance length. This technique could be an efficient tool for species-specific identification and for supporting conservation practices in the future.

KEYWORDS: *Crinum thaianum*, water-onion, *matK*, *rbcL*, *trnH-psbA*, ITS

INTRODUCTION

Crinum (C.) thaianum (water-onion), an aquatic species found only in Thailand, is a native plant of the Southern Provinces of Ranong and Phang Nga [1]. Water-onion is a flowering plant in the family Amaryllidaceae. Its leaves are extremely tough, making it suitable for aquariums with large fish and thus an economic plant that is popular as an ornamental plant in fish tanks and aquariums. In addition, water-onion can be used as an indicator of the quality of stream water because it can only grow in clear, clean water. Furthermore, *C. thaianum* extract has been used in cosmetics and skincare products [2].

Many years ago, during its blooming season, water-onion was promoted by the local tourism industry. At present, it is classified as an endangered species on the International Union for Conservation of Nature (IUCN) Red List due to upstream destruction for flood protection resulting in habitat degradation and reduction [3]. Furthermore, another important issue is an illegal digging of the plant for exportation. These practices have resulted in a substantial reduction of the plant. Although there is a ban on digging up water-onion, it has not been strictly enforced.

DNA barcoding is a concept that applies gene or universal DNA sequence differences to support the identification and classification of organisms [4]. The qualities of the DNA barcoding region must be high interspecific with low intraspecific variation and must

have a conservative region. There are many encoded genes or regions (both nuclear and chloroplast) that can be used as DNA barcodes for plants [5]. The chloroplast gene regions, the ribulose-bisphosphate carboxylase large subunit (*rbcL*) gene and the maturase K (*matK*) gene have been widely used for plant barcoding analysis. In addition, the plastid transfer RNA-histidine-photosystem II protein D1 (*trnH-psbA*) intergenic spacer (non-coding) region has been successfully amplified in many plant species and shows a high power of discrimination with its high substitution rate [6]. Moreover, the chloroplast genomes of bamboo species are being studied to provide data beneficial for future research on systematics, genetic diversity, and evolutionary history [7]. The internal transcribed spacer (ITS) in the nuclear genome is located between the large and small subunits of *ribosomal RNA (rRNA)* genes. Due to the high copy number of *rRNA* genes, it is easy to amplify even from small quantities of DNA [8]. In addition, the ITS region has a high degree of variation even between closely related species, making this region popular for phylogenetic analysis and species identification [9–11].

Although there is a ban on digging up water-onion, it has not been strictly enforced. In addition, genetic information at the molecular level of water-onion has not yet been reported. Thus, it would be useful to have the genetic information water-onion for species-specific identification and its management planning. Species-specific identification in *Crinum* plants is im-

portant to distinguish more abundant species from the endangered one. Therefore, the aim of the current study was to analyze the *matK*, *rbcl*, *trnH-psbA* intergenic spacer, and ITS of *rDNA* regions for information on water-onion genetic diversity and to use the results for the differentiation of water-onion from other *Crinum* plants. The findings would be beneficial for the management, conservation practices, and sustainable uses of water-onion.

MATERIALS AND METHODS

Samples and DNA extraction

Six water-onion (*C. thaianum*) samples were collected from Ranong and Phang Nga Provinces, Southern Thailand and from the White Cane Company, Bangkok, Thailand; including 13 other *Crinum* plants (Fig. 1). Genomic DNAs were extracted from the petal of the *Crinum* plants following the modified CTAB extraction method [12]. The extracted DNA samples were analyzed for quality using electrophoresis in 0.8% agarose gel stained with ethidium bromide to visualize the DNA bands under UV light, and their concentrations were measured using spectrophotometry. Total genomic DNA samples were stored at 4 °C.

PCR amplification

The primers used for the chloroplast-encoded *matK*, *rbcl*, *trnH-psbA* regions and for the nuclear-encoded ITS of *rDNA* region were obtained from other reports [13–16] shown in Table S1. The PCR amplification was conducted using the specific primers of *matK*, *rbcl*, *trnH-psbA*, and ITS. PCR reactions were performed in 25 µl of a mixture containing 100 ng DNA, 5 pmol of each primer, 2.0 mM MgCl₂, 1.25 µM of dNTP, and 2 U of phusion high-fidelity DNA polymerase (Thermo Scientific; USA) in 1X PCR buffer. The amplification conditions were 3 min at 94 °C, followed by 35 cycles of 30 s at 94 °C, 30 s at the annealing temperature (T_a) shown in Table S1, and 1 min at 72 °C; and the extension was completed for 7 min at 72 °C.

DNA sequencing and analysis

PCR products of *matK*, *rbcl*, *trnH-psbA*, and ITS regions, containing the nucleotide sequences of about 900, 600, 700, and 900 bp, respectively, were purified using a FavorPrep gel/PCR purification Kit (Favorgen; Ping-Tung, Taiwan); then, they were electrophoresed in 1% agarose gel, followed by ethidium bromide staining and visualization under UV light. The purified DNA samples were sent for sequencing, except for PCR products of the ITS region which had to be cloned and selected before sequencing to avoid the problem of obtaining multiple peaks of chromatogram. Purified ITS of *rDNA* fragments were cloned into pGEM-T Easy vectors (Promega; WI, USA), and the vectors were

transformed into the *Escherichia coli* strain JM 109. For each sample, about 5 colonies with recombinant vectors were selected and cultured. Plasmids from these cultures were purified and sequenced using a BigDye Terminator v3.1 Cycle Sequencing Kit and an ABI Prism 3730xl Genetic Analyzer (Applied Biosystems; CA, USA). The obtained sequences were aligned using MUSCLE (Multiple Sequence Comparison by Log-Expectation) alignments. The aligned DNA sequence data were analyzed using the maximum likelihood (ML) method, and a phylogenetic tree was constructed using the MEGA 5.0 software [17] with 1,000 bootstrap replications. The genetic distance values were also calculated using pair-wise Tamura-3 parameters by MEGA 5.0 software. These analyses facilitated the examination of how *C. thaianum* diverged from other *Crinum* species, thereby supporting the identification of the species.

RESULTS

In total, 19 DNA sequences for each region of the chloroplast-encoded *matK*, *rbcl*, *trnH-psbA*, and 19 sequences at the nuclear-encoded ITS of six water-onion samples collected from different locations and 13 other *Crinum* species were generated and analyzed. The sequence alignments at each locus were shown in the supplementary data (Figs. S1-A and S1-B). The amplicon lengths of *matK*, *rbcl*, *trnH-psbA*, and ITS were in the expected ranges of approximately 900 bp, 600 bp, 700 bp, and 900 bp, respectively (Table S1). All DNA sequences for each region were aligned using MUSCLE alignments. Variable sites and gaps were found in all 4 regions (Table 1). Then, the model testing of the final sequence data was performed to find a suitable model for phylogenetic tree construction. The ML trees were constructed with 1,000 bootstrap replications based on *matK*, *rbcl*, *trnH-psbA* intergenic spacer and ITS of *rDNA* sequence data, using a Tamura 3-parameter (T92) model. The phylogenetic tree of each region indicated that the water-onion (*C. thaianum*) samples were grouped together and separated from the other *Crinum* plants. The constructed ML phylogenetic tree, based on three chloroplast regions of *matK*, *rbcl* and *trnH-psbA* intergenic spacer indicated that all *Crinum* plants could be separated into two major groups: Group I, *C. natans*; and Group II, the rest of the *Crinum* plants, including *C. thaianum*, which was one of many subgroups in the major Group II (Fig. 2A). The ML tree based on nuclear ITS region revealed that the *Crinum* species were clustered into four groups consisting of: Group I, *C. latifolium*, *C. xanthophyllum*, *C. amoenum*, *C. jagus*, and *Crinum* sp. from Indonesia; Group II, *C. natans*; Group III, *C. asiaticum*, *Crinum* sp., *C. erubescens*, *Crinum* × *amabile*, and *C. japonicum*; and Group IV, six samples of *C. thaianum* (Fig. 2B). The ITS region gave the best result for discrimination of *Crinum* species.

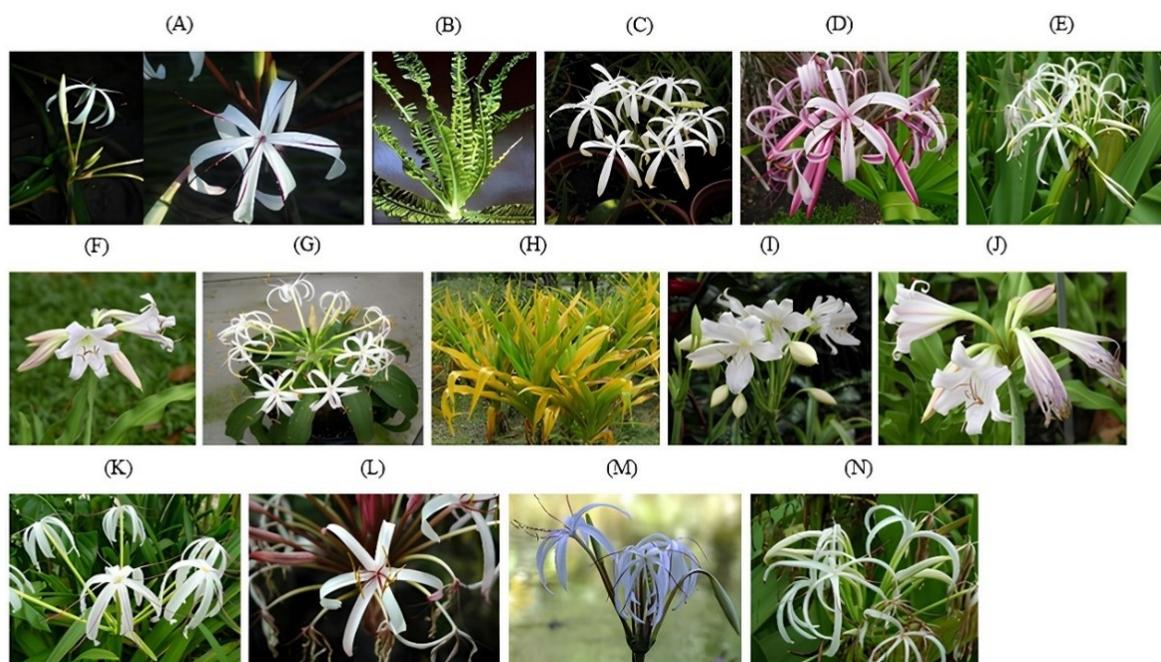


Fig. 1 *Crinum* species used in the present study: (A), *C. thaianum* (SL.382/2558); (B), *C. natans*; (C), *C. amoenum* Ker Gawl. Ex Roxb. (SL.404/2558); (D), *Crinum* × *amabile* Donn ex Ker Gawl. (SL.410/2558); (E), *C. asiaticum* L. (SL.411/2558); (F), *C. latifolium* L. (SL.412/2558); (G), *C. japonicum* (SL.413/2558); (H), *C. xanthophyllum* (SL.414/2558); (I), *C. jagus* (J.Thomps.) Dandy (SL.415/2558); (J), *C. latifolium* L. (SL.416/2558); (K), *C. erubescens* L.f. ex Aiton (SL.417/2558); (L), *Crinum* sp. (SL.434/2558); (M), *C. asiaticum* L. var. *anomalum* Baker (SL.003/2559); and (N), *Crinum* sp. (Indonesia). SL is the Suan Luang Rama IX Park accession number.

Table 1 Number of nucleotides and nucleotide substitutions of four barcoding regions in *Crinum* species.

Sample	Number of nucleotides (bp)				Number of nucleotide substitutions*			
	<i>matK</i>	<i>rbcL</i>	<i>trnH-psbA</i>	ITS	<i>matK</i>	<i>rbcL</i>	<i>trnH-psbA</i>	ITS
<i>C. thaianum</i> (SL.382/2558)	765	507	628	823	–	–	–	–
<i>C. thaianum</i> _1 (Triam canal, Phangnga province)	765	507	628	823	–	–	1	–
<i>C. thaianum</i> _2 (White Cane Co.)	765	507	628	823	–	–	–	–
<i>C. thaianum</i> _3 (Ta-put canal, Phangnga province)	765	507	628	823	–	–	–	–
<i>C. thaianum</i> _4 (Kura canal, Phangnga province)	765	507	628	823	–	–	–	–
<i>C. thaianum</i> _5 (Naka canal, Ranong province)	765	507	626	823	–	–	2	1
<i>C. natans</i> (White Cane Co.)	765	507	615	824	50	18	39	9
<i>C. amoenum</i> Ker Gawl. Ex Roxb. (SL.404/2558)	765	507	628	827	3	2	4	25
<i>Crinum</i> × <i>amabile</i> Donn ex Ker Gawl. (SL.410/2558)	765	507	627	830	3	1	5	12
<i>C. asiaticum</i> L. (SL.411/2558)	765	507	627	826	4	1	4	31
<i>C. latifolium</i> L. (SL.412/2558)	765	507	628	830	3	1	4	12
<i>C. japonicum</i> (SL.413/2558)	793	507	627	830	66	1	3	13
<i>C. xanthophyllum</i> (SL.414/2558)	765	507	628	826	4	1	3	35
<i>C. jagus</i> (J.Thomps.) Dandy (SL.415/2558)	759	507	628	826	6	2	2	31
<i>C. latifolium</i> L. (SL.416/2558)	765	507	628	826	4	1	2	35
<i>C. erubescens</i> L.f. ex Aiton (SL.417/2558)	765	507	628	830	8	1	12	12
<i>Crinum</i> sp. (SL.434/2558)	765	507	628	830	3	1	4	12
<i>C. asiaticum</i> L. var. <i>anomalum</i> Baker (SL.003/2559)	765	505	628	830	3	7	5	12
<i>Crinum</i> sp. (Indonesia)	765	505	627	826	5	6	5	36

* Number of nucleotide substitutions compared with nucleotide sequence of *C. thaianum* (SL.382/2558).

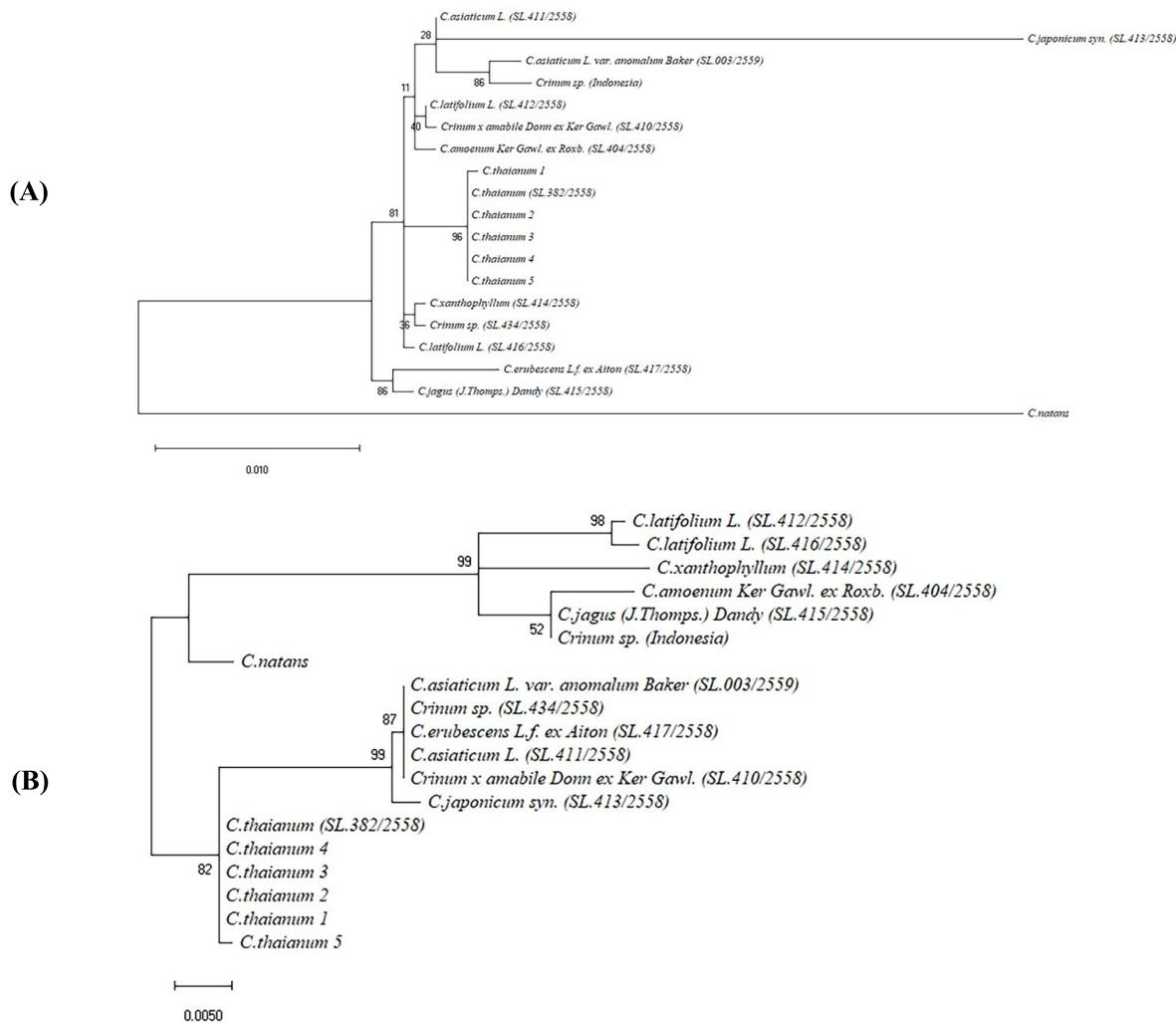


Fig. 2 Phylogenetic tree of 19 samples of *Crinum* species based on ML analysis of specific gene sequences: (A), three chloroplast-encoded gene regions, *matK*, *rbcL*, and *trnH-psbA* intergenic spacer; (B), nuclear-encoded ITS of *rDNA* region.

Sequence analysis of three chloroplast-encoded gene regions

The assembled chloroplast sequences obtained for each specimen were aligned (Fig. S1-A). Then, the phylogenetic tree was generated, and the values of genetic distance (GD) were calculated. The results indicated that the *C. thaianum* samples were grouped together and separated from the other *Crinum* plants, which were clustered in a complex pattern (Fig. 2A). GD values among *Crinum* plants were in the range of 0.0005–0.0883 with a mean distance of 0.0163, while the distances between *C. thaianum* and the other *Crinum* plants were in the range of 0.0037–0.0596 with a mean value of 0.0120. The highest GD value was between *C. thaianum* and *C. natans* (Table 2).

Sequence analysis of *matK*

The *matK* sequences of 759–793 bp were amplified from the *Crinum* species. The obtained sequences were submitted to the GenBank database (OL598039–OL598057). The sequences of *C. thaianum* were identical but differed from the sequences of the other *Crinum* species by 3–66 nucleotide substitutions, as shown in Table 1. All 19 sequences of the *Crinum* species were aligned, and a phylogenetic tree was constructed. The constructed ML tree, based on the *matK* region, revealed that the water-onion (*C. thaianum*) samples were grouped together and separated from the other *Crinum* plants (Fig. S2). However, this dendrogram did not provide clear differentiation among the other *Crinum* plants. The GD values among

Table 2 Genetic distances of pair-wise Tamura-3 parameters determined between studied samples based on three chloroplast-encoded gene regions (*matK*, *rbcL*, and *trnH-psbA* intergenic spacer).

<i>Crinum</i> plant	1	2	3	4	5	6	7	8	9	10	11	12	13
<i>C. thaianum</i>													
<i>C. natans</i>	0.0596												
<i>C. amoenum</i> (SL.404/2558)	0.0046	0.0578											
<i>Crinum</i> × <i>amabile</i> (SL.410/2558)	0.0046	0.0584	0.0021										
<i>C. asiaticum</i> (SL.411/2558)	0.0046	0.0578	0.0021	0.0010									
<i>C. latifolium</i> (SL.412/2558)	0.0041	0.0578	0.0016	0.0005	0.0016								
<i>C. japonicum</i> (SL.413/2558)	0.0326	0.0883	0.0309	0.0298	0.0287	0.0303							
<i>C. xanthophyllum</i> (SL.414/2558)	0.0043	0.0572	0.0026	0.0016	0.0016	0.0021	0.0293						
<i>C. jagus</i> (SL.415/2558)	0.0068	0.0575	0.0052	0.0031	0.0042	0.0037	0.0331	0.0047	0.0332	0.0047			
<i>C. latifolium</i> (SL.416/2558)	0.0037	0.0572	0.0021	0.0021	0.0021	0.0016	0.0293	0.0016	0.0042				
<i>C. erubescens</i> (SL.417/2558)	0.0109	0.0607	0.0073	0.0084	0.0079	0.0079	0.0369	0.0089	0.0063	0.0084			
<i>Crinum</i> sp. (SL.434/2558)	0.0043	0.0578	0.0026	0.0016	0.0016	0.0021	0.0293	0.0010	0.0047	0.0016	0.0089		
<i>C. asiaticum</i> (SL.003/2559)	0.0078	0.0613	0.0052	0.0031	0.0042	0.0037	0.0331	0.0047	0.0084	0.0052	0.0116	0.0047	
<i>Crinum</i> sp. (Indonesia)	0.0085	0.0613	0.0068	0.0058	0.0047	0.0063	0.0326	0.0052	0.0090	0.0058	0.0132	0.0052	0.0037
Average	0.0163												
Max	0.0883												
Min	0.0005												

the *Crinum* plants were in the range of 0.0000–0.1625 with a mean value of 0.0249. The GD values between *C. thaianum* and the other *Crinum* plants were in the range of 0.0039–0.0937 with a mean GD of 0.0172. The highest GD value was between *C. thaianum* and *C. japonicum* (SL.413/2558). The ML tree after adding the outgroups, including *Allium cepa* (NC 024813.1), *Zea mays* (NC 001666.2), *Arabidopsis thaliana* (NC 000932.1) and *Vauquelinia californica* (AF288129.1) indicated that *Crinum* plants were closely related to the monocots *A. cepa* and *Z. mays* by sharing a recent common ancestor with *A. cepa* (Fig. S2).

Sequence analysis of *rbcL*

The *rbcL* barcoding sequences of 505–507 bp were amplified from the *Crinum* species and submitted to the GenBank database (OL598058–OL598076). The sequences of all *C. thaianum* samples were identical; however, 1–18 nucleotide substitutions were found among the *Crinum* species, as shown in Table 1. The phylogenetic tree was generated based on these sequences, and the GD values were calculated. The results indicated that the *C. thaianum* samples were grouped together and separated from the other *Crinum* plants, which were clustered in a complex pattern (Fig. S3). The GD values among the *Crinum* plants were in the range of 0.0000–0.0450 with a mean distance of 0.0087, while the distances between *C. thaianum* and the other *Crinum* plants were in the range of 0.0020–0.0366 with a mean value of 0.0066. The highest GD value was between *C. thaianum* and *C. natans*. The ML tree after adding *A. cepa* (D38294.1), *Z. mays* (NC 001666.2), *A. thaliana* (NC 000932.1), and *Rubus sieboldii* (MZ128458.1) as the outgroups showed that *Crinum* plants were closely related to the monocots *A. cepa* and *Z. mays* by sharing a recent common ancestor with *A. cepa* (Fig. S3).

Sequence analysis of *trnH-psbA* intergenic spacer

The *trnH-psbA* intergenic spacer sequences of the *Crinum* species were submitted to the GenBank database (OL598020–OL598038), and all sequences of 615–628 bp were aligned. Among the water-onion samples, the *trnH-psbA* sequence of *C. thaianum* collected from the Triam Canal differed from those collected from the other locations by one base transversion. Moreover, two bases of the *trnH-psbA* sequence of *C. thaianum* collected from the Naka Canal differed from the others. The sequence of *C. thaianum* differed from the other *Crinum* species by 2–39 substitutions, as shown in Table 1. Then, the ML phylogenetic tree was constructed based on the *trnH-psbA* sequences. Although the *C. thaianum* samples were clustered together, they were in a complex group with the other *Crinum* species (Fig. S4). The GD values among the *Crinum* plants were in the range of 0.0000–0.0746 with a mean value of 0.0157, while the values between *C. thaianum* and the other *Crinum* plants were in the range of 0.0035–0.0692 with a mean value of 0.0122. The highest GD value was between *C. thaianum* and *C. natans*. The ML tree, after adding *Lycoris squamigera* (HM748829.1), *Bulbophyllum cylindraceum* (PQ058145.1), *Anamirta cocculus* (LC506309.1), and *Tinospora sagittata* (JF708221.1) as the outgroups showed that *Crinum* plants were clustered with the monocots *L. squamigera* and *B. cylindraceum*. The most distinct *Crinum* species from the *Crinum* plants studied was *C. natans* (Fig. S4).

Sequence analysis of nuclear-encoded ITS of *rDNA* region

The obtained ITS of *rDNA* sequences were submitted to the GenBank database (OL584022–OL584040). All sequences of 823–830 bp were aligned (Fig. S1-B), and the results showed that the ITS of *rDNA* sequences of

Table 3 Genetic distances of pair-wise Tamura-3 parameters determined between studied samples based on nuclear-encoded gene region (ITS of *rDNA*).

<i>Crinum</i> plant	1	2	3	4	5	6	7	8	9	10	11	12	13
<i>C. thaianum</i>													
<i>C. natans</i>	0.0125												
<i>C. amoenum</i> (SL.404/2558)	0.0317	0.0340											
<i>Crinum</i> × <i>amabile</i> (SL.410/2558)	0.0150	0.0249	0.0392										
<i>C. asiaticum</i> (SL.411/2558)	0.0150	0.0249	0.0392	0.0000									
<i>C. latifolium</i> (SL.412/2558)	0.0461	0.0392	0.0261	0.0511	0.0511								
<i>C. japonicum</i> (SL.413/2558)	0.0163	0.0287	0.0432	0.0036	0.0036	0.0524							
<i>C. xanthophyllum</i> (SL.414/2558)	0.0449	0.0405	0.0287	0.0538	0.0538	0.0248	0.0580						
<i>C. jagus</i> (SL.415/2558)	0.0396	0.0340	0.0073	0.0472	0.0472	0.0185	0.0513	0.0210					
<i>C. latifolium</i> (SL.416/2558)	0.0447	0.0378	0.0273	0.0496	0.0496	0.0036	0.0510	0.0286	0.0197				
<i>C. erubescens</i> (SL.417/2558)	0.0150	0.0249	0.0392	0.0000	0.0000	0.0511	0.0036	0.0538	0.0472	0.0496			
<i>Crinum</i> sp. (SL.434/2558)	0.0150	0.0249	0.0392	0.0000	0.0000	0.0511	0.0036	0.0538	0.0472	0.0496	0.0000		
<i>C. asiaticum</i> (SL.003/2559)	0.0150	0.0249	0.0392	0.0000	0.0000	0.0511	0.0036	0.0538	0.0472	0.0496	0.0000	0.0000	
<i>Crinum</i> sp. (Indonesia)	0.0396	0.0340	0.0073	0.0472	0.0472	0.0185	0.0513	0.0210	0.0000	0.0197	0.0472	0.0472	0.0472
Average	0.0303												
Max	0.0580												
Min	0.0000												

C. thaianum were identical, except for the sequence of *C. thaianum* from the Naka Canal, which differed from the other *C. thaianum* by one base transition. Table 1 shows the number of polymorphisms in the ITS of *rDNA* region among the *Crinum* species. The phylogenetic tree was generated from all ITS of *rDNA* sequences (Fig. 2B). The result revealed that the *Crinum* species were clustered into four groups as follows: Group I of six *Crinum* plants, Group II of one *Crinum* plant of *C. natans*, Group III of six *Crinum* plants, and Group IV of six samples of *C. thaianum*. As shown in Table 3, the GD values among the *Crinum* plants were in the range of 0.0000–0.0580 with a mean value of 0.0303, while the values between *C. thaianum* and the other *Crinum* plants were in the range of 0.0125–0.0461 with a mean value of 0.0270. The lowest GD value was between *C. thaianum* and *C. natans*, whereas the highest GD value was between *C. thaianum* and *C. latifolium* (SL.412/2558). The genetic relationship patterns among the *Crinum* plants were different based on the chloroplast and the nuclear database. The ML phylogenetic tree after adding the outgroup species, including *A. cepa* (OP617675.1), *Oryza glumipatula* (KR364805.1), *A. thaliana* (X52320.1), and *Clematis viticella* (PQ888957.1), revealed that *Crinum* plants were closely related to the monocots *A. cepa* (OP617675.1) and *O. glumipatula* by sharing the most recent common ancestor with *A. cepa* (Fig. S5).

DISCUSSION

Plant species currently listed as abundant are being threatened by various factors, such as environmental pollution, exportation for commercial operations, and habitat destruction. In Thailand, plant smuggling is another threatening factor which, if not strenuously addressed, could lead to the risk of species extinction. Species identification is one of several options to pro-

tect an endangered plant, and there are various molecular markers that have been developed specifically for plant species identification. One of the interesting molecular techniques for identifying species is DNA barcoding, which has been widely reported in the literature, such as identifying mixed stock of *Ziziphora* species, a medicinally important plant in Iran [18]; and molecular characterization of entomopathogenic fungi [19], using ITS sequences. The *COI* gene has been a useful tool for trade detection of threatened and endangered species in commercial shark products [20] and in marine fish mislabeling investigations in South Korea [21].

The current study used barcoding regions, which included nuclear and chloroplast-encoded genes, to identify *C. thaianum*, an endangered species of Thailand. The Consortium for the Barcode of Life (CBOL) Plant Working Group has recommended the *matK* and *rbcl* genes as a plant barcode for plant identification at the species level [5]. The results from the constructed phylogenetic tree of the *matK* and *rbcl* regions among the *Crinum* species showed that the bootstrap value and GD value of the *C. thaianum* clade from the *matK* ML tree were higher than those from the *rbcl* ML tree. In addition, the GD value between *C. thaianum* and the other *Crinum* plants of the *rbcl* ML tree was lower than that of the *matK* ML tree. However, the results between these two ML trees were not different. *C. thaianum* samples were clustered in a complex pattern to the other *Crinum* plants, and they were not clearly separated. Thus, these two regions were unsuitable for use as water-onion (*C. thaianum*) species identification. In addition, the *rbcl* sequence was also reported to be not variable enough in some plants for separating some species in the same genus [22].

Generally, the *trnH-psbA* intergenic spacer is the best plastid option for sequencing. It has good priming

sites with length and interspecific variations [23]. The *trnH-psbA* intergenic spacer region is located between the *trnH* and *psbA* genes and has high polymorphism that is more suitable for species identification than *rbcl* [24]. Furthermore, the non-coding *trnH-psbA* spacer region has been endorsed as a global land plant barcode that could be utilized for discrimination at the species level [15]. The results from the *trnH-psbA* ML tree in the current study were the same as those from the *matK* and *rbcl* ML trees. However, as the bootstrap value of the *C. thaianum* clade was less than 50, this barcoding region was not effective to identify *C. thaianum* since its lower bootstrap value representing uncertainty for that node.

Analysis of the combined chloroplast regions can provide an accurate result. A combination of the non-coding *trnH-psbA* spacer region and a portion of *rbcl* gene analysis [15] and the *trnH-psbA* region and portions of two coding regions (*matK* and *rpoC1*), or three coding regions combined (*matK*, *rpoB* and *rpoC1*) analysis [25] were previously suggested. In the present study, the three chloroplast regions of *matK*, *rbcl* and *trnH-psbA* intergenic spacer were used to construct a phylogenetic tree. The results indicated that the *C. thaianum* samples were clustered with a higher bootstrap value. Moreover, the complex pattern of some *Crinum* species could be classified. Although the dendrogram obtained from the combined three chloroplast regions was clearer than the dendrogram based on single region analysis, most of the *Crinum* plants could not be distinguished from one another. All *Crinum* plants could be separated into two major groups, Group I consisting of only one sample of *C. natans* and Group II containing the rest of the *Crinum* plants, including *C. thaianum*.

In several researches, the nuclear ribosomal ITS region is recommended as a probable barcoding in plants, fungi and bacteria. The ITS of *rDNA* region is used extensively in phylogenetic analysis and can successfully discriminate species because it provides the highest resolving power for discriminating closely related species of fungi [26]. In addition, it exists in multi-copies and exhibits high levels of within-species sequence differentiation. The ITS1 was earlier suggested as a region for the identification of flowering plants [23]. In the current work, the results based on the ITS of *rDNA* ML tree showed that the *C. thaianum* samples were separated from other *Crinum* species, and they were clustered together, despite being collected from different locations. The other *Crinum* species were clustered into three groups, namely, Group I, consisting of *C. latifolium* (SL.412/2558 and SL.416/2558), *C. xanthophyllum*, *C. amoenum*, *C. jagus* and *Crinum* sp. from Indonesia; Group II, containing only one species, *C. natans*; and Group III, containing *C. asiaticum* (SL.411/2558 and SL.003/2559), *Crinum* sp., *C. erubescens*, *Crinum* × *amablie*, and

C. japonicum. All six samples of *C. thaianum* were clustered together in Group IV. Although it was not possible to distinguish all *Crinum* plants, it was clear that the *C. thaianum* samples were significantly separated from the other *Crinum* species. Even though the ITS of *rDNA* region was unsuitable for identifying some *Crinum* species, it could be used as an optimum tool for the water-onion (*C. thaianum*) identification.

Different sources of gene sequences used for barcoding provide different patterns of genetic relationship. In this study, the genetic relationship patterns among the *Crinum* plants were different based on the chloroplast-encoded *matK*, *rbcl*, *trnH-psbA* intergenic spacer and the nuclear-encoded ITS of *rDNA* data. The chloroplast-encoded genes are maternal inheritance, whereas the nuclear-encoded genes are inherited from both parents.

CONCLUSION

The four DNA barcoding loci, the chloroplast-encoded *matK*, *rbcl*, and *trnH-psbA* intergenic spacer and the nuclear-encoded ITS of *rDNA*, could be used successfully for *C. thaianum* discrimination from other *Crinum* spp. However, the genetic diversity among *Crinum* plants studied, based on nuclear and chloroplast sequence data, resulted in different patterns. The ITS of *rDNA* sequence seemed to give reasonable results. More DNA barcoding loci or DNA markers, or both, should be used to better discern among the *Crinum* plants.

Appendix A. Supplementary data

Supplementary data associated with this article can be found at <https://dx.doi.org/10.2306/scienceasia1513-1874.2025.047>.

Acknowledgements: This research was supported by a scholarship from the Royal Golden Jubilee (RGJ) PhD Program (PHD/0026/2558), the Thailand Research Fund (TRF), and the Kasetsart University Research and Development Institute (KURDI). The authors would like to thank the Andaman Coastal Research Station for Development for kindly providing the *C. thaianum* samples and the Suan Luang Rama IX Park for the other *Crinum* plants.

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Appendix A. Supplementary data

Table S1 Information on primers used in the present study.

Primer name	Primer sequence (5'-3')	Annealing temp. (T _a)	Expected amplicon	Reference
matK_F	ACC CAG TCC ATC TGG AAA TCT TGG TTC	52°C	900 bp	[13]
matK_R	CGT ACA GTA CTT TTG TGT TTA CGA AG			
rbcL_F	ATG TCA CCA CAA ACA GAG ACT AAA GC	52°C	600 bp	[14]
rbcL_R	GTA AAA TCA AGT CCA CCR CG			
trnH_F	CGC GCA TGG TGG ATT CAC AAT CC	56°C	700 bp	[15]
psbA_R	GTT ATG CAT GAA CGT AAT GCT C			
ITS-18S_F	TCG CTC CTA CCG ATT GAA TG	56°C	900 bp	[16]
ITS-26S_R	TCC TCC GCT TAT TGA TAT GC			

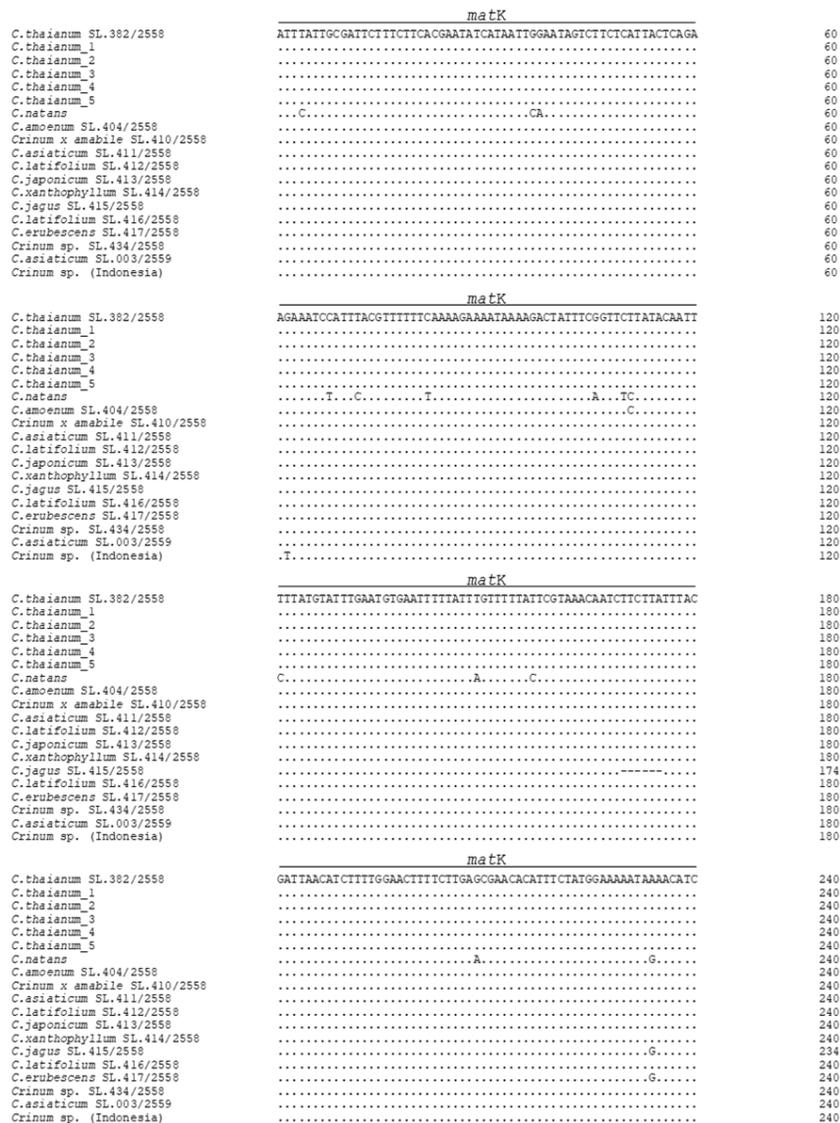


Fig. S1-A Multiple DNA sequence alignment of three chloroplast specific gene regions of *Crinum* plants for phylogenetic analysis.

	<u>matK</u>	
C.thaianum SL.382/2558	TCARATAGAAAATTTATAGTAATATGTCGTACGGATTTTCATAGAACCTTAIGGTTCT	300
C.thaianum_1	300
C.thaianum_2	300
C.thaianum_3	300
C.thaianum_4	300
C.thaianum_5	300
C.natansC...CC...G.....T.....TC.....	300
C.amoenum SL.404/2558	300
Crinum x amabile SL.410/2558	300
C.asiaticum SL.411/2558G.....	300
C.latifolium SL.412/2558	300
C.japonicum SL.413/2558G.....	300
C.xanthophyllum SL.414/2558	300
C.jagus SL.415/2558	294
C.latifolium SL.416/2558	300
C.erubescens SL.417/2558	300
Crinum sp. SL.434/2558	300
C.asiaticum SL.003/2559	300
Crinum sp. (Indonesia)G.....	300
<u>matK</u>		
C.thaianum SL.382/2558	TCRAAGATCCTTTCGTGCATTATGTCGATATCGGGGAAAAGCAATTCITGTTTCAAAGG	360
C.thaianum_1	360
C.thaianum_2	360
C.thaianum_3	360
C.thaianum_4	360
C.thaianum_5	360
C.natansG.....AA..C.....C.....A..	360
C.amoenum SL.404/2558	360
Crinum x amabile SL.410/2558	360
C.asiaticum SL.411/2558	360
C.latifolium SL.412/2558	360
C.japonicum SL.413/2558	360
C.xanthophyllum SL.414/2558	360
C.jagus SL.415/2558A.....	354
C.latifolium SL.416/2558	360
C.erubescens SL.417/2558A.....	360
Crinum sp. SL.434/2558	360
C.asiaticum SL.003/2559	360
Crinum sp. (Indonesia)	360
<u>matK</u>		
C.thaianum SL.382/2558	GGACTCATCTTTCIGATGAAGAAATGGAATATCATTTTGCAATTTCTGGCAATATTATT	420
C.thaianum_1	420
C.thaianum_2	420
C.thaianum_3	420
C.thaianum_4	420
C.thaianum_5	420
C.natansA.....C.....	420
C.amoenum SL.404/2558	420
Crinum x amabile SL.410/2558	420
C.asiaticum SL.411/2558	420
C.latifolium SL.412/2558	420
C.japonicum SL.413/2558	420
C.xanthophyllum SL.414/2558	420
C.jagus SL.415/2558	414
C.latifolium SL.416/2558	420
C.erubescens SL.417/2558A.....	420
Crinum sp. SL.434/2558	420
C.asiaticum SL.003/2559	420
Crinum sp. (Indonesia)	420
<u>matK</u>		
C.thaianum SL.382/2558	TTCCATTTTGGTCTCAACCGTACAGGATCCATATAAATCAACTATCAAATCTTTCT	480
C.thaianum_1	480
C.thaianum_2	480
C.thaianum_3	480
C.thaianum_4	480
C.thaianum_5	480
C.natans	..T.....T.....C...T.....	480
C.amoenum SL.404/2558	480
Crinum x amabile SL.410/2558	480
C.asiaticum SL.411/2558	480
C.latifolium SL.412/2558	480
C.japonicum SL.413/2558	480
C.xanthophyllum SL.414/2558	..A.....	480
C.jagus SL.415/2558	474
C.latifolium SL.416/2558	480
C.erubescens SL.417/2558	480
Crinum sp. SL.434/2558	480
C.asiaticum SL.003/2559	480
Crinum sp. (Indonesia)	480

Fig. S1-A Continued ...

	<u>matK</u>	
C.thaianum SL.382/2558	ATTTTCTGGGTTATCTTTCAAGCCTACTAATAAATCTTCGGCAGTAAGGAATCAAATGT	540
C.thaianum_1	540
C.thaianum_2	540
C.thaianum_3	540
C.thaianum_4	540
C.thaianum_5	540
C.natansA.....T.....T.....G.....G.....	540
C.amoenum SL.404/2558T.....	540
Crinum x amabile SL.410/2558T.....	540
C.asiaticum SL.411/2558T.....	540
C.latifolium SL.412/2558T.....	540
C.japonicum SL.413/2558T.....A.....	540
C.xanthophyllum SL.414/2558T.....	540
C.jagus SL.415/2558T.....	534
C.latifolium SL.416/2558T.....	540
C.erubescens SL.417/2558T.....T.....	540
Crinum sp. SL.434/2558T.....	540
C.asiaticum SL.003/2559T.....	540
Crinum sp. (Indonesia)T.....	540
<u>matK</u>		
C.thaianum SL.382/2558	TAGAGAATTCAATTCTAATAGATACCGTTACTAAGAAATTTGATACCATAGTCCCGATTA	600
C.thaianum_1	600
C.thaianum_2	600
C.thaianum_3	600
C.thaianum_4	600
C.thaianum_5	600
C.natansTC.....T.....A.....AG...	600
C.amoenum SL.404/2558G.....	600
Crinum x amabile SL.410/2558G.....	600
C.asiaticum SL.411/2558G.....	600
C.latifolium SL.412/2558G.....	600
C.japonicum SL.413/2558	G.....A.....A.....T.....G.....	600
C.xanthophyllum SL.414/2558G.....	600
C.jagus SL.415/2558G.....	594
C.latifolium SL.416/2558G.....	600
C.erubescens SL.417/2558G.....	600
Crinum sp. SL.434/2558G.....	600
C.asiaticum SL.003/2559G.....	600
Crinum sp. (Indonesia)G.....	600
<u>matK</u>		
C.thaianum SL.382/2558	TTCTTCTAATGGATCCCTGTCTAAGCTAAATTTGTACCGTATCGGCCATCCTATTA	660
C.thaianum_1	660
C.thaianum_2	660
C.thaianum_3	660
C.thaianum_4	660
C.thaianum_5	660
C.natansTT.....C.....C.....	660
C.amoenum SL.404/2558	660
Crinum x amabile SL.410/2558	660
C.asiaticum SL.411/2558	660
C.latifolium SL.412/2558	660
C.japonicum SL.413/2558	.G.....T.....A.....G.....TGT...T.ATCCTTTC.A.CC..	660
C.xanthophyllum SL.414/2558	660
C.jagus SL.415/2558	654
C.latifolium SL.416/2558	660
C.erubescens SL.417/2558	660
Crinum sp. SL.434/2558	660
C.asiaticum SL.003/2559	660
Crinum sp. (Indonesia)	660
<u>matK</u>		
C.thaianum SL.382/2558	GTAAGCCGATCT-----GGGCCGATTATCAGATT-----CTGATATTCITGATCGAT	708
C.thaianum_1	-----	708
C.thaianum_2	-----	708
C.thaianum_3	-----	708
C.thaianum_4	-----	708
C.thaianum_5	-----	708
C.natansGGGCCGATTATCAGAT.....	706
C.amoenum SL.404/2558	-----	708
Crinum x amabile SL.410/2558	-----	708
C.latifolium SL.412/2558	-----	708
C.japonicum SL.413/2558	T..GTTACTATGGACCTT..T...AA...TCAC.AATCTTGA.T...C...GA...A.A	720
C.xanthophyllum SL.414/2558	-----	708
C.jagus SL.415/2558	-----	702
C.latifolium SL.416/2558	-----	708
C.erubescens SL.417/2558	-----	708
Crinum sp. SL.434/2558	-----	708
C.asiaticum SL.003/2559	-----	708
Crinum sp. (Indonesia)	-----	708

Fig. S1-A Continued ...

<u>matK</u>		
C.thaianum SL.382/2558	TCG-----GTCGGATATGTAGAAATCTTCTCATTATCACAGCGGATCTCAAAA	759
C.thaianum_1	759
C.thaianum_2	759
C.thaianum_3	759
C.thaianum_4	759
C.thaianum_5	759
C.natans	-----ATTGG.....T.....	759
C.amoenum SL.404/2558	759
Crinum x amabile SL.410/2558	759
C.asiaticum SL.411/2558	759
C.latifolium SL.412/2558	759
C.japonicum SL.413/2558	.T.GTTTGGGATT...T.G.AA.CATTG...TAT...C.C.GACT..ATC...T..T..	780
C.xanthophyllum SL.414/2558	759
C.jagus SL.415/2558T.....	753
C.latifolium SL.416/2558	759
C.erubescens SL.417/2558T.....	759
Crinum sp. SL.434/2558	759
C.asiaticum SL.003/2559	759
Crinum sp. (Indonesia)	759
<u>matK</u> <u>rbcl</u>		
C.thaianum SL.382/2558	AACAGGCTTATTATACTCCTGATTACGAAACCAAGATACTGATATCTTGGCAGCATTCC	819
C.thaianum_1	819
C.thaianum_2	819
C.thaianum_3	819
C.thaianum_4	819
C.thaianum_5	819
C.natansA.....T.....	819
C.amoenum SL.404/2558	819
Crinum x amabile SL.410/2558	819
C.asiaticum SL.411/2558	819
C.latifolium SL.412/2558	819
C.japonicum SL.413/2558TT.TA.....	840
C.xanthophyllum SL.414/2558	819
C.jagus SL.415/2558	813
C.latifolium SL.416/2558	819
C.erubescens SL.417/2558	819
Crinum sp. SL.434/2558	819
C.asiaticum SL.003/2559	819
Crinum sp. (Indonesia)	819
<u>rbcl</u>		
C.thaianum SL.382/2558	GAGTAACTCCTCAACCCGGAGTCCCGCTGAAGAGGCAGGGGGTGGGTAGCTGCCGAAT	879
C.thaianum_1	879
C.thaianum_2	879
C.thaianum_3	879
C.thaianum_4	879
C.thaianum_5	879
C.natansT.....A.....G.....	879
C.amoenum SL.404/2558	879
Crinum x amabile SL.410/2558	879
C.asiaticum SL.411/2558	879
C.latifolium SL.412/2558	879
C.japonicum SL.413/2558	900
C.xanthophyllum SL.414/2558	879
C.jagus SL.415/2558	873
C.latifolium SL.416/2558	879
C.erubescens SL.417/2558	879
Crinum sp. SL.434/2558	879
C.asiaticum SL.003/2559	879
Crinum sp. (Indonesia)	879
<u>rbcl</u>		
C.thaianum SL.382/2558	CTTCTACCGGTACATGGACAACCTGTGTGGACTGATGGACTTACCAGCCTTGATCGTTACA	939
C.thaianum_1	939
C.thaianum_2	939
C.thaianum_3	939
C.thaianum_4	939
C.thaianum_5	939
C.natansT.....C..C.....T.....	939
C.amoenum SL.404/2558	939
Crinum x amabile SL.410/2558	939
C.asiaticum SL.411/2558	939
C.latifolium SL.412/2558	939
C.japonicum SL.413/2558	960
C.xanthophyllum SL.414/2558	939
C.jagus SL.415/2558	933
C.latifolium SL.416/2558	939
C.erubescens SL.417/2558	939
Crinum sp. SL.434/2558	939
C.asiaticum SL.003/2559	939
Crinum sp. (Indonesia)	939

Fig. S1-A Continued ...

<u>rbcl</u>		
C.thaianum SL.382/2558	AAGGACGATGCTACCCACATTGAGGCCGTTATGGGGAAGAAATCAATATATGCTTATG	999
C.thaianum_1	999
C.thaianum_2	999
C.thaianum_3	999
C.thaianum_4	999
C.thaianum_5	999
C.natansG.....	999
C.amoenum SL.404/2558G.....	999
Crinum x amabile SL.410/2558G.....	999
C.asiaticum SL.411/2558G.....	999
C.latifolium SL.412/2558G.....	999
C.japonicum SL.413/2558G.....	1020
C.xanthophyllum SL.414/2558G.....	999
C.jagus SL.415/2558T.....G.....	993
C.latifolium SL.416/2558G.....	999
C.erubescens SL.417/2558G.....	999
Crinum sp. SL.434/2558G.....	999
C.asiaticum SL.003/2559G.....	999
Crinum sp. (Indonesia)G.....	999
<u>rbcl</u>		
C.thaianum SL.382/2558	TAGCTTATGCTTTAGACCTTTTTGAGAAGGTTCTGTTACTAACAATGTTACTTCCATTG	1059
C.thaianum_1	1059
C.thaianum_2	1059
C.thaianum_3	1059
C.thaianum_4	1059
C.thaianum_5	1059
C.natans	1059
C.amoenum SL.404/2558	1059
Crinum x amabile SL.410/2558	1059
C.asiaticum SL.411/2558	1059
C.latifolium SL.412/2558	1059
C.japonicum SL.413/2558	1080
C.xanthophyllum SL.414/2558	1059
C.jagus SL.415/2558	1083
C.latifolium SL.416/2558	1059
C.erubescens SL.417/2558	1059
Crinum sp. SL.434/2558	1059
C.asiaticum SL.003/2559	1059
Crinum sp. (Indonesia)	1059
<u>rbcl</u>		
C.thaianum SL.382/2558	TGGGTAATGTATTTGGTTTCAAGGCCCTACGAGCTCTAOSTCTGGAGGATCTGOGAATTC	1119
C.thaianum_1	1119
C.thaianum_2	1119
C.thaianum_3	1119
C.thaianum_4	1119
C.thaianum_5	1119
C.natans	1119
C.amoenum SL.404/2558	1119
Crinum x amabile SL.410/2558	1119
C.asiaticum SL.411/2558	1119
C.latifolium SL.412/2558	1119
C.japonicum SL.413/2558	1140
C.xanthophyllum SL.414/2558	1119
C.jagus SL.415/2558	1113
C.latifolium SL.416/2558	1119
C.erubescens SL.417/2558	1119
Crinum sp. SL.434/2558	1119
C.asiaticum SL.003/2559	1119
Crinum sp. (Indonesia)	1119
<u>rbcl</u>		
C.thaianum SL.382/2558	CCCTGCTTATTCRAAACTTTCCRAAGGCCGCCCATGGCATCCAGTTGAAAGAGATA	1179
C.thaianum_1	1179
C.thaianum_2	1179
C.thaianum_3	1179
C.thaianum_4	1179
C.thaianum_5	1179
C.natans	...A.T.....	1179
C.amoenum SL.404/2558	...C.....	1179
Crinum x amabile SL.410/2558	1179
C.asiaticum SL.411/2558	1179
C.latifolium SL.412/2558	1179
C.japonicum SL.413/2558	1200
C.xanthophyllum SL.414/2558	1179
C.jagus SL.415/2558	1173
C.latifolium SL.416/2558	1179
C.erubescens SL.417/2558	1179
Crinum sp. SL.434/2558	1179
C.asiaticum SL.003/2559	1179
Crinum sp. (Indonesia)	1179

Fig. S1-A Continued ...

	<u>rbcl</u>	
C.thaianum SL.382/2558	AATTGATAAGTACGGTGTCCOCTATTGGGATGACTATTAAACCAAATTTGGGATTAT	1239
C.thaianum_1	1239
C.thaianum_2	1239
C.thaianum_3	1239
C.thaianum_4	1239
C.thaianum_5	1239
C.natansC.....T..C.....	1239
C.amoenum SL.404/2558	1239
Crinum x amabile SL.410/2558	1239
C.asiaticum SL.411/2558	1239
C.latifolium SL.412/2558	1239
C.japonicum SL.413/2558	1260
C.xanthophyllum SL.414/2558	1239
C.jagus SL.415/2558	1233
C.latifolium SL.416/2558	1239
C.erubescens SL.417/2558	1239
Crinum sp. SL.434/2558	1239
C.asiaticum SL.003/2559	1239
Crinum sp. (Indonesia)	1239
	<u>rbcl</u> <u>trnH-psbA</u>	
C.thaianum SL.382/2558	CCGCAAAAAACTACGGTAGAGCGGTTTATGAATTTATCTAGCTAAAGGATTTTTTCTTTT	1299
C.thaianum_1	1299
C.thaianum_2	1299
C.thaianum_3	1299
C.thaianum_4	1299
C.thaianum_5	1299
C.natansC..G.....G.....C.C.....	1299
C.amoenum SL.404/2558	1299
Crinum x amabile SL.410/2558G.-.....	1298
C.asiaticum SL.411/2558	1299
C.latifolium SL.412/2558	1299
C.japonicum SL.413/2558	1320
C.xanthophyllum SL.414/2558	1299
C.jagus SL.415/2558	1293
C.latifolium SL.416/2558	1299
C.erubescens SL.417/2558	1299
Crinum sp. SL.434/2558T...T.TTCC.....	1299
C.asiaticum SL.003/2559T...T.TTCC.....	1299
Crinum sp. (Indonesia)T...T.TTCC.....G.-.....	1298
	<u>trnH-psbA</u>	
C.thaianum SL.382/2558	TTCCATTCAICATTATTGTATTATCTTACCTTCATAC-TTAGATCGAGATATTCTATT	1358
C.thaianum_1	1358
C.thaianum_2	1358
C.thaianum_3	1358
C.thaianum_4	1358
C.thaianum_5	1358
C.natansGC.....G.....	1359
C.amoenum SL.404/2558	1358
Crinum x amabile SL.410/2558	1357
C.asiaticum SL.411/2558	1358
C.latifolium SL.412/2558	1358
C.japonicum SL.413/2558	1379
C.xanthophyllum SL.414/2558	1358
C.jagus SL.415/2558	1352
C.latifolium SL.416/2558	1358
C.erubescens SL.417/2558	1358
Crinum sp. SL.434/2558	1358
C.asiaticum SL.003/2559	1358
Crinum sp. (Indonesia)	1357
	<u>trnH-psbA</u>	
C.thaianum SL.382/2558	GGACATAGAAATGCCAATCTTTAAAATGTAATAAAAGGAGTAATCAGCTGTGGCAGGTTT	1418
C.thaianum_1	1418
C.thaianum_2	1418
C.thaianum_3	1418
C.thaianum_4	1418
C.thaianum_5	1418
C.natansG.....A.....	1418
C.amoenum SL.404/2558	1418
Crinum x amabile SL.410/2558	1417
C.asiaticum SL.411/2558	1418
C.latifolium SL.412/2558	1418
C.japonicum SL.413/2558	1439
C.xanthophyllum SL.414/2558	1418
C.jagus SL.415/2558	1412
C.latifolium SL.416/2558	1418
C.erubescens SL.417/2558	1418
Crinum sp. SL.434/2558	1418
C.asiaticum SL.003/2559	1418
Crinum sp. (Indonesia)	1417

Fig. S1-A Continued ...

	<u>trnH-psbA</u>	
C. thaianum SL.382/2558	ACTAAAAAAAAATCCTTTTGTAGCTAATCATTATCGAGAAAAATTGAAAACTCAACAT	1478
C. thaianum_1	1478
C. thaianum_2	1478
C. thaianum_3	1478
C. thaianum_4	1478
C. thaianum_5	1478
C. natansT.....	1478
C. amoenum SL.404/2558	1478
Crinum x amabile SL.410/2558	1477
C. asiaticum SL.411/2558	1478
C. latifolium SL.412/2558	1478
C. japonicum SL.413/2558	1499
C. xanthophyllum SL.414/2558	1478
C. jagus SL.415/2558	1472
C. latifolium SL.416/2558	1478
C. erubescens SL.417/2558	1478
Crinum sp. SL.434/2558	1478
C. asiaticum SL.003/2559	1478
Crinum sp. (Indonesia)	1477
	<u>trnH-psbA</u>	
C. thaianum SL.382/2558	GAGGGAGGAGAAAGAAATAATAGTACTGGTCTCGGGCATCTACCATTTATAOCCAAAAAT	1538
C. thaianum_1	1538
C. thaianum_2	1538
C. thaianum_3	1538
C. thaianum_4	1538
C. thaianum_5	1538
C. natans	1538
C. amoenum SL.404/2558	1538
Crinum x amabile SL.410/2558	1537
C. asiaticum SL.411/2558	1538
C. latifolium SL.412/2558	1538
C. japonicum SL.413/2558	1559
C. xanthophyllum SL.414/2558	1538
C. jagus SL.415/2558C.....	1532
C. latifolium SL.416/2558	1538
C. erubescens SL.417/2558	1538
Crinum sp. SL.434/2558	1538
C. asiaticum SL.003/2559	1538
Crinum sp. (Indonesia)	1537
	<u>trnH-psbA</u>	
C. thaianum SL.382/2558	GATTGGCCATACAATCGCGATTCAATGGAAGGAACATTTAOCCTATTTATATACAGA	1598
C. thaianum_1	1598
C. thaianum_2	1598
C. thaianum_3	1598
C. thaianum_4	1598
C. thaianum_5	1598
C. natansT.....	1598
C. amoenum SL.404/2558	1598
Crinum x amabile SL.410/2558	1597
C. asiaticum SL.411/2558	1598
C. latifolium SL.412/2558	1598
C. japonicum SL.413/2558	1619
C. xanthophyllum SL.414/2558	1598
C. jagus SL.415/2558	1592
C. latifolium SL.416/2558	1598
C. erubescens SL.417/2558	1598
Crinum sp. SL.434/2558	1598
C. asiaticum SL.003/2559	1598
Crinum sp. (Indonesia)	1597
	<u>trnH-psbA</u>	
C. thaianum SL.382/2558	TCGTAIGGTAGGTCACAAATGGGAGAAITCGGGCCTACTATGACTITCGGAGACATGC	1658
C. thaianum_1	1658
C. thaianum_2	1658
C. thaianum_3	1658
C. thaianum_4	1658
C. thaianum_5	1658
C. natansC.....	1658
C. amoenum SL.404/2558C.....	1658
Crinum x amabile SL.410/2558C.....	1657
C. asiaticum SL.411/2558C.....	1658
C. latifolium SL.412/2558C.....	1658
C. japonicum SL.413/2558C.....	1679
C. xanthophyllum SL.414/2558C.....	1658
C. jagus SL.415/2558C.....	1652
C. latifolium SL.416/2558C.....	1658
C. erubescens SL.417/2558C.....	1658
Crinum sp. SL.434/2558C.G.....	1658
C. asiaticum SL.003/2559C.....	1658
Crinum sp. (Indonesia)C.....	1657

Fig. S1-A Continued ...

<u>trnH-psbA</u>		
C.thaianum SL.382/2558	GAGAAACGATAATAAATCTCGTCGTTAATTAGATATAAATAAAAAATAGATACTTACA	1718
C.thaianum_1	1718
C.thaianum_2	1718
C.thaianum_3	1718
C.thaianum_4	1718
C.thaianum_5	1718
C.natansG.....AC.T.GT.CAT.TA..GA.	1718
C.amoenum SL.404/2558T.....	1718
Crinum x amabile SL.410/2558	1717
C.asiaticum SL.411/2558	1718
C.latifolium SL.412/2558	1718
C.japonicum SL.413/2558	1739
C.xanthophyllum SL.414/2558	1718
C.jagus SL.415/2558	1712
C.latifolium SL.416/2558	1718
C.erubescens SL.417/2558TT.....	1718
Crinum sp. SL.434/2558	1718
C.asiaticum SL.003/2559	1718
Crinum sp. (Indonesia)	1717
<u>trnH-psbA</u>		
C.thaianum SL.382/2558	TTGACGGGGATACCTTATGATAAAGGGRGCCATCTCATATCTTACGAAAAACAAGA	1777
C.thaianum_1	1777
C.thaianum_2	1777
C.thaianum_3	1777
C.thaianum_4	1777
C.thaianum_5	1777
C.natans	TATTGAAGG-----AGCTATATCCCATAGCTTAAAAAACAAGCGG	1758
C.amoenum SL.404/2558	...G.....	1777
Crinum x amabile SL.410/2558	...G.....	1776
C.asiaticum SL.411/2558	...G.....	1777
C.latifolium SL.412/2558	...G.....	1777
C.japonicum SL.413/2558	...G.....	1798
C.xanthophyllum SL.414/2558	...G.....	1777
C.jagus SL.415/2558	...G.....	1771
C.latifolium SL.416/2558	...G.....	1777
C.erubescens SL.417/2558	...G.....	1777
Crinum sp. SL.434/2558	...G.....	1777
C.asiaticum SL.003/2559	...G.....	1777
Crinum sp. (Indonesia)	...G.....	1776
<u>trnH-psbA</u>		
C.thaianum SL.382/2558	-----TATTGGGTATGGCTCTTCAACGATCTTAAATACATTAAGTTAAGACTTCTGTC	1831
C.thaianum_1	-----	1831
C.thaianum_2	-----	1831
C.thaianum_3	-----	1831
C.thaianum_4	-----	1831
C.thaianum_5	-----	1831
C.natans	ATTGCGGG-ATA.CTCCITCAA.....A..CA.....GAGAA...	1818
C.amoenum SL.404/2558	-----	1831
Crinum x amabile SL.410/2558	-----C.....	1830
C.asiaticum SL.411/2558	-----C.....	1831
C.latifolium SL.412/2558	-----C.....	1831
C.japonicum SL.413/2558	-----C.....	1852
C.xanthophyllum SL.414/2558	-----C.....	1831
C.jagus SL.415/2558	-----C.....	1825
C.latifolium SL.416/2558	-----C.....	1831
C.erubescens SL.417/2558	-----C.....	1831
Crinum sp. SL.434/2558	-----C.....	1831
C.asiaticum SL.003/2559	-----C.....	1831
Crinum sp. (Indonesia)	-----C.....	1830
<u>trnH-psbA</u>		
C.thaianum SL.382/2558	TTATCCATTGTAGCTGTAACCTTCAACGACGCTAAGTCTAGAGGGAAAGTGTGAGCATT	1891
C.thaianum_1	1891
C.thaianum_2	1891
C.thaianum_3	1891
C.thaianum_4	1891
C.thaianum_5	1891
C.natansA..A.G.....G.....	1878
C.amoenum SL.404/2558	1891
Crinum x amabile SL.410/2558	1890
C.asiaticum SL.411/2558	1891
C.latifolium SL.412/2558	1891
C.japonicum SL.413/2558	1912
C.xanthophyllum SL.414/2558	1891
C.jagus SL.415/2558G.....G.....	1885
C.latifolium SL.416/2558	1891
C.erubescens SL.417/2558	...A.....G.....G.....A.....T.....	1891
Crinum sp. SL.434/2558	1891
C.asiaticum SL.003/2559	1891
Crinum sp. (Indonesia)C..C.....	1890
<u>trnH-psbA</u>		
C.thaianum SL.382/2558	ACGTTTCATG	1900
C.thaianum_1T.....	1900
C.thaianum_2	1900
C.thaianum_3	1900
C.thaianum_4	1900
C.thaianum_5	1898
C.natans	1887
C.amoenum SL.404/2558T.....	1900
Crinum x amabile SL.410/2558AT.....	1899
C.asiaticum SL.411/2558	...CTTG-	1899
C.latifolium SL.412/2558	...AT..	1900
C.japonicum SL.413/2558	...CATG-	1920
C.xanthophyllum SL.414/2558	1900
C.jagus SL.415/2558	1894
C.latifolium SL.416/2558	1900
C.erubescens SL.417/2558	T.T...T..	1900
Crinum sp. SL.434/2558	1900
C.asiaticum SL.003/2559	...AT..	1900
Crinum sp. (Indonesia)	1899

Fig. S1-A Continued ...

	ITS1	
C.thaianum SL.382/2558	GTCCGGTGAAGTGTTCGGATCGCGCGAGGGGG-TGGTTCGCCGCTCGTG	49
C.thaianum_1	49
C.thaianum_2	49
C.thaianum_3	49
C.thaianum_4	49
C.thaianum_5	49
C.natansG.---.CG.....G.....C.....	47
C.amoenum SL.404/2558G.....C.....	50
Crinum x amabile SL.410/2558	49
C.asiaticum SL.411/2558	49
C.latifolium SL.412/2558A.....G.....C.....	50
C.japonicum SL.413/2558	49
C.xanthophyllum SL.414/2558G.....C.....	50
C.jagus SL.415/2558G.....C.....	50
C.latifolium SL.416/2558A.....G.....C.....	50
C.erubescens SL.417/2558	49
Crinum sp. SL.434/2558	49
C.asiaticum SL.003/2559	49
Crinum sp. (Indonesia)G.....C.....	50
	ITS1	
C.thaianum SL.382/2558	ACGTCGCGAGAAGTTCACCTGAACCTTATCATTAGAGGAAGGAGAAGTTCG	99
C.thaianum_1	99
C.thaianum_2	99
C.thaianum_3	99
C.thaianum_4	99
C.thaianum_5	99
C.natansT.....	97
C.amoenum SL.404/2558T.....	100
Crinum x amabile SL.410/2558	99
C.asiaticum SL.411/2558	99
C.latifolium SL.412/2558T.....	100
C.japonicum SL.413/2558	99
C.xanthophyllum SL.414/2558T.....	100
C.jagus SL.415/2558T.....	100
C.latifolium SL.416/2558T.....	100
C.erubescens SL.417/2558T.....	99
Crinum sp. SL.434/2558T.....	99
C.asiaticum SL.003/2559T.....	99
Crinum sp. (Indonesia)T.....	100
	ITS1	
C.thaianum SL.382/2558	TAACAAGGTTTCGGTAGGTGAACCTGCGGAAGGATCATTGTCGTCGTTTCG	149
C.thaianum_1	149
C.thaianum_2	149
C.thaianum_3	149
C.thaianum_4	149
C.thaianum_5	149
C.natansC.....	147
C.amoenum SL.404/2558C.....	150
Crinum x amabile SL.410/2558C.....	149
C.asiaticum SL.411/2558C.....	149
C.latifolium SL.412/2558C.....	150
C.japonicum SL.413/2558	149
C.xanthophyllum SL.414/2558C.....	150
C.jagus SL.415/2558C.....	150
C.latifolium SL.416/2558C.....	150
C.erubescens SL.417/2558C.....	149
Crinum sp. SL.434/2558C.....	149
C.asiaticum SL.003/2559C.....	149
Crinum sp. (Indonesia)C.....	150
	ITS1	
C.thaianum SL.382/2558	AATAGRATATCGCGRACTCGTAGAGCACCTGCAGGGATCGCAGAGGTTGT	199
C.thaianum_1	199
C.thaianum_2	199
C.thaianum_3	199
C.thaianum_4	199
C.thaianum_5	199
C.natansT.....	197
C.amoenum SL.404/2558T.....C.....	200
Crinum x amabile SL.410/2558G.....	199
C.asiaticum SL.411/2558G.....	199
C.latifolium SL.412/2558T.....T.....C.....	200
C.japonicum SL.413/2558G.....	199
C.xanthophyllum SL.414/2558T.....C.....	200
C.jagus SL.415/2558T.....C.....	200
C.latifolium SL.416/2558T.....T.....C.....	200
C.erubescens SL.417/2558G.....	199
Crinum sp. SL.434/2558G.....	199
C.asiaticum SL.003/2559G.....	199
Crinum sp. (Indonesia)T.....C.....	200

Fig. S1-B Multiple DNA sequence alignment of nuclear ITS of *Crinum* plants for phylogenetic analysis.

ITS1		
C.thaianum SL.382/2558	GGCGATTGCTGCCTGCCTATGCTCTCTGGGTCGATTGCTGCTGCCAATC	249
C.thaianum_1	249
C.thaianum_2	249
C.thaianum_3	249
C.thaianum_4	249
C.thaianum_5	249
C.natans	247
C.amoenum SL.404/2558C..G.....	250
Crinum x amabile SL.410/2558C.....	249
C.asiaticum SL.411/2558C.....	249
C.latifolium SL.412/2558C.....	250
C.japonicum SL.413/2558C.....	249
C.xanthophyllum SL.414/2558G.....	250
C.jagus SL.415/2558C..G.....	250
C.latifolium SL.416/2558C.....	250
C.erubescens SL.417/2558C.....	249
Crinum sp. SL.434/2558C.....	249
C.asiaticum SL.003/2559C.....	249
Crinum sp. (Indonesia)C..G.....	250
ITS1		
C.thaianum SL.382/2558	GTCITGAACCTGGCTGG-GGGGGTG----GCGGGAACAAACATCCGGCGC	293
C.thaianum_1-.....-.....-.....	293
C.thaianum_2-.....-.....-.....	293
C.thaianum_3-.....-.....-.....	293
C.thaianum_4-.....-.....-.....	293
C.thaianum_5-.....-.....-.....	293
C.natansG..A..G..TG--	294
C.amoenum SL.404/2558T..A..G..CG--T.....G.....	297
Crinum x amabile SL.410/2558T.....TGGCG.....T.....	299
C.asiaticum SL.411/2558T.....TGGCG.....T.....	299
C.latifolium SL.412/2558T..A..G..CG--T.....	297
C.japonicum SL.413/2558T.....TGGCG.....T.....	299
C.xanthophyllum SL.414/2558T..AC.G..CG--T.....	297
C.jagus SL.415/2558T..A..G..CG--T.....G.....	297
C.latifolium SL.416/2558T..A..G..CG--T.....	297
C.erubescens SL.417/2558T.....TGGCG.....T.....	299
Crinum sp. SL.434/2558T.....TGGCG.....T.....	299
C.asiaticum SL.003/2559T.....TGGCG.....T.....	299
Crinum sp. (Indonesia)T..A..G..CG--T.....G.....	297
ITS1		
C.thaianum SL.382/2558	GGTGTGCGCCAAGGAGCAAAGGCCTGTTGGGGAGCAGAGTGTGCCAGCAT	343
C.thaianum_1	343
C.thaianum_2	343
C.thaianum_3	343
C.thaianum_4	343
C.thaianum_5	343
C.natans	344
C.amoenum SL.404/2558A..C.....A.....	346
Crinum x amabile SL.410/2558G.....	349
C.asiaticum SL.411/2558G.....	349
C.latifolium SL.412/2558A.....A.....C..T.....	346
C.japonicum SL.413/2558G.....	349
C.xanthophyllum SL.414/2558A.....A.....	346
C.jagus SL.415/2558A..C.....A.....	346
C.latifolium SL.416/2558A.....A.....C..T.....	346
C.erubescens SL.417/2558G.....	349
Crinum sp. SL.434/2558G.....	349
C.asiaticum SL.003/2559G.....	349
Crinum sp. (Indonesia)A..C.....A.....	346
ITS1 5.8S rRNA		
C.thaianum SL.382/2558	GCTTGGTGCTAGAGCTTGGGATGCGATCTTGGTACATCATAACACCTACA	393
C.thaianum_1	393
C.thaianum_2	393
C.thaianum_3	393
C.thaianum_4	393
C.thaianum_5	393
C.natans	394
C.amoenum SL.404/2558	396
Crinum x amabile SL.410/2558 G.....	399
C.asiaticum SL.411/2558 G.....	399
C.latifolium SL.412/2558 T.....G.....	396
C.japonicum SL.413/2558 G.....	399
C.xanthophyllum SL.414/2558 C.....G.....G.....	396
C.jagus SL.415/2558	396
C.latifolium SL.416/2558 G.....T.....G.....	396
C.erubescens SL.417/2558 G.....	399
Crinum sp. SL.434/2558 G.....	399
C.asiaticum SL.003/2559 G.....	399
Crinum sp. (Indonesia)	396

Fig. S1-B Continued ...

5.8S rRNA			
C.thaianum SL.382/2558	TGACTCCC GGCAATGGATACTTTGGCTCTCGCATCGATGAAGGACGTAGC	443	
C.thaianum_1	443	
C.thaianum_2	443	
C.thaianum_3	443	
C.thaianum_4	443	
C.thaianum_5	443	
C.natans	444	
C.amoenum SL.404/2558	446	
Crinum x amabile SL.410/2558	C.....	449	
C.asiaticum SL.411/2558	C.....	449	
C.latifolium SL.412/2558	446	
C.japonicum SL.413/2558	C.....	449	
C.xanthophyllum SL.414/2558	...C.....	446	
C.jagus SL.415/2558	446	
C.latifolium SL.416/2558	446	
C.erubescens SL.417/2558	C.....	449	
Crinum sp. SL.434/2558	C.....	449	
C.asiaticum SL.003/2559	C.....	449	
Crinum sp. (Indonesia)	446	
5.8S rRNA			
C.thaianum SL.382/2558	GAAATGGGATACTTGGTGTGAATTGCAGAACTCGTGAAACCATCGAGTCT	493	
C.thaianum_1	493	
C.thaianum_2	493	
C.thaianum_3	493	
C.thaianum_4	493	
C.thaianum_5	493	
C.natans	494	
C.amoenum SL.404/2558C..C.....	496	
Crinum x amabile SL.410/2558	499	
C.asiaticum SL.411/2558	499	
C.latifolium SL.412/2558C.....	496	
C.japonicum SL.413/2558	499	
C.xanthophyllum SL.414/2558C.....	496	
C.jagus SL.415/2558C..C.....	496	
C.latifolium SL.416/2558C.....	496	
C.erubescens SL.417/2558	499	
Crinum sp. SL.434/2558	499	
C.asiaticum SL.003/2559	499	
Crinum sp. (Indonesia)C..C.....	496	
5.8S rRNA			
C.thaianum SL.382/2558	TTGAACGCAAGTTGCGCCCGAGGTATCTGGCCAAAGGGCAGCGCTGCGCTG	543	
C.thaianum_1	543	
C.thaianum_2	543	
C.thaianum_3	543	
C.thaianum_4	543	
C.thaianum_5	543	
C.natans	544	
C.amoenum SL.404/2558C.....T.....	546	
Crinum x amabile SL.410/2558	549	
C.asiaticum SL.411/2558	549	
C.latifolium SL.412/2558C.....T.....	546	
C.japonicum SL.413/2558	549	
C.xanthophyllum SL.414/2558C.....T.....	546	
C.jagus SL.415/2558C.....T.....	546	
C.latifolium SL.416/2558C.....T.....	546	
C.erubescens SL.417/2558	549	
Crinum sp. SL.434/2558	549	
C.asiaticum SL.003/2559	549	
Crinum sp. (Indonesia)C.....T.....	546	
5.8S rRNA ITS2			
C.thaianum SL.382/2558	GGCATCAGGCTCGTGACGCTTCGGCC	CCTTGCCCTGATCTGGTGACAG	593
C.thaianum_1	593
C.thaianum_2	593
C.thaianum_3	593
C.thaianum_4	593
C.thaianum_5	593
C.natans	594
C.amoenum SL.404/2558C.....T.C.....	596
Crinum x amabile SL.410/2558G.....T.....	599
C.asiaticum SL.411/2558G.....T.....	599
C.latifolium SL.412/2558C.....T.C.....	596
C.japonicum SL.413/2558G.....T.....	599
C.xanthophyllum SL.414/2558C.....C.....T.C.....	596
C.jagus SL.415/2558C.....T.C.....	596
C.latifolium SL.416/2558C..A..T.C.....	596
C.erubescens SL.417/2558G.....T.....	599
Crinum sp. SL.434/2558G.....T.....	599
C.asiaticum SL.003/2559G.....T.....	599
Crinum sp. (Indonesia)C.....T.C.....	596

Fig. S1-B Continued ...

	ITS2	
C. thaianum SL.382/2558	GCGGCACCTGGTTCGAACGTGGAGATTGGCCCOCTGTGCGTCATCGGCGG	643
C. thaianum_1	643
C. thaianum_2	643
C. thaianum_3	643
C. thaianum_4	643
C. thaianum_5	643
C. natans	644
C. amoenum SL.404/2558G...T...	646
Crinum x amabile SL.410/2558	649
C. asiaticum SL.411/2558	649
C. latifolium SL.412/2558	.T...G.....T...	646
C. japonicum SL.413/2558G.....	649
C. xanthophyllum SL.414/2558	T.....T...	646
C. jagus SL.415/2558	.T.....G...T...	646
C. latifolium SL.416/2558	.T...G.....T...	646
C. erubescens SL.417/2558	649
Crinum sp. SL.434/2558	649
C. asiaticum SL.003/2559	649
Crinum sp. (Indonesia)	.T.....G...T...	646
ITS2		
C. thaianum SL.382/2558	GTTGGTTGAAGTGTGGGCCGTTGGCGGTCGGATGCGCGAGTGGTGGAG	693
C. thaianum_1	693
C. thaianum_2	693
C. thaianum_3	693
C. thaianum_4	693
C. thaianum_5C.....	693
C. natans	694
C. amoenum SL.404/2558C.....	696
Crinum x amabile SL.410/2558T.....	699
C. asiaticum SL.411/2558T.....	699
C. latifolium SL.412/2558C.....	696
C. japonicum SL.413/2558T.....	699
C. xanthophyllum SL.414/2558C.....	696
C. jagus SL.415/2558C.....	696
C. latifolium SL.416/2558T.....	696
C. erubescens SL.417/2558T.....	699
Crinum sp. SL.434/2558T.....	699
C. asiaticum SL.003/2559T.....	699
Crinum sp. (Indonesia)C.....	696
ITS2		
C. thaianum SL.382/2558	AA-GACACGCACGGCGTGGTGAAGTGTGCTGCTGACGCGGTCATTG	742
C. thaianum_1	..-.....	742
C. thaianum_2	..-.....	742
C. thaianum_3	..-.....	742
C. thaianum_4	..-.....	742
C. thaianum_5	..-.....	742
C. natans	..-.....C..C.....	743
C. amoenum SL.404/2558	..A.....	746
Crinum x amabile SL.410/2558	..A.....	749
C. asiaticum SL.411/2558	..A.....	749
C. latifolium SL.412/2558	..-.....C..C.....	745
C. japonicum SL.413/2558	..A.....	749
C. xanthophyllum SL.414/2558	..-.....C..CA.....	745
C. jagus SL.415/2558	..-.....C..C.....	745
C. latifolium SL.416/2558	..-.....C..C.....	745
C. erubescens SL.417/2558	..A.....	749
Crinum sp. SL.434/2558	..A.....	749
C. asiaticum SL.003/2559	..A.....	749
Crinum sp. (Indonesia)	..-.....C..C.....	745
ITS2		
C. thaianum SL.382/2558	GAGGACCCCATGCTGGTGGTGGCGAGTGGACCCCTGGACACAGATCC	792
C. thaianum_1	792
C. thaianum_2	792
C. thaianum_3	792
C. thaianum_4	792
C. thaianum_5	792
C. natansC.....	793
C. amoenum SL.404/2558	796
Crinum x amabile SL.410/2558	799
C. asiaticum SL.411/2558	799
C. latifolium SL.412/2558C...C.....G.....	795
C. japonicum SL.413/2558C.....	799
C. xanthophyllum SL.414/2558GC.T...G.....	795
C. jagus SL.415/2558C.....G.....	795
C. latifolium SL.416/2558C...C.....G.....	795
C. erubescens SL.417/2558	799
Crinum sp. SL.434/2558	799
C. asiaticum SL.003/2559	799
Crinum sp. (Indonesia)C.....G.....	795
ITS2		
C. thaianum SL.382/2558	CAGGTGAGTGGGGACACCGCTGAGTTAA	823
C. thaianum_1	823
C. thaianum_2	823
C. thaianum_3	823
C. thaianum_4	823
C. thaianum_5	823
C. natans	824
C. amoenum SL.404/2558	827
Crinum x amabile SL.410/2558	830
C. asiaticum SL.411/2558	830
C. latifolium SL.412/2558C.....	826
C. japonicum SL.413/2558	830
C. xanthophyllum SL.414/2558C..G.....	826
C. jagus SL.415/2558C.....	826
C. latifolium SL.416/2558C.....	826
C. erubescens SL.417/2558	830
Crinum sp. SL.434/2558	830
C. asiaticum SL.003/2559	830
Crinum sp. (Indonesia)C.....	826

Fig. S1-B Continued ...

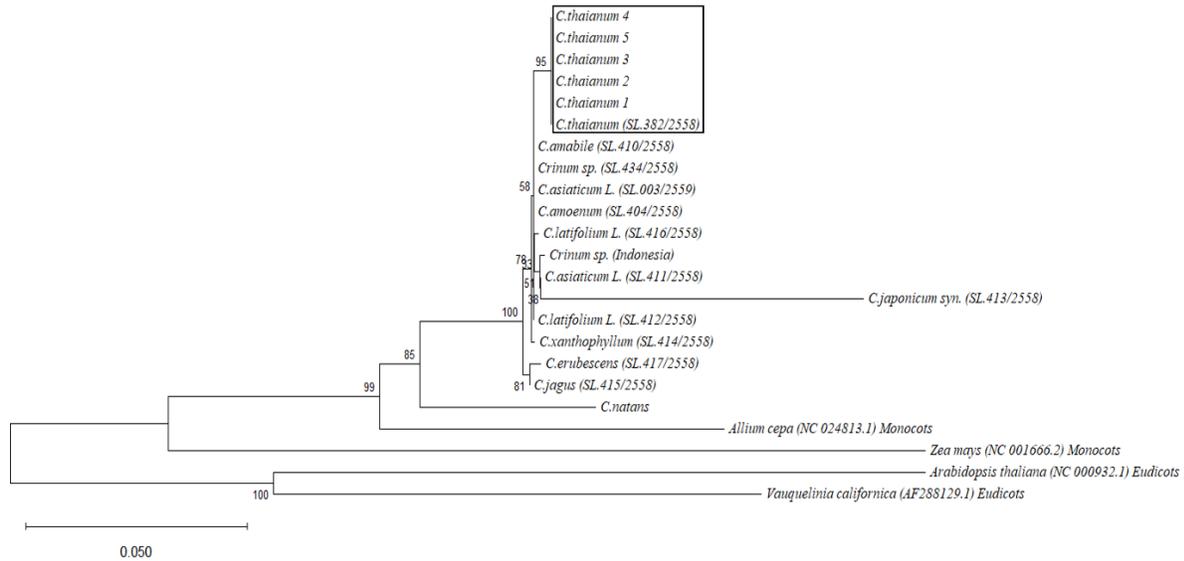


Fig. S2 Phylogenetic tree of 19 samples of *Crinum* species based on maximum-likelihood analysis of *matK* sequences, including *A. cepa* (NC 024813.1), *Z. mays* (NC 001666.2), *A. thaliana* (NC 000932.1) and *V. californica* (AF288129.1) as outgroup species.

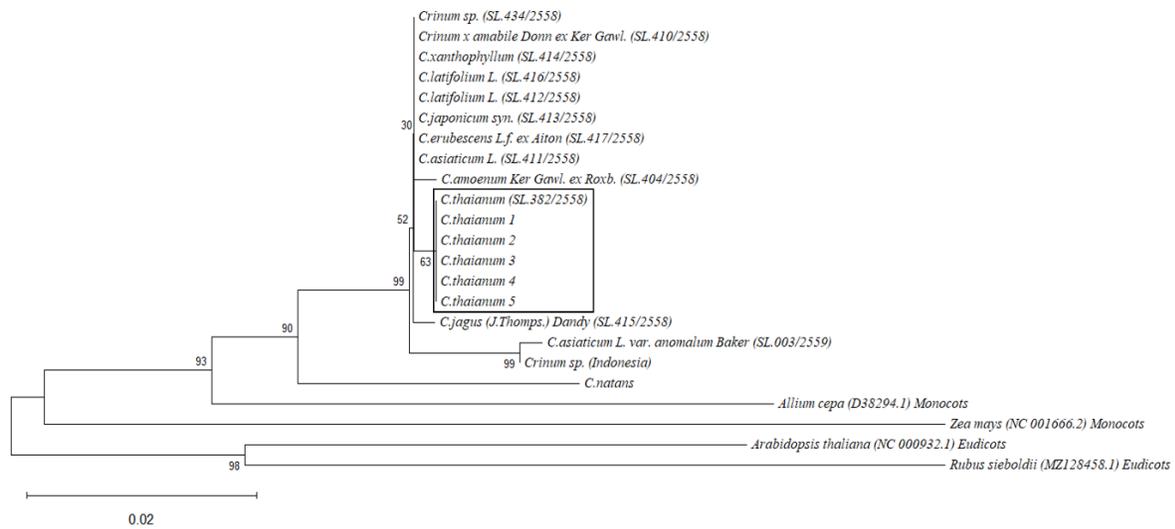


Fig. S3 Phylogenetic tree of 19 samples of *Crinum* species based on maximum-likelihood analysis of *rbcL* sequences, including *A. cepa* (D38294.1), *Z. mays* (NC 001666.2), *A. thaliana* (NC 000932.1), and *R. sieboldii* (MZ128458.1) as outgroup species.

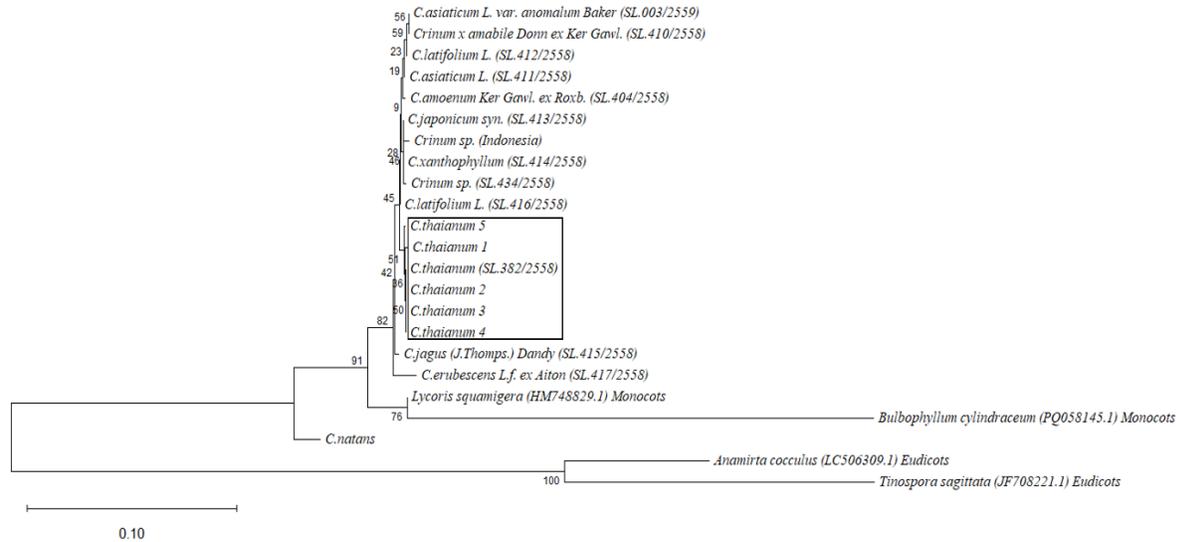


Fig. S4 Phylogenetic tree of 19 samples of *Crinum* species based on maximum-likelihood analysis of *trnH-psbA* intergenic spacer sequences, including *L. squamigera* (HM748829.1), *B. cylindraceum* (PQ058145.1), *A. cocculus* (LC506309.1), and *T. sagittata* (JF708221.1) as outgroup species.

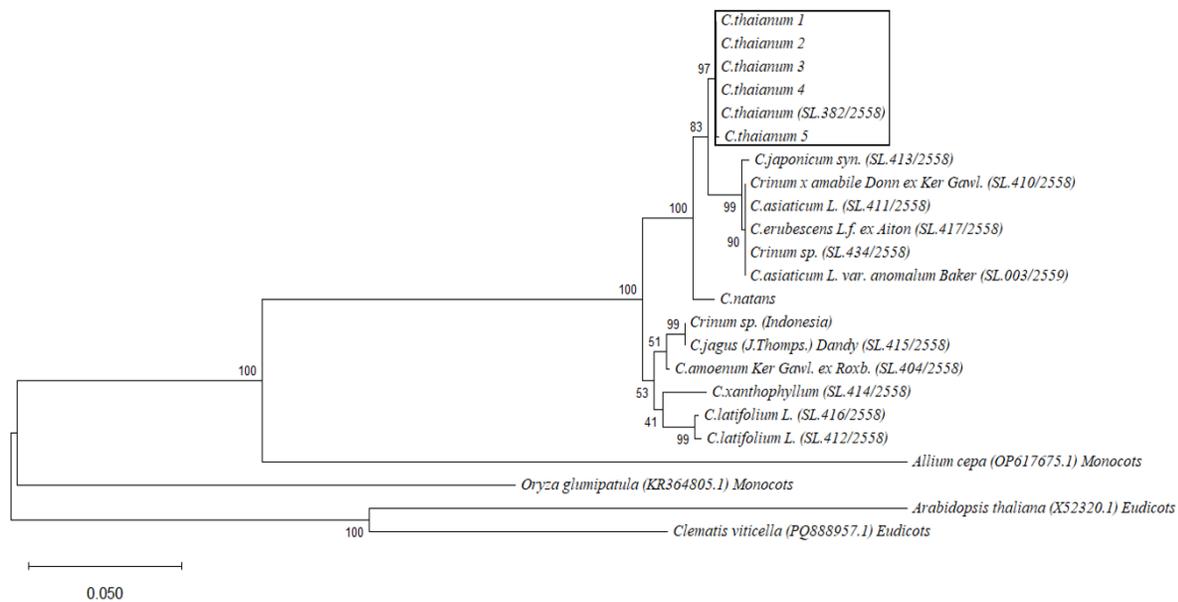


Fig. S5 Phylogenetic tree of 19 samples of *Crinum* species based on maximum-likelihood analysis of Nuclear-encoded ITS of *rDNA* sequences, including *A. cepa* (OP617675.1), *O. glumipatula* (KR364805.1), *A. thaliana* (X52320.1), and *C. viticella* (PQ888957.1) as outgroup species.