CHAPTER 4

RESULTS

4.1 DNA extraction

DNeasy® Plant MiniKit (QIAGEN) was firstly used to extract DNA from dry leaf specimens. Genomic DNA of five Cassia specimens (C. fistula, C. bakeriana, C. javanica and C. spectabilis) were extracted. The extracted DNA were in good quality after checked with 0.8% agarose gel electrophoresis. However, the DNA of C. spectabilis was not able to yield any PCR products, although its amplifications had been attempted for three times and the plant was even reextracted with the QIAGEN kit. Nucleospin® DNA miniKit then was subsequently chosen to solve this problem. This was because the Nucleospin kit contains an extraction buffer claimed to be specific to legume plants (i.e. Pisum sativum). Fortunately, the extracted genomic DNA of C. spectabilis using the Nucleospin kit was successly amplified, given the PCR product visualisable on 0.8% agarose gel electrophoresis. By this mean, all remaining specimens were extracted by the Nucleospin kit. So far, genomic DNA extracted with the Nucleospin® DNA miniKit showed as good quality as that with the DNeasy® Plant MiniKit. Note that although smear DNA bands caused by DNA fragmentation along extraction occurred in most samples, no amplification problem was found. Although, the genomic DNA bands of C. pumila and C. leschenaultiana could not be seen with gel electrophoresis, these DNA could nicely give PCR amplified products.

4.2 PCR amplification

4.2.1 PCR amplification of trnL intron

Amplifications of *tmL* intron regions of all *Cassia* specimens were performed using the *tmL*-C primer as a forward primer and the *tmL*-D primer as a reverse primer. The size of PCR products was around 600 bp compared to 100 bp ladder standard marker. Only *C. siamea* was not able to be amplified while the remaining specimens were easy to get PCR products. Primer dimers occurred in all of these samples and the control reaction (without DNA added). None of non-specific band was found in any lanes (Fig.15).



Fig. 15 PCR products of *tm*L intron (size around 600 bp) compared with 100 bp ladder marker.

M = 1 kb ladder marker

c = control (blank)

1 = C. javanica

5 = C. surattensis

2 = C. spectabilis

6 = C. pumila

3 = C. bakeriana

7 = C. leschenaultiana

4 = C. fistula

4.2.2 PCR amplification of ITS regions

To amplify both ITS1 and ITS2 regions included 5.8S subunit all together, the 5P primer was used as a forward primer and the 8P (or 4P for *C. timoriensis*) primer as a reverse primer. The size of PCR products was around 800 bp compared to standard marker. Non-specific band was not found from all amplification. There were four *Cassia* not successfully amplified: *C. siamea, C. garrettiana, C. pumila* and *C. leschenaultiana*. Other remaining species were amplifiable except *C. timoriensis* which was necessary to use the 4P primer instead of the 8P as a reverse primer and also had to decrese the annealing temperature from 55°C to 50°C in the PCR programme. Primer dimers were not found in all samples and the control reaction (Fig. 16).

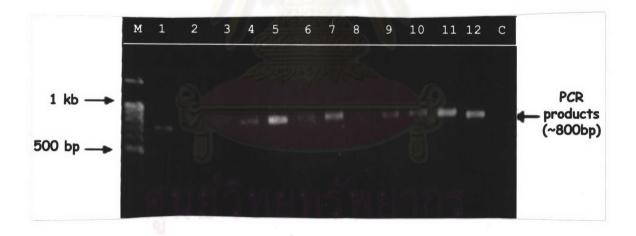


Fig. 16 PCR products of ITS regions of nrDNA (~800bp) compared with 100 bp ladder marker

M = 1 kb ladder marker	5 = C. sophera	10 = C. hirsuta
1 = C. grandis	6 = C. surattensis	11 = C. occidenatalis
2 = C. javanica	7 = C. bakeriana	12 = C. obtusifolia
3 = C. spectabilis	8 = C. fistula	c = control
4 = C. tora	9 = C. alata	

4.3 PCR product purification and DNA sequencing

QIAquick® PCR Purification Kit (QIAGEN) was used to purify the PCR samples which had no or few primer-dimer. Thirteen samples found having primerdimers were purified with QIAquick® gel extraction (QIAGEN) with additional gelslicing procedure. These Cassia samples yeilded trnL intron PCR products of C. grandis, C. bakeriana, C. tora, C. sophera, C. surattensis, C. javanica, C. spectabilis, C. fistula, C. alata, C. hirsuta, C. occidentalis, C. obtusifolia and C. pumila. The purified PCR product was clean and ready to sequence (Fig. 17). After DNA sequencing was performed in both forward and reverse directions, Chromas computer program was used to compare each couple of the complementary sequences (Fig. 18 and Fig. 19). Most electropherogram graphs appeared to be clear without contaminated sequence signals from other plant samples or primer-dimers. Although the trnL intron and ITS sequences of almost all samples region were clear and easy to analyse, the sequence results of ITS regions of C. tora, C. bakeriana, C. obtusifolia and C. surattensis were not clear in both forward and reverse directions (Fig. 20). Sequencing experiments were redone several times for these particularly species but not only in the case of C. surattensis. In this case, multiple copies of ITS were strong, but re-sequencing and comparing base by base each time could help to get an accurately data. The DNA sequences were converted to FASTA format (Fig. 21) before further analysed with Clustal X alignment program. Note that band of C. grandis was not equally to other members because of the shortest sequences of this species while compared to the others.

Among *tm*L intron sequences of all *Cassia*, the sequence of *C. leschenaultiana* was the longest one with 607 bp long while that of *C. grandis* was the shortest with 548 bp. For ITS sequences, without 16S and 28S regions, the longest total ITS1-5.8S-ITS2 sequence was that of *C. bakeriana* (674 bp) and the shortest one was to *C. grandis* (560bp). Average lengths of both sequence regions

were 570 bp and 645 bp (*trn*L intron and ITS regions, respectively). Moreover, these two regions had different characteristics. The *tm*L intron, sequences were easily alignable because they had high similarity to each other in all taxa while alignment of the ITS sequences were much more difficult. GCcontent percentage of each sequence was also observed from nucleotide comparison. The percentages of GC contents of *tm*L intron sequences were range from 35.03% in *C. sophera* and *C. spectabilis* to 36.80% in *C. grandis*. In ITS regions, %GC contents were from 51.61% in *C. grandis* to 62.46% in *C. spectabilis*.



Fig. 17 purified PCR product of tmL intron compare with 100 bp ladder marker.

M = 1 kb ladder marker

1 = C. obtusifolia

2 = C. occidentalis

3 = C. hirsuta

4 = C. alata

5 = C. fistula

6 = C. bakeriana

7 = C. spectabilis

8 = C. javanica

c = control

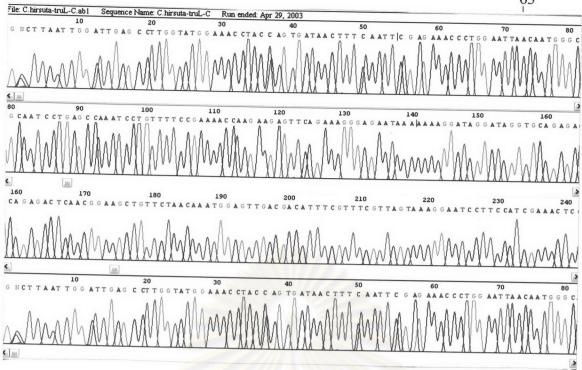


Fig. 18 four-coloured electropherogram of *trn*L intron sequence of *C. hirsuta* with blue peaks represent Cytocine (C), red Thymine (T), green Adenine (A) and cyan Guanine (G) nucleotides.

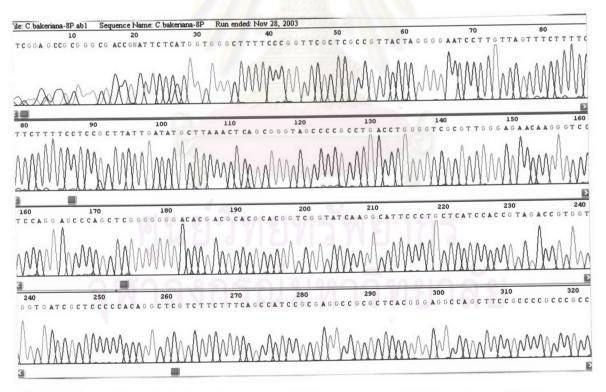


Fig. 19 four-coloured electropherogram of ITS sequence of *C. bakeriana* with blue peaks represent Cytocine (C), red Thymine (T), green Adenine (A) and cyan Guanine (G) nucleotides.

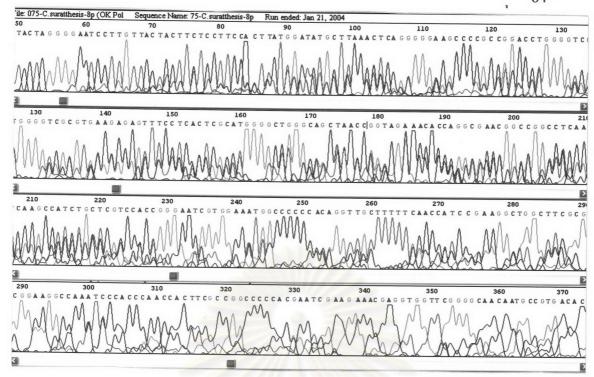


Fig. 20 four-coloured electropherogram of ITS sequence of *C. surattensis* with blue peaks represent Cytocine (C), red Thymine (T), green Adenine (A) and cyan Guanine (G) nucleotides.

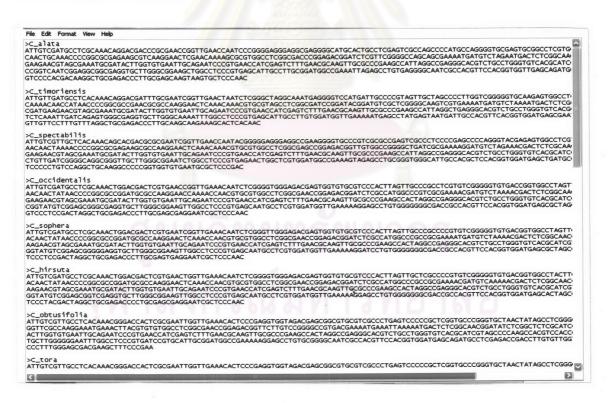


Fig. 21 a sample of FASTA sequence format of tmL intron sequences

4.4 Alignment of DNA sequences

After converting DNA sequences to FASTA format, the Clustal X computer program was used to align the FASTA file. Three types of sequence alignments were performed: 1.) an alignment of ITS sequences of Thai Cassia, 2.) an alignment of trnL intron of Thai Cassia and 3.) an alignment of trnL intron of Thai Cassia compared with those of Cassia from other countries. These additional tmL data for the third alignment were the sequences of C. grandis (AF365092), Senna crassiramea (AF365090), S. lindheimeriana (AF365089), S. bauhinioides (AF365087), S. wislizeni (AF365028), S. bacillaris (AF365031), Chamaecrista nictitans (AF365093), Ch. sp. Klitgaad (AF365093) and Ch. sp. Breteler (AF365094). When completed, the lengths of these character-taxon matrices were 911 bp (excluded 206 bp before doing phylogenetic tree reconstruction which belong to 16S small and 28S large subunit), 646 bp and 657 bp, respectively. These charactertaxon matrices (Fig. 22) were then transformed to NEXUS file format (Fig. 23) for further phylogenetic tree reconstruction.

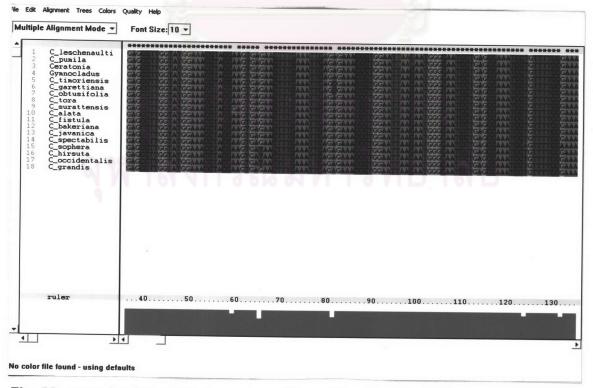


Fig. 22 a sample of an aligned sequence data matrix using ClustalX program

#NEXUS					
begin data;					
<pre>dimensions ntax=18 nchar=: format missing=? gap=- mage options gapmode=missing; matrix</pre>		atatype=dna	symbols = '	"01";	
Ceratonia siliqua AF365075	GTCGACTTTA	GAAAT-CGTG	AG		
Gymnocladus dioica AF365095	GTCGACTTTA	GAAAT-CGTG	AGG		
C. leschenaultiana	GTCGACTTTA	GAAAT-CGTG	AGGGTTCAAG	TCCTTCCTAT	CCCCAA
C. pumila	GTCGACTTTA	GAAAT-CGTG	AGGG		
C. grandis	GTCGACTTTA	GAAAT-CG	-GGG		
C. javanica	GTCGACTTTA	GAAAT-CG			
C. bakeriana	GTCGACTTTA	GAAAT-CGTG	AG		
C. fistula	GTCGACTTTA	GAAAT-CG-G	A		
C. sophera	GTCGACTTTA	GAAAT-CG-G	GG		
C. occidentalis	GTCGACTTTT	GAAAT-CGTG	A		
C. hirsuta	GTCGACTTTA	GAAAT-CGTG	AGGGTTCAAG	TCCCTT	
C. obtusifolia	GTCGACTTTA	GAAATGCG-G	AG		
C. tora	GTCGACTTTA	GAAAT-CGTG	AG		
C. surattensis	GTCGACTTTA	GAAAT-CG-G	AG		
C. timoriensis	GTCGACTTTA	GAAAT-CGTG	AGGGTTCAAG	TCC	
C. garettiana	GTCGACTTTA	GAAAT-CGTG	AGGGTTCAAG	TCCTCTATCC	CCAAC-
C. alata	GTCGACTTTA	GAAAT-CG-G	A		
C. spectabilis	GTCGACTTTA	GAAAT-CG			
end;					

Fig. 23 a sample of NEXUS file format using for phylogenetic analyses in the program PAUP*.

4.5 Phylogenetic analysis

4.5.1 trnL intron sequence data set (see Fig. 24)

- trnL intron sequence data set of 16 Thai Cassia sensu lato

After automatically aligned by ClustalX program and transformed to NEXUS file format, each sequence matrix was adjusted manually to get a highest level of homology before phylogenetically analysed. Some nucleotide positions appeared to be too ambiguous to align and necessarily to be excluded. The beginning and the ending regions of some sequences were also blocked out as incomplete or missing data. Symbols '01' were added to the DNA data matrix to increase informative characters.

Gymnocladus dioica AF365095 7????????? ????????? ?GACTTAATT GGATTGAGCC TY C. (Ch.) leschenaultiana TCGAAATCGG TAGACGCTAC GGACTTAATT GGATTGAGCC TY C. grandis 7???????? ???????? ???????? GGACTTAATT GGATTGAGCC TY C. javanica 7???????? GTGACGCTAC GGACTTAATT GGATTGAGCC TY C. bakeriana 7???????? GTGACGCTAC GGACTTAATT GGATTGAGCC TY C. fistula 7???????? TAGACGCTAC GGACTTAATT GGATTGAGCC TY C. (S.) sophera 7???????? GTGACGCTAC GGACTTAATT GGATTGAGCC TY C. (S.) occidentalis 7???????? GTGACGCTAC GGACTTAATT GGATTGAGCC TY	50 TTGGTATGGA TTGGTATGGA
Ceratonia siliqua AF365075 Gymnocladus dioica AF365095 C.(Ch.) leschenaultiana C.(Ch.) pumila C. grandis C. javanica C. javanica C. bakeriana C. fistula C. (S.) sophera C. (S.) occidentalis C: erratonia siliqua AF365095 C: erratoria siliqua AF365095 C: erratoria siliqua AF365095 C: erratoria siliqua AF365095 C: erratoria a F365095 C: erratoria a F366000 C: erratoria a F3	TTGGTATGGA
Gymmocladus dioica AF365095 C. (Ch.) leschenaultiana TCGAAATCGG TAGACGCTAC GGACTTAATT GGATTGAGCC TT. C. (Ch.) pumila ?????????? ??????TAC GGACTTAATT GGATTGAGCC TT. C. grandis ????????? ????????? GGACTTAATT GGATTGAGCC TT. C. javanica ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TT. C. bakeriana ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TT. C. fistula ????????? TAGACGCTAC GGACTTAATT GGATTGAGCC TT. C. (S.) sophera ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TT. C. (S.) occidentalis ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TT.	TTGGTATGGA
C. (Ch.) leschenaultiana TCGAAATCGG TAGACGCTAC GGACTTAATT GGATTGAGCC TOUR C. (Ch.) pumila ?????????????? ????????? GGACTTAATT GGATTGAGCC TOUR C. grandis C. javanica ?????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TOUR C. bakeriana ?????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TOUR C. fistula ????????? TAGACGCTAC GGACTTAATT GGATTGAGCC TOUR C. (S.) sophera ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TOUR C. (S.) occidentalis ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TOUR C. (S.) occidentalis	
C. (Ch.) pumila ????????????? ??????TAC GGACTTAATT GGATTGAGCC TT C. grandis ?????????? ????????? ????????? GGACTTAATT GGATTGAGCC TT C. javanica ?????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TT C. fistula ???????? GTGACGCTAC GGACTTAATT GGATTGAGCC TT C. (S.) sophera ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TT C. (S.) occidentalis ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC TT	
C. grandis ????????? ???????? ???????? GGATTGAGCC T. C. javanica ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC T. C. bakeriana ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC T. C. fistula ????????C TAGACGCTAC GGACTTAATT GGATTGAGCC T. C.(S.) sophera ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC T. C.(S.) occidentalis ????????C GTGACGCTAC GGACTTAATT GGATTGAGCC T.	TTGGTATGGA
C. javanica ????????? ???????? GACCTTAATT GGATTGAGCC T. C. bakeriana ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC T. C. fistula ???????CG TAGACGCTAC GGACTTAATT GGATTGAGCC T. C.(S.) sophera ????????? ???????? GGATTGAGCC T. C.(S.) occidentalis ????????C GTGACGCTAC GGACTTAATT GGATTGAGCC T.	TTGGTATGGA
C. bakeriana ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC T. C. fistula ???????CG TAGACGCTAC GGACTTAATT GGATTGAGCC T. C.(S.) sophera ????????? ???????? GGATTGAGCC T. C.(S.) occidentalis ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC T.	TTGGTATGGA
C. fistula ???????CG TAGACGCTAC GGACTTAATT GGATTGAGCC TT C.(S.)sophera ????????? ???????? ???????T GGATTGAGCC TT C.(S.)occidentalis ????????C GTGACGCTAC GGACTTAATT GGATTGAGCC TT	TTGGTATGGA
C.(S.)sophera ????????? ????????? ???????T GGATTGAGCC T. C.(S.)soccidentalis ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC T.	TTGGTATGGA
C.(S.)occidentalis ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC T	TTGGTATGGA
	TTGGTATGGA
	TTGGTATGGA
C.(S.)hirsuta ?????????????? GACCTTAATT GGATTGAGCC T	TTGGTATGGA
C.(S.) obtusifolia . ??????CGTAG ACGACGCTAC GGACTTAATT GGATTGAGCC T	TTGGTATGGA
C.(S.)tora ????????? ???????? ?GACTTAATT GGATTGAGCC T	TTGGTATGGA
C.(S.) surattensis ????????? ????????? GACCTTAATT GGCTTGAGCC T	TTGGTATGGA
C.(S.) timoriensis ????????? ???ACGCTAC GGACTTAATT GGATTGAGCC T	TTGGTATGGA
C.(S.) garettiana ????????? TAGACGCTAC GGACTTAATT GGATTGAGCC T	TTGGTATGGA
C.(S.)alata ????????? GTGACGCTAC GGACTTAATT GGATTGAGCC T	TTGGTATGGA
C.(S.) spectabilis ?????????? ???????? GACCTTAATT GGATTGAGCC T	TTGGTATGGA

Fig. 24 a 646 bp character-taxon matix of 16 Thai Cassia species based on trnL intron sequences. Asterisks * and * represent excluded and gap-matrix sites from analyses, respectively. Gap symbol (-) indicates insertion or deletion at the site. ? symbol shows missing nucleotide data.

	60	70	80	90	10.0
Ceratonia siliqua AF365075	AACCTACCAA	GTGAGAACTT	TCAAATTCAG	AGAAACCCTG	GAATTAACAA
Gymnocladus dioica AF365095		GTGAGAACTT			
C. (Ch.) leschenaultiana		GTGAGAACTT			
C. (Ch.) pumila		GTGAGAACTT			
C. grandis		GTGAGAACTT GTGAGAACTT			
C. javanica C. bakeriana		GTGAGAACTT			
C. fistula		GTGAGAACTT			
C.(S.) sophera		GTGATAACTT			
C.(S.)occidentalis		GTGATAACTT			
C.(S.)hirsuta		GTGATAACTT			
C.(S.)obtusifolia		GTGAGAACTT			
C.(S.) tora C.(S.) surattensis		GTGAGAACTT GTGAGAACTT			
C.(S.) timoriensis		GTGAGAACTT			
C. (S.) garettiana		GTGAGAACTT			
C.(S.)alata		GTGAGAACTT			
C.(S.) spectabilis	AACCTACCAA	GTGAGAACTT	TCAAATTCAG	AGAAACCCTG	GAATTAACAA
	110	120	130	140	150
Ceratonia siliqua AF365075		TGAGCCAAAT			
Gymnocladus dioica AF365095 C.(Ch.)leschenaultiana		TGAGCCAAAT TGAGCCAAAT			
C. (Ch.) pumila		TGAGCCAAAT			
C. grandis		TGAGCCAAAT			
C. javanica	TGGGCAATCC	TGAGCCAAAT	CCTGTTTTCC	GAAAACCAAG	AAGAGTTCAG
C. bakeriana		TGAGCCAAAT			
C. fistula		TGAGCCAAAT			
C.(S.) sophera		TGAGCCAAAT TGAGCCAAAT			
C.(S.)occidentalis C.(S.)hirsuta		TGAGCCAAAT			
C.(S.)obtusifolia		TGAGCCAAAT			
C. (S.) tora		TGAGCCAAAT			
C.(S.) surattensis		TGAGCCAAAT			
C. (S.) timoriensis		TGAGCCAAAT			
C.(S.) garettiana		TGAGCCAAAT			
C. (S.) alata	and the same and the same and the	TGAGCCAAAT			
C.(S.) spectabilis	TGGGCAATCC	TOAGCCAAAT	CCMCITITOC	ESESESES CONTROL	MADAGIIOAG
	160	170	180	190	200
Ceratonia siliqua AF365075		*** TAAAAAAA	******	GATAGGTGCA	GAGACTCAAT
Gymnocladus dioica AF365095		TAAAACAA			
C. (Ch.) leschenaultiana		TAAAAAAAA-			
C. (Ch.) pumila		TAAAAAAAA-			
C. grandis		TAAAAAAAA-			
C. javanica		TAAAAAAA-			
C. bakeriana		TAAAAAAAAA TAAAAAAAAA			
C. fistula C.(S.) sophera		TAAAAAAAA TAAAAAAA			
C.(S.) occidentalis		TAAAAAAA			
C. (S.) hirsuta		TAAAAAA			
C.(S.) obtusifolia		TAAAAAAA			
C. (S.) tora		TAAAAAAA			
C. (S.) surattensis		AAAAAAAAA			
C.(S.) timoriensis		TAAAAAAA			
C.(S.) garettiana C.(S.) alata		TAAAAAAA			
C.(S.) spectabilis		TAAAAAA			

Fig. 24 (continue)

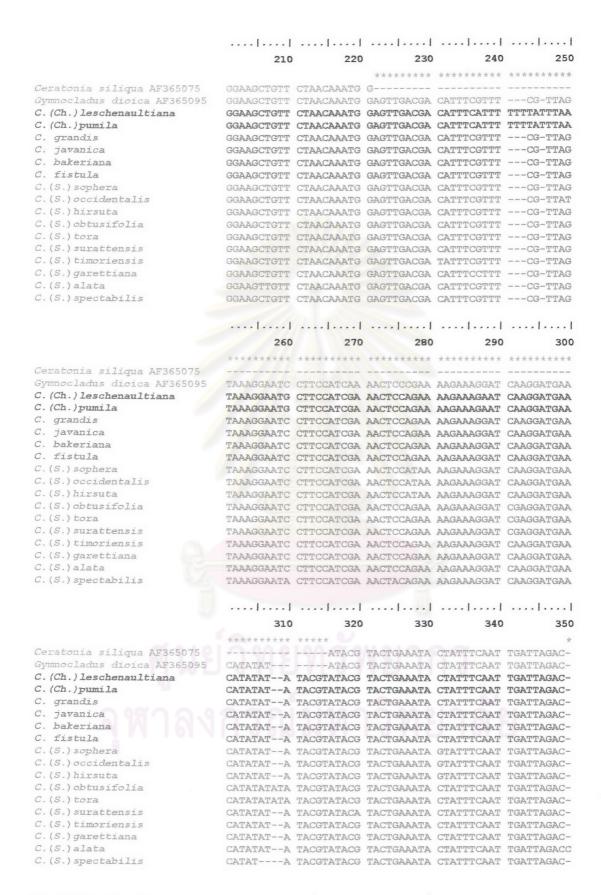


Fig. 24 (continue)

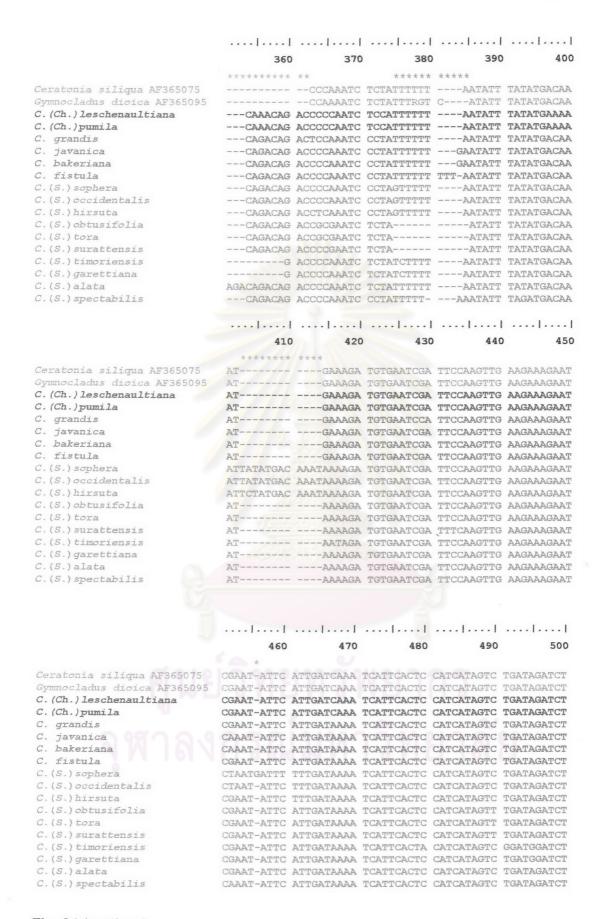


Fig. 24 (continue)

	1 1				
	510	520	530	540	550

Ceratonia siliqua AF365075		AAAACTGATT			
Gymnocladus dioica AF365095	TTTGA	AGAACTGATT	AATCGGACGA	GAATAAAGAT	AGAGTCCCAT
C. (Ch.) leschenaultiana	TTTGA	AGAACTGATT	AATCGGACGA	GAATAAAGAT	AGAGTCCCAT
C. (Ch.) pumila	TTTGA	AGAACTGATT AGAACTGATT	AATCGGACGA	GAATAAAGAT	AGAGTCCCAT
C. grandis C. javanica	TTTGA	AGAACTGATT	AATCGGACGA	GAATAAAGAT	AGAGTCCCAT
C. bakeriana		AGAACTGATT			
C. fistula		AGAACTGATT			
C.(S.) sophera		AGAACTGATT			
C.(S.)occidentalis		AGAACTGATT			
C. (S.) hirsuta		AGAACTGATT			
C. (S.) obtusifolia		AGAACTGATT			
C.(S.) tora		AGAACTGATT AGAACTGATT			
C.(S.) surattensis C.(S.) timoriensis		AGAACTGATT			
C. (S.) garettiana		AGAACTGATT			
C.(S.) alata		AGAACTGATT			
C.(S.) spectabilis		AGAACTTATT			
	560	570	580	590	600
Ceratonia siliqua AF365075	TCTACATGTC	AATACCGACA	ACAATGAAAT	TTATAGTAAG	AGGAAAATCC
Gymnocladus dioica AF365095	TCTACATGTC	AATACCGACA	ACAATGAAAT	TTATAGTAAG	AGGAAAATCC
C. (Ch.) leschenaultiana		AATACCGACA			
C. (Ch.) pumila		AATACCGACA			
C. grandis		AATACCGACA			
C. javanica C. bakeriana		AATACCGACA AATACCGACA			
C. fistula		AATACCGACA			
C.(S.) sophera		AATACCGACA			
C.(S.)occidentalis		AATACCGACA			
C.(S.) hirsuta		AATACCGACA			
C.(S.) obtusifolia		AATACCGACA			
C.(S.) tora		AATACCGACA			
C. (S.) surattensis		AATACCGACA			
C.(S.) timoriensis		AATACCGACA AATACCGACA			
C.(S.) garettiana C.(S.) alata		AATACCGACA			
C.(S.) spectabilis		AATACCGACA			
0. (0.) 57.000002225					
	610	620	630	640	1
		* **	******	*****	****
Ceratonia siliqua AF365075		GAAAT-CGTG			
Gymnocladus dioica AF365095		GAAAT-CGTG			
C. (Ch.) leschenaultiana		GAAAT-CGTG			
C. (Ch.) pumila		GAAAT-CGTG GAAAT-CG??			
C. grandis C. javanica		GAAAT-CG??			
C. bakeriana		GAAAT-CGTG			
C. fistula		GAAAT-CG?G			
C.(S.) sophera		GAAAT-CG?G			
C.(S.)occidentalis		GAAAT-CGTG			
C. (S.) hirsuta		GAAAT-CGTG			
C. (S.) obtusifolia		GAAATGCG?G			
C.(S.)tora		GAAAT-CGTG			
C.(S.) surattensis		GAAAT-CG?G GAAAT-CGTG			
C.(S.) timoriensis C.(S.) garettiana		GAAAT-CGTG			
C. (S.) garettiana C. (S.) alata		GAAAT-CG?G			
C.(S.) spectabilis		GAAAT-CG??			

Fig. 24 (continue)

Branch-and-bound searching strategy was used to analyse a data matrix of 597 bp trnL intron sequences of Thai *Cassia* 16 species without *C. siamea* (not amplified both *trn*L intron and ITS regions) included with a 20-position gap matrix (0, 1 symbols). The fully unexcluded matrix had 646 characters, but 62 nucleotides (the first position to the 30th, the 375th to the 385th and 619th to the last one) needed to be excluded. Gap were treated as missing data. *Gymnocladus dioica* (AF365095) and *Ceratonia siliqua* (AF365075) were included into the analysis as outgroup taxa (sequences retrieved from GenBank). All characters used in phylogenetic tree reconstruction were unordered and equally weighted with 37 characters (6.2%) were parsimony-informative as synapomorphy (shared-derived character) and 37 characters were parsimony-uninformative as autapomorphy specifically for each taxon. There were 14 most parsimonious trees found from this data set, with 87 steps in lenth (Fig. 25). Consistency index (CI) was 0.9195 and Homoplasy index (HI) was 0.0805. Retention index (RI) was 0.9041 and rescale consistency index (RC) was 0.8314.

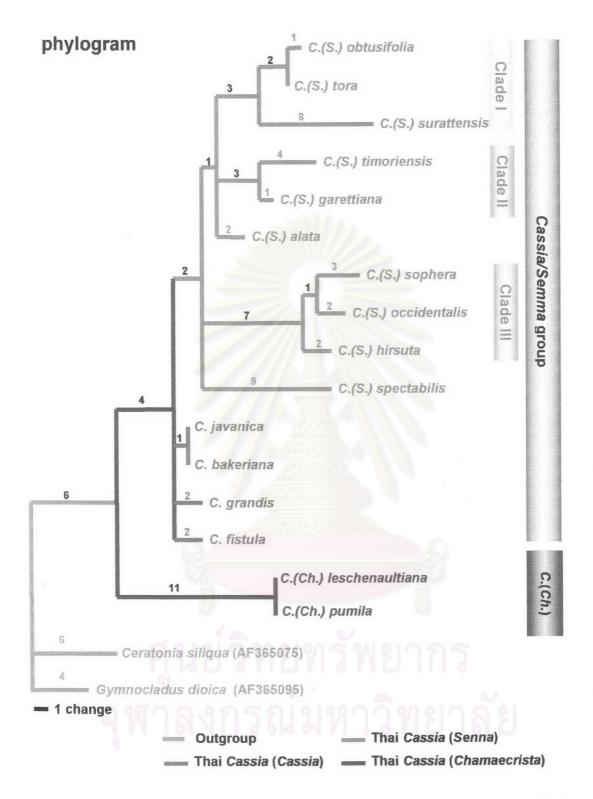


Fig. 25 one phylogram of 14 equally most parsimonious trees (87 steps in length) for 16 Cassia in Thailand based on tmL intron sequence data with Ceratonia siliqua (AF365075) and Gymnocladus dioica (AF365095) as outgroups (retrieved from GenBank). Black numbers along branches are amounts of synapomorphy and colouring numbers are amounts of autapomorphy. [CI = 0.9195, RI = 0.9041, RC = 0.8314]

Bootstrap (BS) and jackknife (JK) supporting values were calculated to confirm a reliability of each clade. Some branches were collapsed when these supporting-values were less than 50%. Strict (Fig. 26), semistrict (Fig. 27) and 50% majority-rule (Fig. 28) consensus trees were made from the 14 most parsimonious trees (MPTs). All consensus trees were similar to each other that *Gymnocladus dioica* and *Ceratonia siliqua* the two outgroups were clustered while all Thai *Cassia* species were grouped together with very high bootstrap and jackknife supporting-values (97%, 93%), respectively. Within the Thai *Cassia* group, there were two major clades separated distinctively. One clade contained Thai *Cassia* species that moved to genus *Senna* (blue branches) based on Flora Malesiana and some other species remaining to be in the genus *Cassia* (dark-red branches). The other group had two Thai *Cassia* species which moved to the genus *Chamaecrista*: *Cassia*(*Chamaecrista*) *leschenaultiana* and *C.(Ch.) pumila* (green branches).

The first Cassia/Senna group, with 66% BS and 61% JK, composes of Cassia (Senna) obtusifolia, C.(S.) tora, C.(S.) surattensis, C.(S.) timoriensis, C.(S.) garrettiana, C.(S.) alata, C.(S.) sophera, C.(S.) occidentalis, C.(S.) hirsuta, C.(S.) spectabilis, C. javanica, C. bakeriana, C. grandis and C. fistula. The other major group had only two species: C.(Ch.) pumila and C.(Ch.) leschenaultiana, with very high robustness of bootstrap (100%). Considering subgroupings in the first Cassia/Senna group, the cluster could be subdivided into three minor clades. The first clade contained C.(S.) obtusifolia, C.(S.) tora and C.(S.) surattensis with strong supporting-values (80% BS and 78% JK). The clade II composed of C.(S.) timoriensis and C.(S.) garrettiana with even higher bootstrap (91%) and jackknife (81%) supporting-values. The last clade III of C.(S.) sophera, C.(S.) occidentalis, and C.(S.) hirsuta had highest supporting-values (100% BS and 99% JK).

Some differences were also found between the strict, semistrict and 50% majority-rule consensus trees. The strict consensus tree showed that there were some remained taxa ungrouped as a clade. These taxa were C.(S.) alata, C.(S.)

spectabilis, C. javanica, C. bakeriana, C. grandis and C. fistula. Grouping between any of these species may have been collapsed after strict consensus analysis to form an unresolved polytomic backbone for the three previously recognised clades. In contrast, the semistrict consensus tree suggested two more low-supported clades. The fourth grouping contained C. grandis and C. fistula whereas the fifth minor clade composed of C. javanica and C. bakeriana. Moreover, these four Thai Cassia (Cassia) formed a distinctive group with each other in the 50% majority-rule consensus tree, though with low supporting-values. Note that C. javanica and C. bakeriana were clustered in this group. This newly recognised clade therefore had all members belonging to Cassia species not moved to the genera Senna and Chamaecrista. Cassia (Senna) spectabilis and C.(S.) alata were left as unresolved polytomic taxa to other species in the Cassia/Senna group in both semistrict and 50% majority-rule consensus trees.

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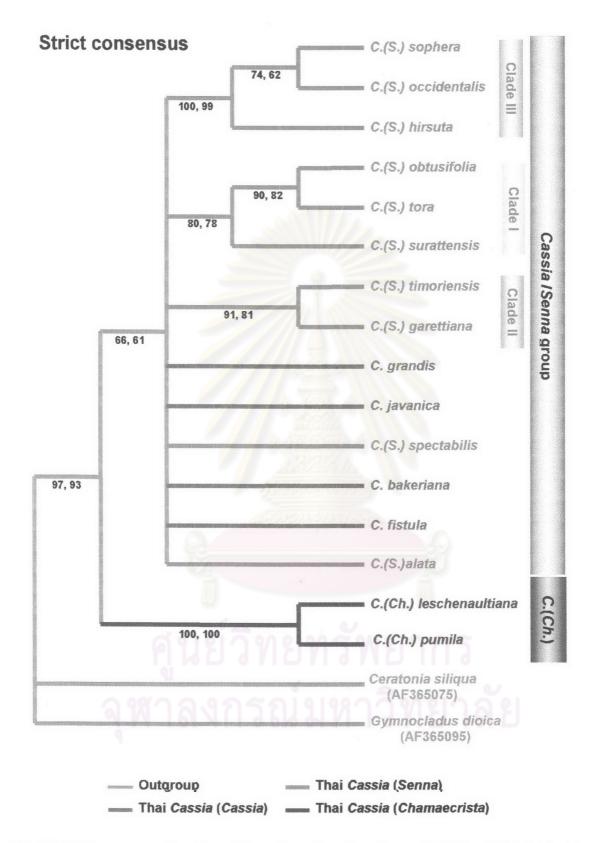


Fig. 26 strict consensus tree from 14 most parsimonious trees of 16 *Cassia* in Thailand based on *trn*L intron sequence data with *Ceratonia siliqua* and *Gymnocladus dioica* as outgroups (retrieved from GenBank). The two numbers along branches are 1000-replicate bootstrap and jackknife supporting-values, respectively.

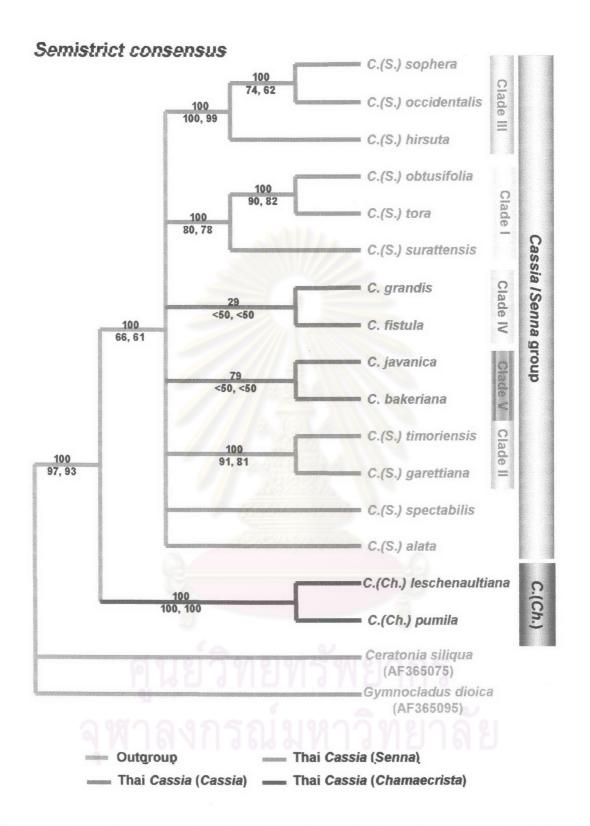


Fig. 27 semistrict consensus tree from 14 most parsimonious trees of 16 Cassia in Thailand based on trnL intron sequence data with Ceratonia siliqua and Gymnocladus dioica as outgroups (retrieved from GenBank). The upper numbers are percentages of congruent MPTs on the consensus trees and the lower numbers are 1000-replicate bootstrap and jackknife supporting-values of each clade, respectively.

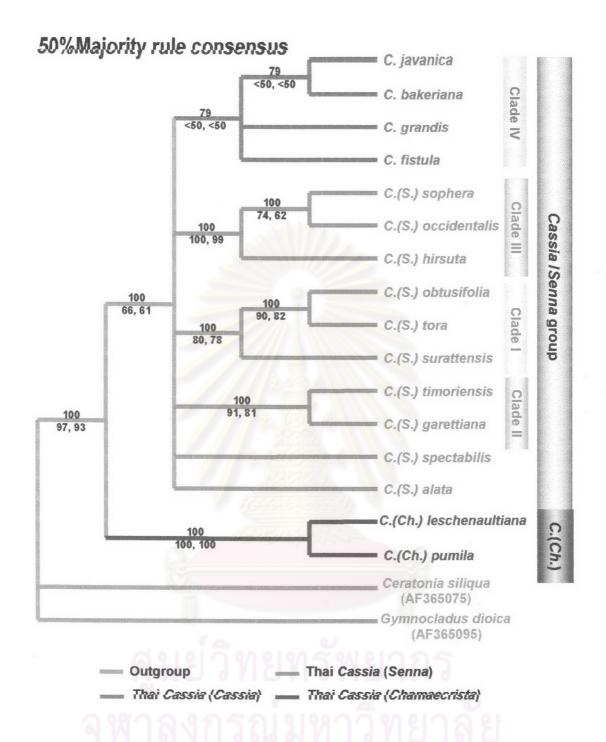


Fig. 28 50% majority-rule consensus tree from 14 most parsimonious trees of 16 Cassia in Thailand based on trnL intron sequence data with Ceratonia siliqua and Gymnocladus dioica as outgroups (retrieved from GenBank). The upper numbers are percentages of similar MPTs tree on the consensus. The lower numbers are 1000-replicate bootstrap and jackknife supporting-values of each clade, respectively.

For distance method analysis, neighbour-joining (NJ) tree was drawn to compare with results from maximum parsimony analyses. The NJ tree showed that *Gymnocladus dioica* was separated from Thai *Cassia* but *Ceratonia siliqua* formed a low supported group with Thai *Cassia* (*Chamaecrsita*). *Cassia* (*Chamaecriata*) *leschenaultiana* and *C.(Ch.) pumila* were paired with each other like in the parsimony analysis with very high supporting values (100% bootstrap and 100% jackknife). *Cassia* (*Senna*) *sophera*, *C.(S.) occidentalis* and *C.(S.) hirsuta* formed their own group with 100% BS and 100% JK supporting-values while *C.(S.) sophera* were specifically sistered to *C.(S.) occidentalis* in the group. *Cassia* (*Senna*) *obtusifolia* was paired with *C.(S.) tora* and both were grouped to *C.(S.) surattensis* with 80% BS and 76% JK. The next grouping was that of *C.(S.) alata* forming a cluster with *C.(S.) garrettiana* and *C.(S.) timoriensis*. Unexpectedly, *C.(S.) spectabilis* was transgressed into a group of four still-unmoved *Cassia* species (*C. javanica*, *C. bakeriana*, *C. grandis* and *C. fistula*).

ศูนย์วิทยทรัพยากร จุฬาลงกรณ์มหาวิทยาลัย

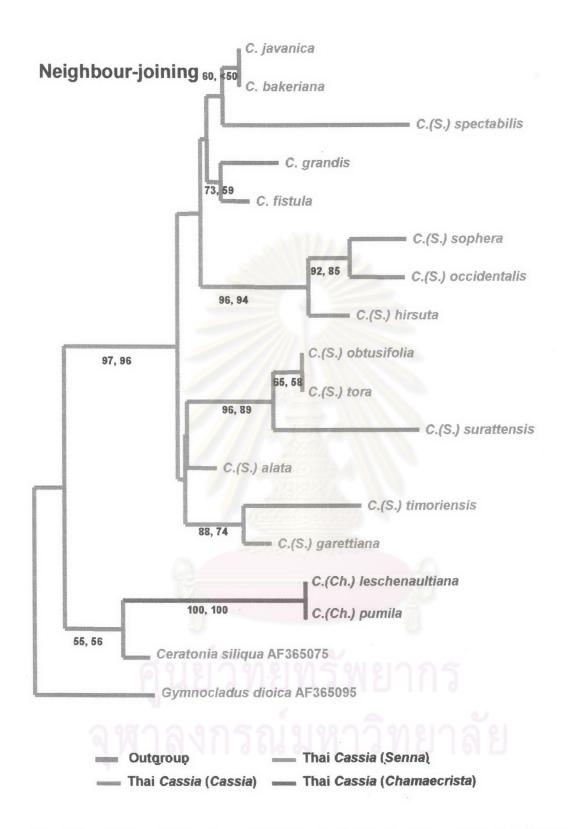


Fig. 29 neighbour-joining tree of 16 Cassia in Thailand based on tmL intron sequence data with Ceratonia siliqua and Gymnocladus dioica as outgroups (retrieve from GenBank). The numbers along branches are 1000-replicate bootstraps and jackknife supporting-values, respectively. Note that supporting-values less than 50% were not shown in the tree.

- trnL sequence data set of Cassia sensu lato 16 species in Thailand compared with those of other members in the subtribe Cassiinae (see Fig. 30)

After the *tm*L character-taxon data matrix of 16 cassia in Thailand was analysed and there were two distinctive major groups were found the next stepwas to ass nine more sequences of other Cassiinae species which were not found in Thailand but their sequences retrieved from GenBank to the analysis. These were *Chamaecrista nictitans* (AF365093), *Ch.* sp. Klitgaad (AF365093), *Ch.* sp. Breteler (AF365094), *Senna crassiramea* (AF365093), *S. lindheimeriana* (AF365089), *S. bauhinioides* (AF365087), *S. wislizeni* (AF365028), *S. bacillaris* (AF365031) and *Cassia grandis* (AF365092). Their trnL sequences were used to align together with 16 *Cassia* species from the previous data set. The new character-taxon matrix was shown in Fig. 30.

		1		1	
	10	20	30	40	50
	*****	******	*****	*****	******
Ceratonia siliqua AF365075	222222222	222222255	?GACTTAATT	GGATTGAGCC	TTGGTATGGA
Gymnocladus dioica AF365095	2222222222	222222222	?GACTTAATT	GGATTGAGCC	TTGGTATGGA
Ch nictitans AF365093	222222222	222222222	?GACTTAATT	GGATTGAGCC	TTGGTATGGA
Ch. sp. Klitgaad AF365093	2222222222	??????????	?GACTTAATT	GGATTGAGCC	TTGGTATGGA
Ch. sp. Breteler AF365094	222222222	5555555555	?GACTTAATT	GGATTGAGCC	TTGGTATGGA
S. crassiramea AF365090	2772772777	2223233333	?GACTTAATT	GGATTGAGCC	TTGGTATGGA
S. lindheimeriana AF365089	3333333333	2555555555	?GACTTAATT	GGATTGAGCC	TTGGTATGGA
S. bauhinioides AF365087	2222222222	5555555555	?GACTTAATT	GGATTGAGCC	TTGGTATGGA
5. wislizeni AF36502B	2222222222	2272222222	PGACTTAATT	GGATTGAGCC	TTGGTATGGA
S. bacillaris AF365031	222222222	2222222222	?GACTTAATT	GGATTGAGCC	TTGGTATGGA
C. grandis AF365092	222222222	??????????	222222222	??????????	555555555
C. leschenaultiana	TCGAAATCGG	TAGACGCTAC	GGACTTAATT	GGATTGAGCC	TTGGTATGGA
C. pumila	??????????	???????TAC	GGACTTAATT	GGATTGAGCC	TTGGTATGGA
C. grandis	??????????	??????????	??????????	GGATTGAGCC	
C. javanica	??????????	??????????	GACCTTAATT	GGATTGAGCC	
C. bakeriana	222222222	GTGACGCTAC	GGACTTAATT	GGATTGAGCC	TTGGTATGGA
C. fistula	????????CG	TAGACGCTAC	GGACTTAATT	GGATTGAGCC	
C. (S.) sophera	??????????	??????????	?????????T	GGATTGAGCC	TTGGTATGGA
C. (S.) occidentalis	333333333C	GTGACGCTAC	GGACTTAATT	GGATTGAGCC	
C. (S.) hirsuta	??????????	??????????	GACCTTAATT	GGATTGAGCC	
C. (S.) obtusifolia	?????CGTAG	ACGACGCTAC	GGACTTAATT	GGATTGAGCC	
C. (S.) tora	5555555555	??????????	?GACTTAATT	GGATTGAGCC	
C. (S.) surattensis	3555555555	333333333	GACCTTAATT	GGCTTGAGCC	
C. (S.) timoriensis	3333333333	???ACGCTAC	GGACTTAATT		
C. (S.) garettiana	3555555555	TAGACGCTAC	GGACTTAATT		
C. (S.) alata	??????????	GTGACGCTAC	GGACTTAATT		
C. (S.) spectabilis	555555555	5555555555	GACCTTAATT	GGATTGAGCC	TTGGTATGGA

Fig. 30 a 657 bp character-taxon matrix of 16 Thai Cassia species based on trnL intron sequences compared with some additional new-world Cassiinae species and two other outgroups. Asterisks * and * represent excluded and gap-matrix sites from analyses, respectively. Gap symbol (-) indicates insertion or deletion at the site. ? symbol shows missing nucleotide data.

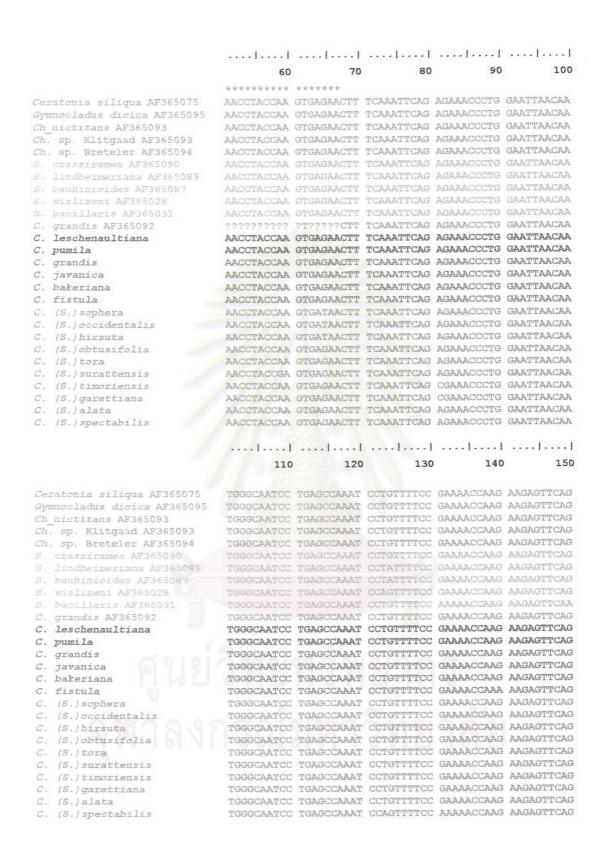


Fig. 30 (continue)

	160				
		***	****	****	
Ceratonia siliqua AF365075	AAAGCGCGAA	TAAAAAAA	GGATAG	GTGCA	GAGACTCAAT
Gymnocladus dioica AF365095	AAAGCGAGAA	TAAAACAA	GGATTG	GTGCA	GAGACTCAAT
Ch nictitans AF365093	AAAGGGAGAA	TAAAAAAAA-	GGATAG	GTGCA	GAGACTCAAT
Ch. sp. Klitgaad AF365093	AAAGGGAGAA	TAAAAAAAA-	GGATAG	GTGCA	GAGACTCAAT
Ch. sp. Breteler AF365094	AAAGGGAGAA	TAAAAAAA	GGATAG	GTGCA	GAGACTCAAT
S. crassiramea AF365090	AAAGGGAGAA	TAAAAAAA	GGATAG	GTGCA	GAGACTCAAC
S. lindheimeriana AF365089		TAAAAAA			
S. bauhinioides AF365087		TAAAAAA			
S. wislizeni AF365028		TAAAAAAA			
S. bacillaris AF365031		TAAAAAAA			
C. grandis AF365092		TAAAAAAA-			
C. (Ch.) leschenaultiana		TAAAAAAAA-			
C. (Ch.) pumila		TAAAAAAAA-			
C. grandis		TAAAAAAAA-			
C. javanica C. bakeriana		TAAAAAAAA-			
C. fistula		TAAAAAAAA-			
C. (S.) sophera		TAAAAAAAA TAAAAAAA			
C. (S.) occidentalis		TAAAAAAA			
C. (S.) hirsuta		TAAAAAAA			
C. (S.) obtusifolia		TAAAAAAA			
C. (S.) tora		TAAAAAAA			
C. (S.) surattensis		AAAAAAAAA			
C. (S.) timoriensis		TAAAAAAA			
C. (S.) garettiana	AAAGGGAGAA	TAAAAAAA	GGATAG	GTGCA	GAGACTCAAC
C. (S.) alata	AAAGGGAGAA	TAAAAAAA	GGATAG	GTGCA	GAGACTCAAC
C. (S.) spectabilis	AAAGGGAGAA	TAAAAAA	GGATAG	GTGCA	GAGACTCAAC
	ll		230	240	250
Ceratonia siligua AF365075	210	220	230	240	250
Ceratonia siliqua AF365075 Gymnocladus dioica AF365095	210 GGAAGCTGTT	220 CTAACAAATG	230 ******	240	250
Ceratonia siliqua AF365075 Gymnocladus dioica AF365095 Ch nictitans AF365093	210 GGAAGCTGTT GGAAGCTGTT	220 CTAACAAATG	230 ******* G GAGTTGACGA	240 ******** CATTTCGTTT	250 ******* CGTT-AG
Gymnocladus dioica AF365095	GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT	220 CTAACAAATG CTAACAAATG	230 ******* G GAGTTGACGA GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT	250 ********CGTT-AG TTTTATTGAA
Gymnocladus dioica AF365095 Ch nictitans AF365093	GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT	220 CTAACAAATG CTAACAAATG CTAACAAATG	230 ******* G GAGTTGACGA GAGTTGACGA GAGTTGACGA	240 ******* CATTTCGTTT CATTTCATTT CATTTCATTT	250 *******CGTT-AG TTTTATTGAA TTTTATTGAA
Gymnocladus dioica AF365095 Ch_nictitans AF365093 Ch. sp. Klitgaad AF365093	GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT	CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG	230 ******* G GAGTTGACGA GAGTTGACGA GAGTTGACGA GGGTTGACGA	240 ******* CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCATTT	250 *******CGTT-AG TTTTATTGAA TTTTATTGAA TTTTATG
Gymnocladus dioica AF365095 Ch_nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094	GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT	CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG	230 ******* G GAGTTGACGA GAGTTGACGA GAGTTGACGA GGGTTGACGA GGGTTGACGA GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCATTT	250 *******CGTT-AG TTTTATTGAA TTTTAG CGTTAG
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087	GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT	CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG	230 ******* G GAGTTGACGA GAGTTGACGA GAGTTGACGA GGGTTGACGA GGGTTGACGA GAGTTGACGA GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT CATTTCGTTT CATTTCGTTT	250 *******
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028	GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT GGAAGCTGTT	CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG	230 ******** G GAGTTGACGA GAGTTGACGA GAGTTGACGA GAGTTGACGA GAGTTGACGA GAGTTGACGA GAGTTGACGA GAGTTGACGA GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT	250 ********
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031	GGAAGCTGTT	CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG	230 ******** G GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT	250 ********
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092	GGAAGCTGTT	CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG CTAACAAATG	230 ******** G GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT	250 *******
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C. (Ch.) leschenaultiana	GGAAGCTGTT	CTAACAAATG	230 ******** G GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCGTTT	250 *******
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C. (Ch.) leschenaultiana C. (Ch.) pumila	GGAAGCTGTT	CTAACAAATG	230 ******** G GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT CATTTCATTT	250 ********
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365031 C. grandis AF365031 C. grandis AF365092 C. (Ch.) leschenaultiana C. (Ch.) pumila C. grandis	GGAAGCTGTT	CTAACAAATG	230 ******** G GAGTTGACGA	240 ********* CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT CATTTCATTT	250 ********
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C. (Ch.) leschenaultiana C. (Ch.) pumila C. grandis C. javanica	GGAAGCTGTT	CTAACAAATG	******** G GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT CATTTCATTT	250 ********CGTT-AG TTTTATTGAA TTTTAT-GA TTTTAG CGTTAG
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C. (Ch.)leschenaultiana C. (Ch.)pumila C. grandis C. javanica C. bakeriana	GGAAGCTGTT	CTAACAAATG	******** G GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCATTT	250 ********CGTT-AG TTTTATTGAA TTTTATTGAA TTTTAG CGTTAG
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C.(Ch.)leschenaultiana C.(Ch.)pumila C. grandis C. javanica C. bakeriana C. fistula	GGAAGCTGTT	CTAACAAATG	******** G GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCATTT	250 ********
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C.(Ch.)leschenaultiana C.(Ch.)pumila C. grandis C. javanica C. bakeriana C. fistula C. (S.)sophera	GGAAGCTGTT	CTAACAAATG	******** G GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCGTTT CATTTCATTT	250 *******
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C.(Ch.)leschenaultiana C.(Ch.)pumila C. grandis C. javanica C. bakeriana C. fistula C. (S.)sophera C. (S.)occidentalis	GGAAGCTGTT	CTAACAAATG	230 ******** G GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT	250 ********
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365021 C. grandis AF365092 C.(Ch.)leschenaultiana C.(Ch.)pumila C. grandis C. javanica C. javanica C. bakeriana C. fistula C. (S.)sophera C. (S.)occidentalis C. (S.)hirsuta	GGAAGCTGTT	CTAACAAATG	230 ******** G GAGTTGACGA	240 ******** CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT	250 ********
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C.(Ch.)leschenaultiana C.(Ch.)pumila C. grandis C. javanica C. bakeriana C. fistula C. (S.)sophera C. (S.)occidentalis	GGAAGCTGTT	CTAACAAATG	******** G GAGTTGACGA	240 ********* CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT	250 ********
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C.(Ch.)leschenaultiana C.(Ch.)pumila C. grandis C. javanica C. bakeriana C. fistula C. (S.)sophera C. (S.)occidentalis C. (S.)hirsuta C. (S.)obtusifolia	GGAAGCTGTT	CTAACAAATG	******** G GAGTTGACGA	240 ********* CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT	250 ********
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C. (Ch.) leschenaultiana C. (Ch.) pumila C. grandis C. javanica C. bakeriana C. fistula C. (S.) sophera C. (S.) occidentalis C. (S.) hirsuta C. (S.) obtusifolia C. (S.) tora	GGAAGCTGTT	CTAACAAATG	******** G GAGTTGACGA	********* CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT	250 ********
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C. (Ch.) leschenaultiana C. (Ch.) pumila C. grandis C. javanica C. bakeriana C. fistula C. (S.) sophera C. (S.) occidentalis C. (S.) hirsuta C. (S.) tora C. (S.) tora C. (S.) surattensis	GGAAGCTGTT	CTAACAAATG	******** G GAGTTGACGA GAGTTGACGA	********* CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT TATTTCGTTT	250 ********CGTT-AG TTTTATTGAA TTTTATTGAA TTTTAT-GG CGTTA-GG
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C. (Ch.) leschenaultiana C. (Ch.) pumila C. grandis C. javanica C. bakeriana C. fistula C. (S.) sophera C. (S.) occidentalis C. (S.) hirsuta C. (S.) obtusifolia C. (S.) tora C. (S.) surattensis C. (S.) timoriensis	GGAAGCTGTT	CTAACAAATG	******** G GAGTTGACGA	240 ********* CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT	250 ********CGTT-AG TTTTATTGAA TTTTATTGAA TTTTAT-G CGTTA-G
Gymnocladus dioica AF365095 Ch nictitans AF365093 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 S. crassiramea AF365090 S. lindheimeriana AF365089 S. bauhinioides AF365087 S. wislizeni AF365028 S. bacillaris AF365031 C. grandis AF365092 C. (Ch.) leschenaultiana C. (Ch.) pumila C. grandis C. javanica C. bakeriana C. fistula C. (S.) sophera C. (S.) occidentalis C. (S.) hirsuta C. (S.) obtusifolia C. (S.) tora C. (S.) timoriensis C. (S.) garettiana	GGAAGCTGTT	CTAACAAATG	******** G GAGTTGACGA	240 ********* CATTTCGTTT CATTTCATTT CATTTCATTT CATTTCGTTT	250 ********CGTT-AG TTTTATTGAA TTTTATTGAA TTTTATTGAA TTTTATG CGTTAG

Fig. 30 (continue)

				[]	
	260	270	280	290	300
	******	*******	******	*******	******
Ceratonia siliqua AF365075	*25 MM 100 (MM 400 MM 900 MM 400 MM				
Symmocladus dioica AF365095	TAAAGGAATC	CTTCCATCAA	AACTCCCGAA	AA	GAAAGGA
Ch nictitans AF365093	TAAAGGAATG	CTTCCATCGA	AACTCCAGAA	AA	GAAAGAA
Th. sp. Klitgaad AF365093	TAAAGGAATG	CTTCCATCGA	AACTCCAGAA	AA	GAAAGAA
h. sp. Breteler AF365094	TAAAGGAATC	CCCCCATCGA	AACTCCAGAA.	AAAGA	AAAGAAAGGA
. crassiramea AF365090	TAAAGGAATC	CTTCCATCGA	AACTCCAGAA	AAGAAAGAGA	AAAGAAAGGA
. lindheimeriana AF365089	TAAAGGAATC	CTTCCATCGA	AACTCCATAA	AA	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
. bauhinioides AF365087	TAAAGGAATC	CTTCCATCGA	AACTCCATAA	AA	GAAAGGA
. wislizeni AF365028	TAAAGGAATC	CTTCCATCGA	AACTCCAGAA	AA	GAAAGGA
. bacillaris AF365031	TAAAGGAATC	CTTCCATCAA	AACTACAGAG	AA	GAAAGGA
. grandis AF365092	TAAAGGAATC	CTTCCATCGA	AACTCCAGAA	AA	GAAAGGA
. (Ch.) leschenaultiana	TAAAGGAATG	CTTCCATCGA	AACTCCAGAA	AA	GAAAGAA
.(Ch.)pumila	TAAAGGAATG	CTTCCATCGA	AACTCCAGAA	AA	GAAAGAA
grandis	TAAAGGAATC	CTTCCATCGA	AACTCCAGAA	AA	GAAAGGA
. javanica	TAAAGGAATC	CTTCCATCGA	AACTCCAGAA	AA	GAAAGGA
. bakeriana	TAAAGGAATC	CTTCCATCGA	AACTCCAGAA	AA	GAAAGGA
fistula				AA	
. (S.) sophera	TAAAGGAATC	CTTCCATCGA	AACTCCATAA	AA	GAAAGGA
. (S.)occidentalis				AA	
(S.) hirsuta				AA	
. (S.) obtusifolia				AA	
. (S.) tora				AA	
(S.) surattensis				AA	
. (S.) timoriensis				AA	
(S.) garettiana				AA	
(S.)alata	TAAAGGAATC				MESSAGE ACTION OF THE SECOND
		CITCEATCEA	AALTELAHAA	AA	GAAAGGA
C. (S.)spectabilis	TAAAGGAATA	CTTCCATCGA	AACTACAGAA	AA	GAAAGGA
. (S.) spectabilis	TAAAGGAATA	CTTCCATCGA	AACTACAGAA	.1	GAAAGGA
. (S.)spectabilis	TAAAGGAATA	CTTCCATCGA	AACTACAGAA	.1	gaaagga
	TAAAGGAATA	CTTCCATCGA	AACTACAGAA	.1	GAAAGGA -
eratonia siliqua AF365075	TAAAGGAATA	. 10 3.	AACTACAGAA	.1	GAAAGGA
eratonia siliqua AF365075 yymocladus dioica AF365095	TAAAGGAATA 3 ******** TCAAGGATG	1	AACTACAGAA . 20 3 ** *****ATA	AA30 3	T ACTATTC
eratonia siliqua AF365075 ymnocladus dioica AF365095 n_nictitans AF365093	TAAAGGAATA ******** TCAAGGATG TCAAGGATG	CTTCCATCGA I III A ACATATATA A ACATATATA	AACTACAGAA .i	AA 30 3 AC GTACTGAAA	T ACTATTC T ACTATTC
eratonia siliqua AF365075 gmnocladus dioica AF365095 n_nictitans AF365093 n. sp. Klitgaad AF365093	TAAAGGAATA ******** TCAAGGATG TCAAGGATG TCAAGGATG	CTTCCATCGA . 10 3. ** ******** A ACATATATA A ACATATATA A ACATATATA	AACTACAGAA .i	AA 30 3 AC GTACTGAAA AC GTACTGAAA AC GTACTGAAA	T ACTATTC T ACTATTC T ACTATTC T ACTATTC T ACTATTC
eratonia siliqua AF365075 mmocladus dioica AF365095 nnictitans AF365093 n. sp. Klitgaad AF365093 n. sp. Breteler AF365094	TAAAGGAATA ******** TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG	CTTCCATCGA . 10 3: ** ******** A ACATATATA A ACATATATA A ACATATATA A ACATATATA A ACATATATA	AACTACAGAA . 20 3 ** *****AT#AT# AT ACGTAT# AT ACGTAT# AT ACGTAT#	AA 30 3 AC GTACTGAAA AC GTACTGAAA AC GTACTGAAA AC GTACTGAAA	T ACTATTC
eratonia siliqua AF365075 pmocladus dioica AF365095 nnictitans AF365093 n. sp. Klitgaad AF365093 n. sp. Breteler AF365094 crassiramsa AF365090	TAAAGGATA ******* TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG	CTTCCATCGA . 10 3: ** ******* A ACATATATA A ACATATATA A ACATATATA A ACATATATA A ACATATATA A ACATATATA	AACTACAGAA . 20 3 ** *****AT#AT# AT ACGTAT# AT ACGTAT# AT ACGTAT# AT ACGTAT# AT ACGTAT#	AA 30 3- AC GTACTGAAA AC GTACTGAAA AC GTACTGAAA AC GTACTGAAA	T ACTATTC
eratonia siliqua AF365075 pmocladus dioica AF365095 n nictitans AF365093 n. sp. Klitgaad AF365093 n. sp. Breteler AF365094 crassiramsa AF365090 lindheimeriana AF365089	TAAAGGATA ******* TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG	CTTCCATCGA . 10 3: ** ******* A ACATATATA	AACTACAGAA . 20 3 ** *****ATIATI AT ACGTATI AT ACGTATI AT ACGTATI AT ACGTATI AT ACGTATI AT ACGTATI	AA	T ACTATTC
eratonia siliqua AF365075 mmocladus dioica AF365095 n nictitans AF365093 n. sp. Klitgaad AF365093 sp. Breteler AF365094 crassiramea AF365090 lindheimeriana AF365089 bauhinioides AF365087	TAAAGGATA ******* TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG	CTTCCATCGA . 10 3 ** ******* 6A ACATATATA	AACTACAGAA . 20 3 ** ***** AT# AT ACGTAT#	AA	T ACTATTC
eratonia siliqua AF365075 mmocladus dioica AF365095 n nictitans AF365093 n. sp. Klitgaad AF365093 n. sp. Breteler AF365094 crassiramea AF365090 lindheimeriana AF365089 bauhinioides AF365087 wislizeni AF365028	TAAAGGATA ******* TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG	CTTCCATCGA 10 3 ** ******* 5A ACATATATA 5A ACATATATA 5A ACATATATA 5A ACATATATA 5A ACATATATA 6A ACATATATA	AACTACAGAA .	AA	T ACTATTC
eratonia siliqua AF365075 gmnocladus dioica AF365095 n nictitans AF365093 n. sp. Klitgaad AF365094 crassiramea AF365090 lindheimeriana AF365089 bauhinioides AF365087 wislizeni AF365028	TAAAGGATA ******* TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG	CTTCCATCGA 10 3. ********* 5A ACATATATA 5A ACATATATA 5A ACATATATA 6A ACATATATA	AACTACAGAA 1	AA	T ACTATTC
eratonia siliqua AF365075 gmnocladus dioica AF365095 n nictitans AF365093 n. sp. Klitgaad AF365094 crassiramsa AF365090 lindheimeriana AF365089 bauhinioides AF365087 wislizeni AF365028 bacillaris AF365031 grandis AF365092	TAAAGGAATA ******** TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG TCAAGGATG	CTTCCATCGA 10 3. ********* 5A ACATATATA 5A ACATATATA 6A ACATATATA	AACTACAGAA 1	AA	T ACTATTC
eratonia siliqua AF365075 gymocladus dioica AF365095 n nictitans AF365093 n. sp. Klitgaad AF365094 crassiramea AF365090 lindheimeriana AF365089 bauhinioides AF365087 wislizeni AF365028 bacillaris AF365031 grandis AF365092	TAAAGGATA ******* TCAAGGATG	CTTCCATCGA 10 3 ** ******* 3A ACATATATA	AACTACAGAA 1	AA	T ACTATTC
eratonia siliqua AF365075 gamocladus dioica AF365095 n nictitans AF365093 n. sp. Klitgaad AF365094 crassiramsa AF365090 lindheimeriana AF365089 bauhinioides AF365028 bacillaris AF365021 grandis AF365092 (Ch.) leschenaultiana (Ch.) pumila	TAAAGGATA ******* TCAAGGATG	CTTCCATCGA 10 3: ********* SA ACATATATA	AACTACAGAA 1	AA	T ACTATTC
eratonia siliqua AF365075 gmocladus dioica AF365095 n nictitans AF365093 n. sp. Klitgaad AF365094 crassiramsa AF365090 lindheimeriana AF365089 bauhinioides AF365028 wislizeni AF365028 bacillaris AF365031 grandis AF365092 (Ch.) leschenaultiana (Ch.) pumila grandis	TAAAGGAATA ******** TCAAGGATG	CTTCCATCGA 10 3 ** ******* GA ACATATATA GA ACATATATATA GA ACATATATA CA ACATATATATA CA ACATATATA CA ACATATATA CA ACATATATATA CA ACATATATA CA ACATA	AACTACAGAA 1	AA	T ACTATTC
eratonia siliqua AF365075 comocladus dioica AF365095 n.nictitans AF365093 n. sp. Klitgaad AF365094 n. crassiramsa AF365094 n. crassiramsa AF365090 lindheimeriana AF365089 bauhinioides AF365028 bacillaris AF365028 bacillaris AF365031 ngrandis AF365092 (Ch.) leschenaultiana (Ch.) pumila ngrandis javanica	TAAAGGAATA ******* TCAAGGATG	CTTCCATCGA 10 3. ********* A ACATATATA	AACTACAGAA 1	AA	T ACTATTC
eratonia siliqua AF365075 pumocladus dioica AF365095 nictitans AF365093 n. sp. Klitgaad AF365093 n. sp. Breteler AF365094 ccassiramea AF365090 lindheimeriana AF365089 bauhinioides AF365087 wislizeni AF365028 bacillaris AF365031 grandis AF365092 (Ch.)leschenaultiana (Ch.)pumila grandis javanica bakeriana	TAAAGGAATA ******* TCAAGGATG	CTTCCATCGA 1	AACTACAGAA 1	AA	T ACTATTC
eratonia siliqua AF365075 comocladus dioica AF365095 nictitans AF365093 n. sp. Klitgaad AF365093 n. sp. Breteler AF365094 crassiramea AF365089 hauhinioides AF365087 wislizeni AF365028 hacillaris AF365031 grandis AF365092 (Ch.) leschenaultiana (Ch.)pumila grandis javanica hakeriana fistula	TAAAGGAATA ******* TCAAGGATG	CTTCCATCGA 1	AACTACAGAA 20 3 ** ***** ATM T ACGTATM	AA	T ACTATTC
eratonia siliqua AF365075 emocladus dioica AF365095 nictitans AF365093 n. sp. Klitgaad AF365093 n. sp. Breteler AF365094 crassiramea AF365090 lindheimeriana AF365089 bauhinioides AF365087 wislizeni AF365028 bacillaris AF365031 grandis AF365092 (Ch.) leschenaultiana (Ch.) pumila grandis javanica bakeriana fistula (S.) sophera	TAAAGGATA ******* TCAAGGATG	CTTCCATCGA 10 3. ********* 5A ACATATATA 5A ACATATATA 5A ACATATATA 6A ACATATATATA 6A ACATATATA	AACTACAGAA 1	AA	T ACTATTC
eratonia siliqua AF365075 procladus dioica AF365095 nictitans AF365093 n. sp. Klitgaad AF365093 n. sp. Breteler AF365094 crassiramea AF365090 lindheimeriana AF365089 bauhinioides AF365087 wislizeni AF365028 bacillaris AF365028 bacillaris AF36501 grandis AF365092 (Ch.)leschenaultiana (Ch.)pumila grandis javanica bakeriana fistula (S.)sophera (S.)occidentalis	TAAAGGAATA ******** TCAAGGATG	CTTCCATCGA 10 3. ********* ACATATATA	AACTACAGAA 20 3 ** ***** ATA AT ACGTATA	AA	T ACTATTC
eratonia siliqua AF365075 yymocladus dioica AF365095 h nictitans AF365093 h. sp. Klitgaad AF365093 h. sp. Breteler AF365094 crassiramsa AF365090 lindheimeriana AF365089 bauhinioides AF365087 wislizeni AF365028 bacillaris AF365031 grandis AF365092 (Ch.)leschenaultiana (Ch.)pumila grandis javanica bakeriana fistula (S.)sophera (S.)occidentalis (S.)hirsuta	TAAAGGAATA ******** TCAAGGATG	CTTCCATCGA 10 3. ********* SA ACATATATA S	AACTACAGAA 20 3 ** ***** ATA AT ACGTATA	AA	T ACTATTC T ACTA
eratonia siliqua AF365075 yymocladus dioica AF365095 h nictitans AF365093 h. sp. Klitgaad AF365093 h. sp. Breteler AF365090 lindheimeriana AF365089 bauhinioides AF365087 wislizeni AF365028 bacillaris AF365031 grandis AF365092 (Ch.)leschenaultiana (Ch.)pumila grandis javanica bakeriana fistula (S.)sophera (S.)occidentalis (S.)hirsuta (S.)obtusifolia	TAAAGGAATA ******** TCAAGGATG	CTTCCATCGA 10 3: ********* SA ACATATATA S	AACTACAGAA 20 3 ** ***** ATA AT ACGTATA AT ACG	AA	T ACTATTC
eratonia siliqua AF365075 yymnocladus dioica AF365095 h nictitans AF365093 h. sp. Klitgaad AF365093 h. sp. Breteler AF365090 clandheimeriana AF365089 bauhinioides AF365087 vislizeni AF365028 bacillaris AF365031 grandis AF365092 (Ch.)leschenaultiana (Ch.)pumila grandis javanica bakeriana fistula (S.)sophera (S.)occidentalis (S.)hirsuta (S.)obtusifolia (S.)tora	TAAAGGAATA ******** TCAAGGATG	CTTCCATCGA 10 3: ********* **A ACATATATA **A ACATATATA* **A ACA	AACTACAGAA 20 3 ** ***** ATA ACGTATA	AA	T ACTATTCA
eratonia siliqua AF365075 yymnocladus dioica AF365095 h nictitans AF365093 h. sp. Klitgaad AF365094 crassiramsa AF365094 crassiramsa AF365090 lindheimeriana AF365087 wislizeni AF365028 bacillaris AF365028 bacillaris AF365031 grandis AF365092 (Ch.) leschenaultiana (Ch.) pumila grandis javanica bakeriana fistula (S.) sophera (S.) occidentalis (S.) hirsuta (S.) obtusifolia (S.) tora (S.) surattensis	TAAAGGAATA ******** TCAAGGATG	CTTCCATCGA 10 3: ********* 5A ACATATATA 5A ACATATATA 5A ACATATATA 5A ACATATATA 5A ACATATATA 6A ACATATATA 6	AACTACAGAA 20 3 ** ***** ATA ACGTATA	AA	T ACTATTC
eratonia siliqua AF365075 yymnocladus dioica AF365095 h nictitans AF365093 h. sp. Klitgaad AF365093 h. sp. Breteler AF365094 . crassiramsa AF365090 lindheimeriana AF365089 bauhinioides AF365028 bacillaris AF365021 grandis AF365021 grandis AF365092 (Ch.) leschenaultiana (Ch.) pumila grandis javanica bakeriana fistula (S.) sophera (S.) occidentalis (S.) hirsuta (S.) otra (S.) surattensis (S.) timoriensis	TAAAGGAATA ******** TCAAGGATG	CTTCCATCGA 10 3 ********* SA ACATATATA SA	AACTACAGAA 20 3 ** *****ATA AT ACGTATA AT A	AA	T ACTATTC
eratonia siliqua AF365075 ymnocladus dioica AF365095 h nictitans AF365093 h. sp. Klitgaad AF365094 . crassiramaa AF365090 lindheimeriana AF365089 lbauhinioides AF365087 wislizeni AF365028 lbacillaris AF365031 grandis AF365092 (Ch.) leschenaultiana (Ch.) pumila grandis javanica lbakeriana fistula (S.) sophera (S.) occidentalis (S.) hirsuta (S.) obtusifolia (S.) tora (S.) surattensis	TAAAGGAATA ******** TCAAGGATG	CTTCCATCGA 10 3. ********* GA ACATATATA CA ACATATATA CA ACATATATA CA ACATATATA CA ACATATATA CA ACATATATA	AACTACAGAA 20 3 ** ***** ATA AT ACGTATA AT ACG	AC GTACTGAAA	T ACTATTCA

Fig. 30 (continue)

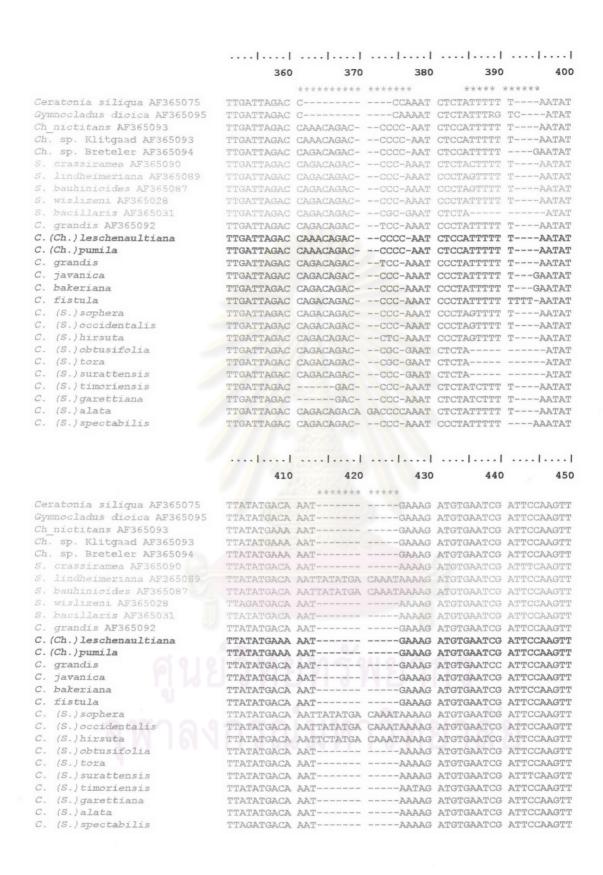


Fig. 30 (continue)

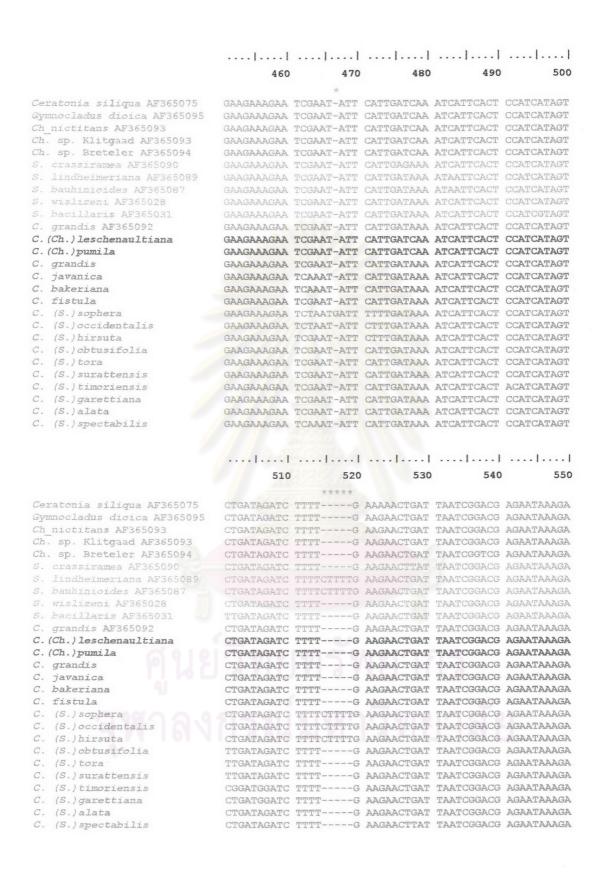


Fig. 30 (continue)

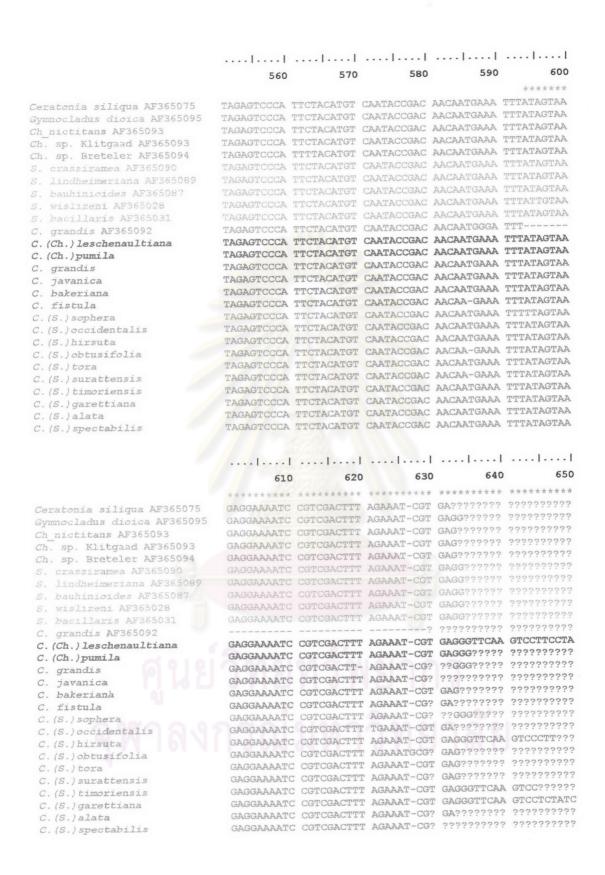


Fig. 30 (continue)

...... ***** Ceratonia siliqua AF365075 222222 Gymnocladus dioica AF365095 Ch nictitans AF365093 ??????? 222222 Ch. sp. Klitgaad AF365093 Ch. sp. Breteler AF365094 5. crassiramea AF365090 5. lindheimeriana AF365089 S. bacillaris AF365031 C. grandis AF365092 C. (Ch.) leschenaultiana TCCCCAA C. (Ch.) pumila ??????? C. grandis ??????? C. javanica ??????? C. bakeriana ??????? C. fistula C. (S.) sophera C. (S.) occidentalis ??????? C. (S.) hirsuta C. (S.) obtusifolia 5555555 C. (S.) tora C.(S.) surattensis 2222222 C. (S.) timoriensis C. (S.) garettiana 2222222 C. (S.) alata C. (S.) spectabilis Fig. 30 (continue)

A 586 bp *tm*L intron sequences of Thai *Cassia* 16 species (no *C. siamea*) and other New-World Cassiinae was analysed using branch-and-bound searching strategy. A 35 position gap matrix (0, 1 symbols) was included. The full data matrix had 657 characters but 107 nucleotides (the first position to the 67th, the 385th to the 395th and the 629th to the 657th) were necessary to be excluded. Gaps were treated as missing data. *Gymnocladus dioica* (GenBank AF365095) and *Ceratonia siliqua* (AF365075) were included into the analysis as outgroup taxa. All characters used in phylogenetic tree reconstruction were unordered and equally weighted with 57 characters (9.7%) were parsimony-informative as synapomorphy and 46 characters were parsimony-uninformative as autapomorphy. There were 6 most parsimonious trees found from this data set, with 127 steps in length (Fig. 31). Consistency index (CI) was 0.8425 and homoplasy index (HI) was 0.1575. Retention index (RI) was 0.8788 and rescaled consistency index (RC) was 0.7404.

ศูนย์วิทยทรัพยากร หาลงกรณ์มหาวิทยาลัย

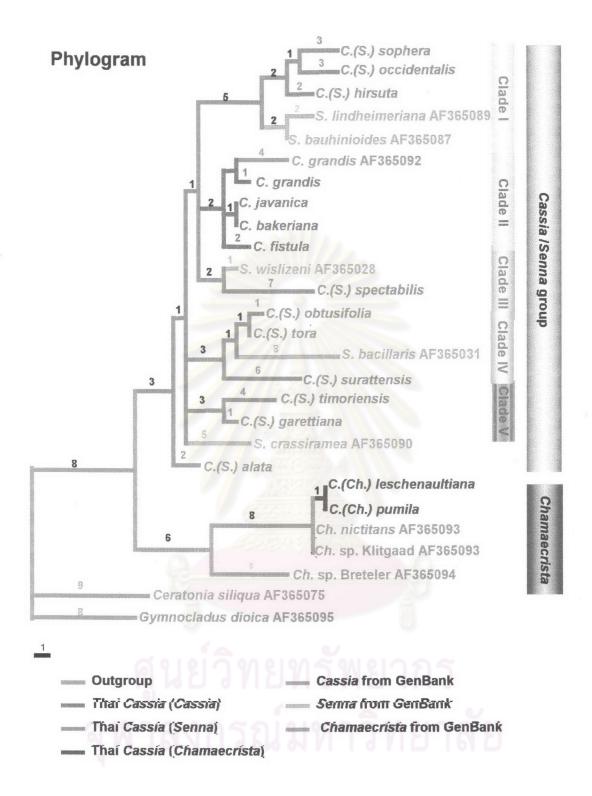


Fig. 31 one phylogram of 6 equally most parsimonious trees (127 steps in length) for 16 Cassia in Thailand based on *trn*L intron sequence data compared with nine additional Cassiinae New-World species and two outgroups, *Ceratonia siliqua* and *Gymnocladus dioica*. Numbers in black are amounts of synapomorphy and colouring numbers are amounts of autapomorphy. [CI = 0.8425, RI = 0.8788, RC = 0.7404]

All nine most equally most parsimonious trees (MPTs) were further analysed to produce strict (Fig. 32), semistrict (Fig. 33) and 50% majority-rule (Fig. 34) consensus trees. All three consensus trees were similar to each other that all members of Cassiinae were grouped together with high bootstrap and jackknife supporting-values (99%, 98%), respectively, while the two outgroups *Gymnocladus dioica* (AF365095) and *Ceratonia siliqua* (AF365075) were clustered. Within the Cassiinae group, there were two major clades separated distinctively. The fist clade had *C.(Ch.) leschenaultiana* and *C.(Ch.) pumila* which moved to the genus *Chamaecrista* based on Flora Malesiana, grouped with other New-World *Chamaecrista* species: *Chamaecrista nictitans*, *Ch.* sp. Klitgaad and *Ch.* sp. Breteler, with very high robustness of bootstrap (97%) and jackknife (95%) supporting-values. The other group contained all Thai *Cassia* species not moved to the genus *Chamaecrista*, clustered with other New-World *Senna* species and *C. grandis* (AF365092) from GenBank.

The Cassia/Senna group (85% BS and 82% JK) composed of Cassia (Senna) sophera, C.(S.) occidentalis, C.(S.) hirsuta, Senna lindheimeriana, S. bauhinioides, S. wislizeni, C. grandis (AF365092), C. grandis, C. javanica, C. bakeriana, C. fistula, C.(S.) spectabilis, C.(S.) obtusifolia, C.(S.) tora, S. bacillaris, C.(S.) surattensis, C.(S.) timoriensis, C.(S.) garrettiana, S. crassiramea and C.(S.) alata. Considering subgroupings in this Cassia/Senna group, the clade could be subdivided into five minor clades. The first clade contained three Thai Cassia (Senna), (C.(S.) sophera, C.(S.) occidentalis and C.(S.) hirsuta) and New-World Senna (S. lindheimeriana and S. bauhinioides) with very high supporting-values (99% BS and 97% JK). The clade II composed of New-World C. grandis and all Thai Cassia (Cassia) species with 65% BS and 53% JK supporting-values. The clade III contained S. wislizeni and C.(S.) spectabilis with 68% BS and 64% JK supporting-values. The fouth clade composed other three Thai Cassia (Senna) (C.(S.) obtusifolia, C(S.) tora and C.(S.) surattensis)

and S. bacillaris (69% both BS and JK). The last clade of C.(S.) timoriensis and C.(S.) garrettiana had high supporting-values (94% BS and 86% JK).

Apart from the similarity between the strict, semistrict and 50% majority-rule consensus trees as above, the strict onsensus tree however indicated that there were two remaining taxa unable to be grouped as a clade. These taxa were *S. crassiramea* and *C.(S.)* alata, though *S. crassiramea* was being a less significant member of the clade IV of the semitrict consensus tree. Moreover, the semistrict and 50% majority-rule revealed that *Ch. nictitans* paired with *Ch.* sp. Klitgaad and *C.(Ch.)* leschenaultiana coupled with *C.(Ch.)* pumila within the Cassia (Chamaecrista) group, though with low supporting-values. Note that *C.(S.)* alata was always not able to form a resolved grouping with other species in any kind of consensus trees.

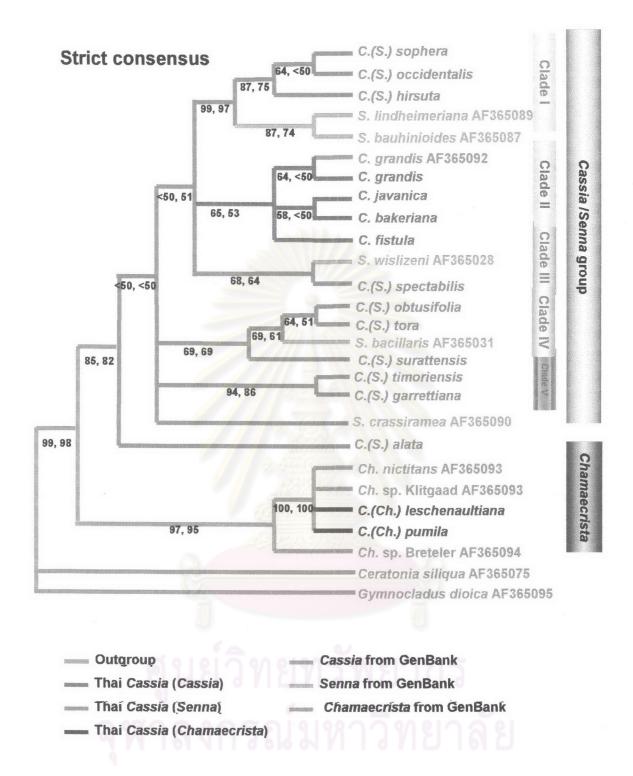


Fig. 32 strict consensus tree from 6 most parsimonious trees of 16 Cassia in Thailand based on trnL intron sequence data compared with nine additional Cassiinae new-world species, Ceratonia siliqua and Gymnocladus dioica as outgroups (retrieved from GenBank). The numbers along branches are 1000-replicate bootstrap and jackknife supporting-values of each clade, respectively.

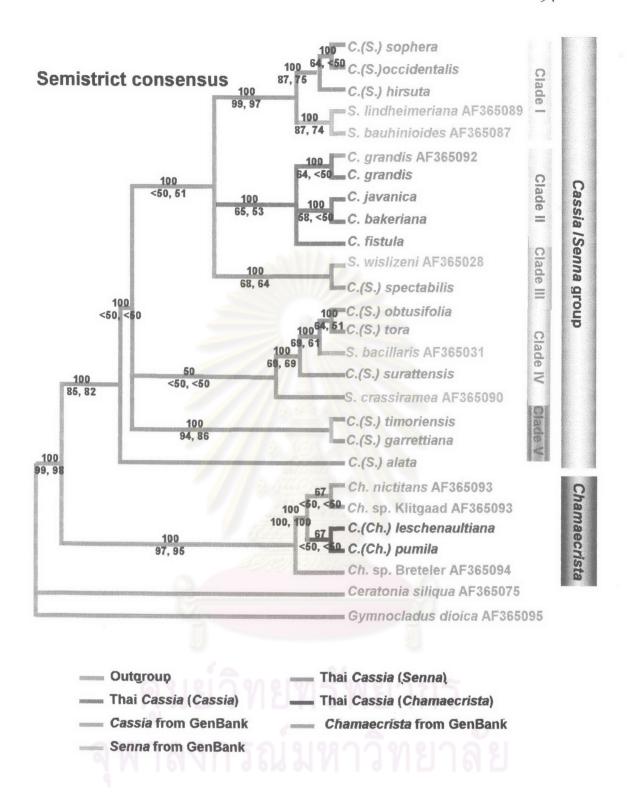


Fig. 33 semistrict consensus tree from 6 most parsimonious trees of 16 Cassia in Thailand based on trnL intron sequence data compared with nine additional Cassiinae new-world species, Ceratonia siliqua and Gymnocladus dioica as outgroups (retrieved from GenBank). The upper numbers are percentages of congruent MPTs on the consensus tree and the lower numbers are 1000-replicate bootstrap and jackknife supporting-values of each clade, respectively.

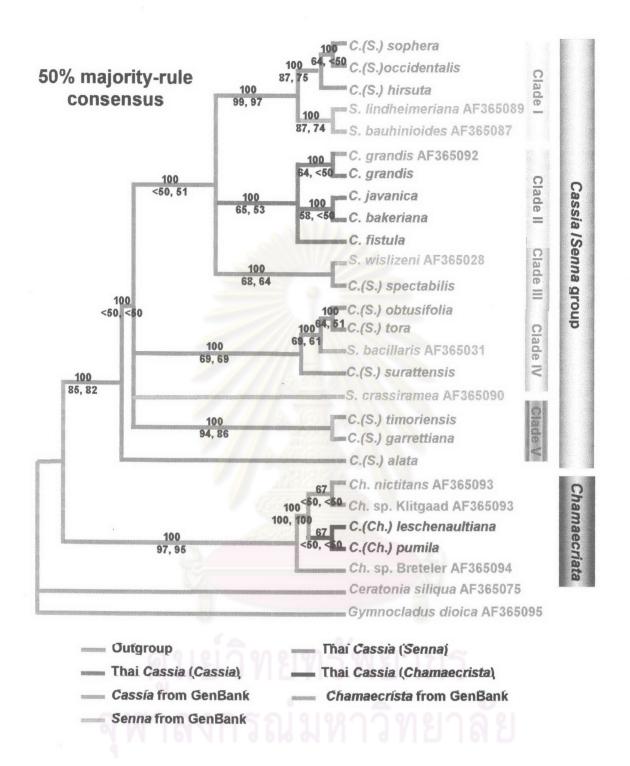


Fig. 34 50% majority-rule consensus tree from 6 most parsimonious trees of 16 Cassia in Thailand based on trnL intron sequence data compared with nine additional Cassiinae new-world species, Ceratonia siliqua and Gymnocladus dioica as outgroups (retrieved from GenBank). The upper numbers are amounts of similarity MPTs on the consensus trees and the lower numbers are 1000-replicate bootstrap and jackknife supporting-values of each clade, respectively.

Neighbour-joining (NJ) tree was also made for this new data matrix to compare with the results from maximum parsimony analyses. The NJ tree showed that all Thai Cassia species suggested to be Chamaecrista (C.(Ch.) leschenaultiana and C.(Ch.) pumila) were grouped as sister with each other to other New-World Chamaecrista as in result of parsimony analysis. Four true Thai Cassia (Cassia) species were also clustered as a unique group with 65% BS and 53% JK. Several more resolved groups were found from NJ tree but two taxa C.(S.) alata and S. crassiramea were still unable to group with any other Cassiinae.



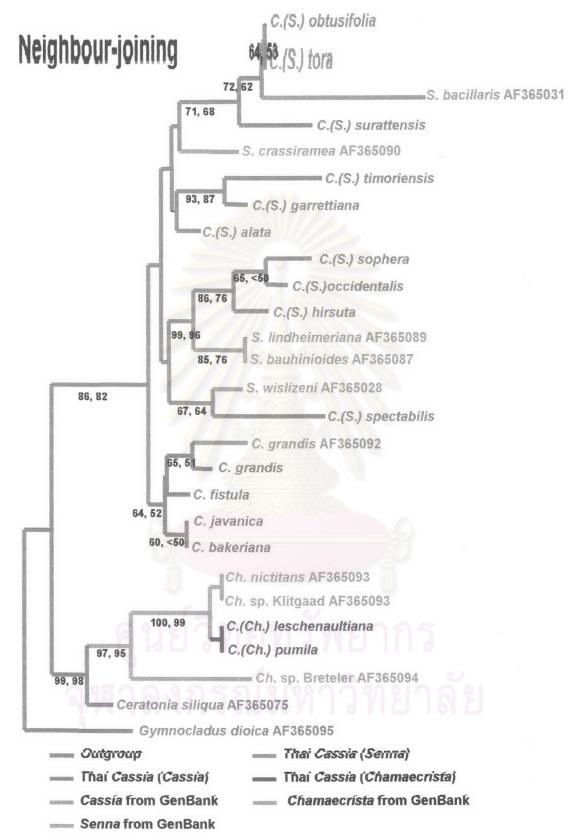


Fig. 35 neighbour-joining tree of 16 Cassia in Thailand based on trnL intron sequence data compared with nine additional Cassiinae New-World species, Ceratonia siliqua and Gymnocladus dioica as outgroups (retrieve from GenBank). The numbers along branches are 1000-replicate bootstraps and jackknife supporting-values, respectively. Note that supporting-values less than 50% were not shown in the tree.

4.5.2 ITS1-5.8S-ITS2 sequences data set (see Fig. 36)

A total ITS1-5.8S-ITS2 sequences data matrix of 13 Thai *Cassia* was also prepared and phylogenetically analysed. Partial sequences of 16S small and 28S large subunits of nuclear ribosomal DNA were prior excluded. The sequence matrix was automatically aligned by Clustal X program and transformed to NEXUS file format, and adjusted manually to get a highest level of homology before phylogenetically analyses (Fig. 40). Gaps were treated as missing data. The data set composed of 913 bp sequence data which the 290 bp belong to the ITS1 regions, 160 bp to the 5.8S subunit and 255 bp to the ITS2 region. The DNA data matrix had total ITS sequences of 13 Thai *Cassia* species. Those of *C.(S.) siamea*, *C.(S.) garrettiana*, *C.(Ch.) pumila* and *C.(Ch.) leschenaultiana* could not be obtained because of difficulty in PCR amplification. The 206 bp regions of 16S (the first position to the 53rd position) and 28S subunits (the 759 position to the last one) were excluded before analysed and were not shown in the data matrix. Sequences of *Gymnocladus dioica* (AF510030, 33) and *Ceratonia siliqua* (AJ245575) retrieved from GenBank were included into the analysis as outgroup taxa.

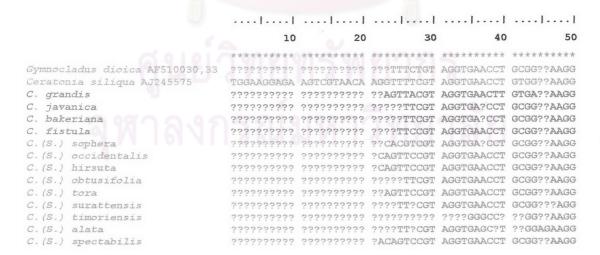


Fig. 36 a 913 bp character taxa matrix of Thai Cassia based on ITS regions sequences for doing tree reconstruction. Asterisks *, *, *, * and * represent 18S, ITS1, 5.8S, ITS2 and 26S regions, respectively. Gaps symbols (-) indicates insertion or deletion at the site. ? symbol shows missing nucleotide data.

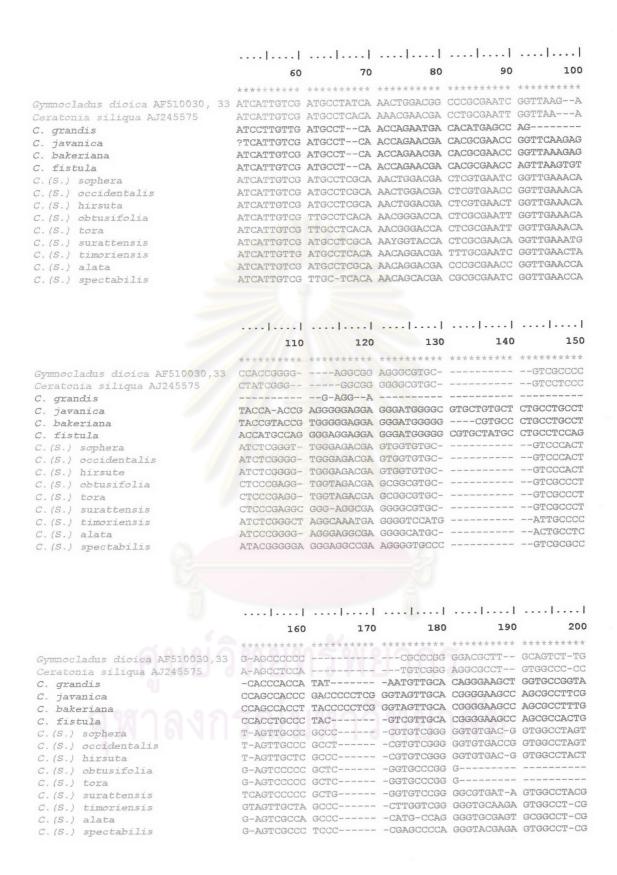


Fig. 36 (continue)

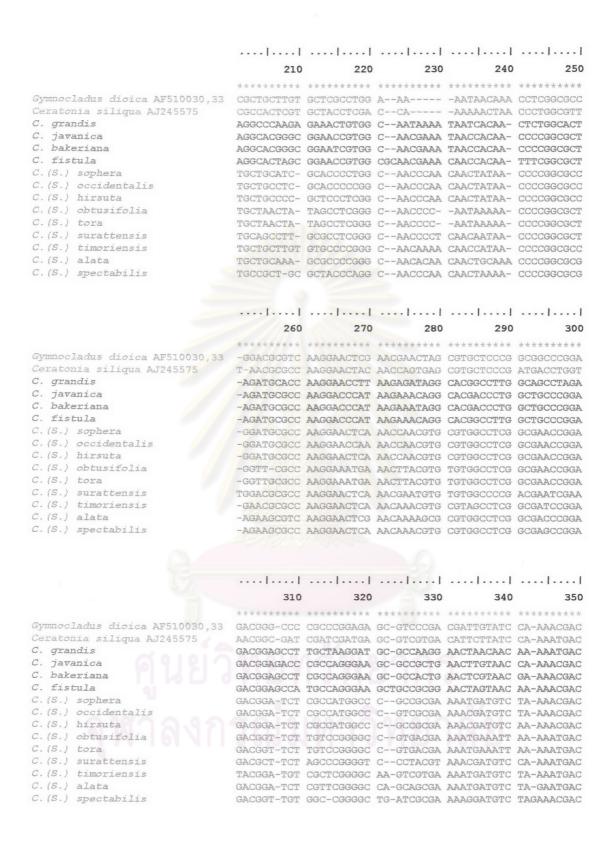


Fig. 36 (continue)

	360	370	380	390	400
	******	******	******	******	******
Gymnocladus dioica AF510030,33			GCTCTCGCAT		
Ceratonia siliqua AJ245575			GCTCTCG		
C. grandis			GCTCTCACAT		
C. javanica			GCTCTCGCAT		
C. bakeriana			GCTCTCGCAT		
C. fistula			GCTCTCGCAT		
C.(S.) sophera			GCTCTCGCAT		
C. (S.) occidentalis			GCTCTCGCAT		
C. (S.) hirsuta			GCTCTCGCAT		
C.(S.) obtusifolia			GCTCTCGCAT		
C. (S.) tora			GCTCTCGCAT		
C. (S.) surattensis			GCTCTCGCAT		
C. (S.) timoriensis			GCTCTCGCAT		
C.(S.) alata			GCTCTCGCAT		
C.(S.) spectabilis	TCTCG-CAAC	GGATATCTCG	GCTCTCGCAT	CGATGAAGAA	CGTAGCGAAA
	410	420	430	440	450
	******	*******	******	******	******
Gymnocladus dioica AF510030,33	TGCGATACTT	GGTGTGAATT	GCAGAATCCC	GCGAACCATC	GAGTCTTTGA
Ceratonia siliqua AJ245575	TGCAATACTT	GGTGTGAATT	GCAGAATCTT	GTGAACCATC	AAGTCTTTGA
C. grandis	TGCGATACTT	AGTGTGAGTT	GCAGAATCCC	ATGAACAATC	GAGTCTTTGA
C. javanica	TGCGATACTT	GGTGTGAATT	GCAGAATCCC	GTGAACCATC	GAGTCTTTGA
C. bakeriana			GCAGAATCCC		
C. fistula	TGCGATACTT	GGTGTGAATT	GCAGAATCCC	GTGAACCATC	GAGTCTTTGA
C.(S.) sophera	TGCGATACTT	GGTGTGAATT	GCAGAATCCC	GTGAACCATC	GAGTCTTTGA
C.(S.) occidentalis	TGCGATACTT	GGTGTGAATT	GCAGAATCCC	GTGAACCATC	GAGTCTTTGA
C.(S.) hirsuta			GCAGAATCCC		
C.(S.) obtusifolia	TGCGATACTT	GGTGTGAATT	GCAGAATCCC	GTGAACCATC	GAGTCTTTGA
C.(S.) tora			GCAGAATCCC		
C.(S.) surattensis			GCAGAATCCC		
C. (S.) timoriensis			GCAGAATCCC		
C.(S.) alata			GCAGAATCCC		
C.(S.) spectabilis	TGCGATACTT	GGTGTGAATT	GCAGAATCCC	GTGAACCATC	GAGTCTTTGA
			5		
	460	470	480	490	500

Gymnocladus dioica AF510030,33	ACGCAAGTTG	CGCCCGAAGC	CACTAGGCCG	AGGGCACGTC	TGCCTGGGTG
Ceratonia siliqua AJ245575			CATCAAGCCG		
C. grandis	ATGCAAGTTA	CGCCCGAAGC	CATTAGGCCG	AGGGCACGTC	TGCTTAGGCG
C. javanica	ACGCAAGTTG	CGCCCGAAGC	CACTAGGCCG	AGGGCACGTC	TGCCTGGGCG
C. bakeriana	ACGCAAGTTG	CGCCCGAAGC	CACTAGGCCG	AGGGCACGTC	TGCCTGGGCG
C. fistula	ACGCAAGTTG	CGCCCGAAGC	CACTAGGCCG	AGGGCACGTC	TGCCTGGGCG
C.(S.) sophera	ACGCAAGTTG	CGCCCGAAGC	CACTAGGCCG	AGGGCACGTC	TGCCTGGGTG
C.(S.) occidentalis			CACTAGGCCG		
C.(S.) hirsuta			CACTAGGCCG		
C.(S.) obtusifolia			CACTAGGCCG		
C.(S.) tora	ACGCAAGTTG	CGCCCGAAGC	CACTAGGCCG	AGGGCACGTC	TGCCTGGGTG
C.(S.) surattensis	ACGCAAGTTG	CGCCCGAAGC	CACTAGGCCA	AGGGCACGTC	TGCCTGGGTG
C.(S.) timoriensis			CATTAGGCTG		
C.(S.) alata	ACGCAAGTTG	CGCCCGAAGC	CATTAGGCCG	AGGGCACGTC	TGCCTGGGTG
			CATTAGGCCG		

Fig. 36 (continue)

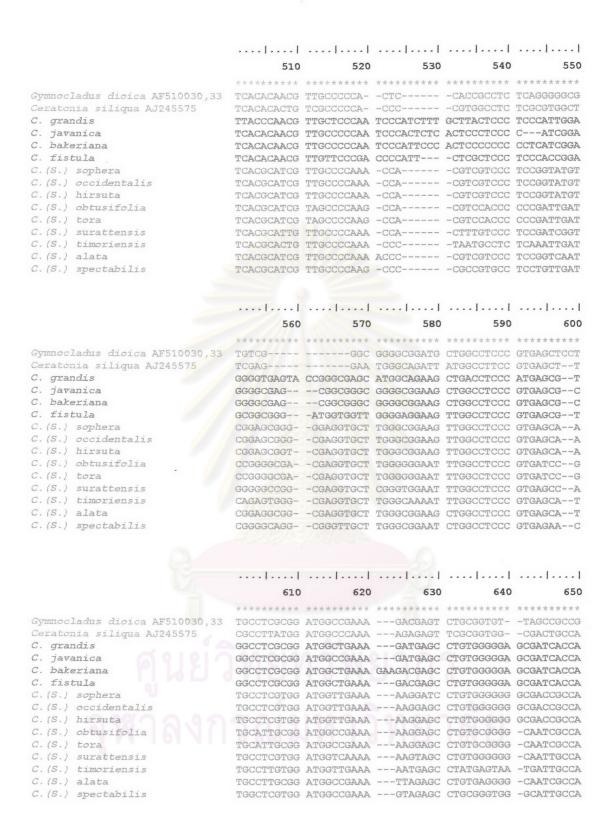


Fig. 36 (continue)

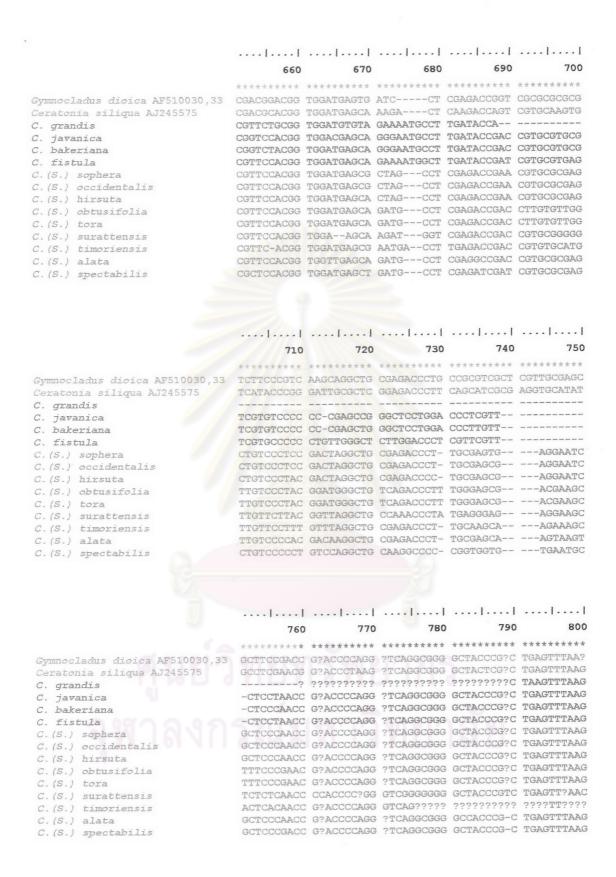


Fig. 36 (continue)

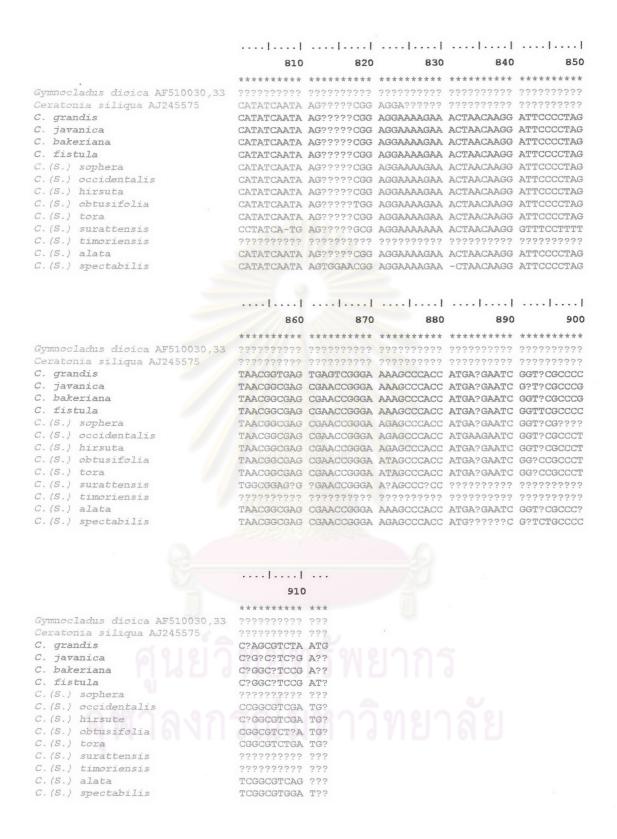


Fig. 36 (continue)

Branch-and-bound searching strategy was used to analyse this ITS data matrix. All characters used in phylogenetic tree reconstruction were unordered and equally weighted and unordered with 295 parsimony-informative characters (41.7%) and parsimony-uninformative 136 characters.

There was only one most parsimonious tree found from this data set, with 956 steps in length (Fig. 37). Consistency index (CI) was 0.7103 and homoplasy index (HI) was 0.2897. Retention index (RI)was 0.6884 and rescaled consistency index (RC) was 0.4889. Bootstrap and jackknife supporting values were calculated. Strict, semistrict and 50% majority-rules consensus trees were not necessary to perform. The phylogenetic tree was fully-resolved; the two outgroups, *Gymnocladus dioica* and *Ceratonia siliqua*, were clustered while all *Cassia* were grouped together with high bootstrap and jackknife supporting-values (98% and 98%, respectively). Within the Thai *Cassia* group, there were two major clades separated distinctively; the group of Thai *Cassia* species that moved to genus *Senna* (blue branches) based on Flora Malesiana, and the other group composed of species remaining to be in the genus *Cassia* (dark-red branches).

The first Cassia (Senna) clade, with 70% BS and 68% JK, composed of C. (S.) occidentalis, C.(S.) sophera, C.(S.) hirsuta, C.(S.) obtusifolia, C.(S.) tora, C.(S.) surattensis, C.(S.) alata, C.(S.) timoriensis and C.(S.) spectabilis. The other clade had four Cassia (Cassia) species: C. javanica, C. bakeriana, C. grandis and C. fistula with very high robustness of bootstrap (100%) and jackknife (100%) supporting-values. Considering subgroupings in the first Cassia (Senna) group, two subclade could recognized from the phylogeny. The first minor clade contained C.(S.) occidentalis, C.(S.) sophera and C.(S.) hirsuta with strongest supporting-values (100% BS and 100% JK). The other clade composed of C.(S.) obtusifolia, C.(S.) tora and C.(S.) surattensis with slightly lower bootstrap (98%) and jackknife (97%) supporting-values than the previous one. Moreover, another weak subclade (<50% of both BS and JK), C.(S.) alata and C.(S.) timoriensis was also drawn. For the Cassia

(Cassia) major clade, there were two recognizable minor clades: C. bakeriana paired with C. javanica with highest supporting-values (100% of both BS and JK) and C. grandis sistered to C. fistula with very weak supporting-values (55% BS and < 50% JK).



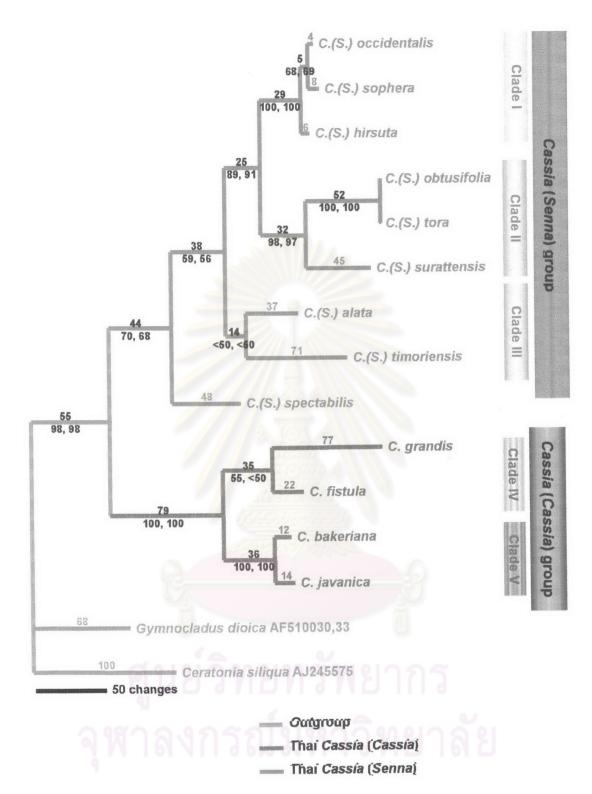


Fig. 37 only one most parsimonious trees (956 steps in length) found from ITS data matrix of 13 *Cassia* species in Thailand based on ITS region sequence data with two outgroups, *Ceratonia siliqua* and *Gymnocladus dioica* the upper numbers are amounts of synapomorphy and the coloured numbers are amounts of autapomorphy. The lower numbers are 1000-replicate bootstrap and jackknife supporting-values of each clade, respectively. [CI = 0.7103, RI = 0.6884, RC = 0.4889]

ITS phylogenetic tree from parsimony analysis was compared with the neibour-joining (NJ) tree of the same data set. The NJ tree also showed that both *Gymnocladus dioica and* ITS sequences were very much different from those of Thai *Cassia* as seen previously in the results of *tmL* intron analyses. Neighbour-joining distance analysis of the ITS sequence data fully supported taxon-arrangement topology on the tree from the parsimony analysis in *Cassia* (*Senna*) group. The second *Cassia* (*Cassia*) group revealed a slightly difference within this group; that is *C. bakeriana* was paired with *C. javanica* before grouped firstly to *C. fistula* and then to *C. grandis*.

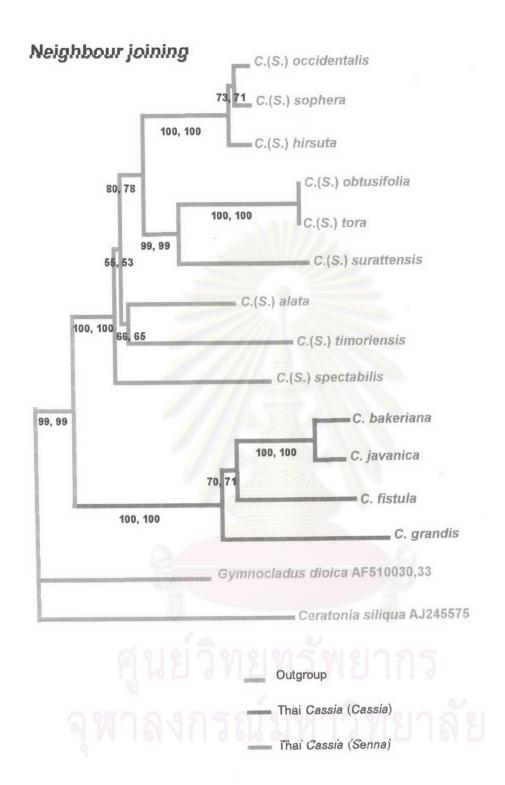


Fig. 38 Neighbour-joining tree of 13 Cassia in Thailand based on ITS regions sequence data with Ceratonia siliqua and Gymnocladus dioica as outgroups (retrieve from GenBank).

4.5.3 Combined sequence data of trnL intron and ITS regions

One best way to make a phylogenetic conclusion from two different DNA data sets is to combine both sequence matrices and rerun an analysis. A combined data matrix between sequences data sets of *tmL* intron and ITS regions of Thai *Cassia* species was prepared. Again, branch-and-bound searching strategy was used to analyse the combined data matrix which had 1303 bp long (597 bp belong to *tmL* intron sequence and 706 bp to the ITS regions). Only 13 Thai *Cassia* species were suitable to be in the analysis as the others (*C. siamea*, *C. garrettinana*, *C. pumila* and *C. leschenaultiana*) could not be PCR amplified either form *tmL* intron or ITS regions. *Gymnocladus dioica* and *Ceratonia siliqua* were still the only two most suitable outgroups from this matrix. Three hundred and nineteen characters (24.5%) were parsimony-informative as synapomorphy (shared-derived characters) and 177 characters were parsimony-uninformative as autapomorphy specifically for each taxon.

As expected, there was only one most parsimonious tree found from this newly combined data set, with 1030 steps in length (Fig. 39). Consistency index (CI) was 0.7243 and homoplasy index (HI) was 0.2757. Retention index (RI)was 0.6072 and rescaled consistency index (RC) was 0.5050. Reliability of each internal branch was estimated using bootstrap and jackknife analyses. The new phylogeny had the same topology as the tree resulted from ITS data alone. The fully-resolved phylogram from combined data set show that *Gymnocladus dioica* and *Ceratonia siliqua* were separated as an outgroup clade while all Thai *Cassia* species were grouped together with full bootstrap and jackknife supporting-values (both 100%). Two major clades were found within the Thai *Cassia* group. As same as from ITS only, both Thai *Cassia* species that moved to the genus *Senna* (blue branches) based on Flora Malesiana are *Cassia* species remaining to be in the genus *Cassia* (dark-red branches) had their own distinctive clades. The *Cassia* (*Senna*) clade (67%

BS and 66% JK) composed of *C.(S.) occidentalis*, *C.(S.) sophera*, *C.(S.) hirsuta*, *C.(S.) obtusifolia*, *C.(S.) tora*, *C.(S.) surattensis*, *C.(S.) alata*, *C.(S.) timoriensis* and *C.(S.) spectabilis*. *C. javanica*, *C. bakeriana*, *C. grandis* and *C. fistula* were grouped together with 100% bootstrap and jackknife branch supporting-values. Within *Cassia* (*Senna*) group, three minor clades could be pointed out: the first clade 100% BS and JK contained *C.(S.) occidentalis*, *C.(S.) sophera* and *C.(S.) hirsuta*; the second clade composed of *C.(S.) obtusifolia*, *C.(S.) tora* and *C.(S.) surattensis* (99% BS and JK); and the last clade of *C.(S.) alata* and *C.(S.) timoriensis* with weak supporting-values (<50% of both BS and JK). Considering subgrouping in the second major clade of Cassia (Cassia) species, there were two minor clades found that *C. bakeriana* paired with *C. javanica* (100% of both BS and JK) and *C. grandis* paired with *C. fistula* with weak supporting-values (54% of BS and 52% of JK).

ศูนย์วิทยทรัพยากร จุฬาลงกรณ์มหาวิทยาลัย

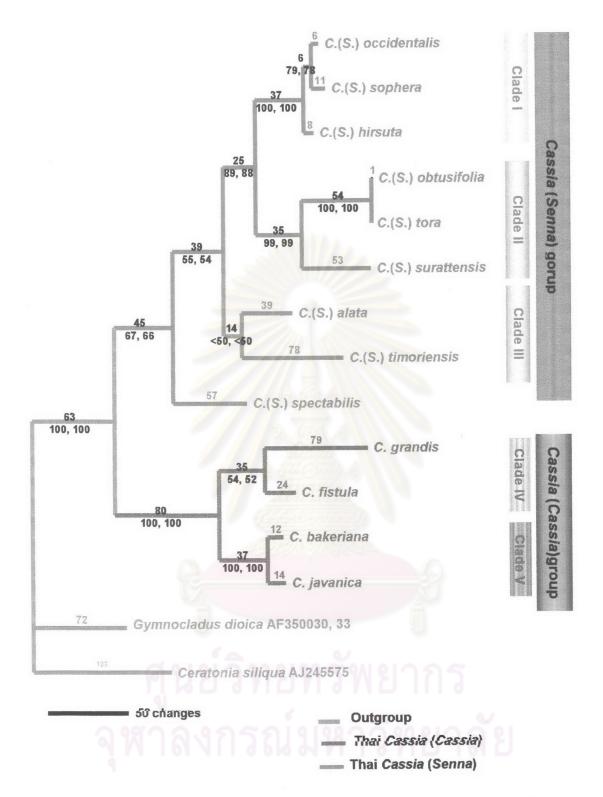


Fig. 39 only one most parsimonious trees (1030 steps in length) found from ITS data matrix of 13 *Cassia* species in Thailand based on combined *trn*L intron and ITS region sequence data with two outgroups, *Ceratonia siliqua* and *Gymnocladus dioica*. The upper in black numbers are amounts of synapomorphy and the coloured numbers are amounts of autapomorphy. The lower numbers are 1000-replicate bootstrap and jackknife supporting-values of each clade, respectively. [CI = 0.7243, RI = 0.6972, RC = 0.5050]

To complete the phylogenetic analysis procedure, NJ method was also performed with the combined DNA matrix. The NJ tree showed the same result as the analysis of ITS data alone that *Gymnocladus dioica* and *Ceratonia siliqua* were separated from all 13 Thai *Cassia* taxa. Neighbour-joining result from ITS sequence data fully supported the parsimony analysis in the first major clade (*Cassia* (*Senna*) clade). While the second major clade (*Cassia* (*Cassia*) clade) were slightly different from parsimony method that this clade had *C. bakeriana* paired with *C. javanica* before grouping to *C. fistula* and *C. grandis*, respectively.

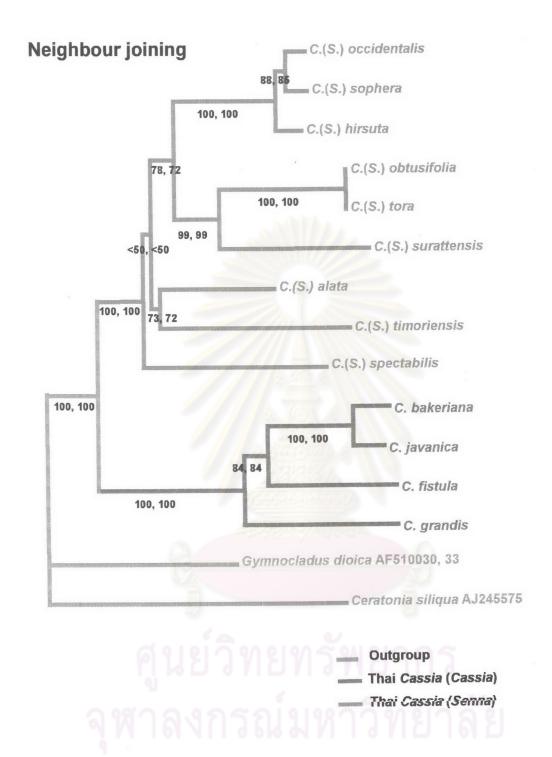


Fig. 40 Neighbour-joining tree of 13 Cassia in Thailand based on ITS regions sequence data with Ceratonia siliqua and Gymnocladus dioica as outgroups (retrieve from GenBank).

4.6 Cytogenetic study

Cytogenetic study of some Cassia in Thailand was performed. Two species (C. timoriensis and C. tora) were studied on somatic cells from their root tips. Other ten species (C. occidentalis, C. surattensis, C. siamea, C. garrettiana, C. fistula, C. sophera, C. javanica, C. spectabilis, C. timoriensis and C. tora) were investigated cytogenetically on their germline cells (Fig. 41 to Fig. 50). The chromosome number of most species could be counted more or less from their bivalent numbers in the late prophase to late metaphase stage. So far, the cytogenetic results were not good enough for karyotyping analysis because the chromosomes were too small and the chromosome from root tips were too difficult to be counted because of contaminated bacteria. The chromosome numbers reporting from meiotic study were not exact as a single number (Fig. 42 to Fig. 50). Only the chromosome numbers C. occidentalis (Fig. 41) could be counted ambiguously as 2n=26 while those of the other nine species (Fig. 42 to Fig. 50) were recorded from estimates. For instance, both chromosome numbers of C. surattensis (Fig. 42) and C. tora (Fig. 43) were revealed to be 2n=56 since 28 bivalent pairs per cell were found in the metaphase I stage. Another four species C. siamea, C. fistula, C. sophera and C. timoriensis could be estimated to be 2n=28 as in the Fig. 44, 46, 47 and 50, respectively. The estimated chromosome numbers from the other three remaining species, however, were unclear as around 12-14 bivalent pairs in C. garrettiana (Fig. 45), 13-14 in C. javanica (Fig. 48) and 11-12 in C. spectabilis (Fig. 49).

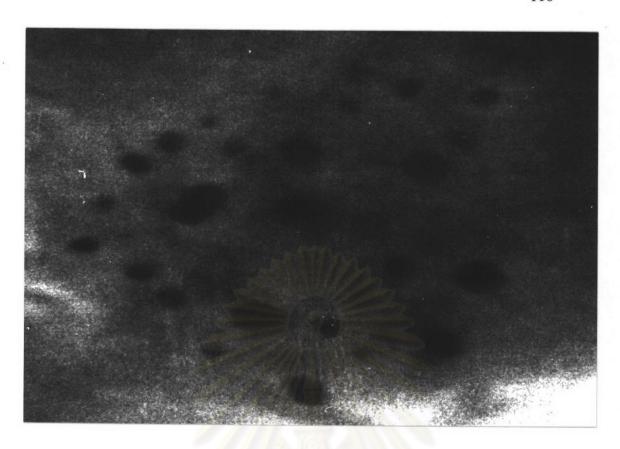


Fig. 41 late metaphase in microsporocyte of *C. occidentalis* (estimated 2n = 26)

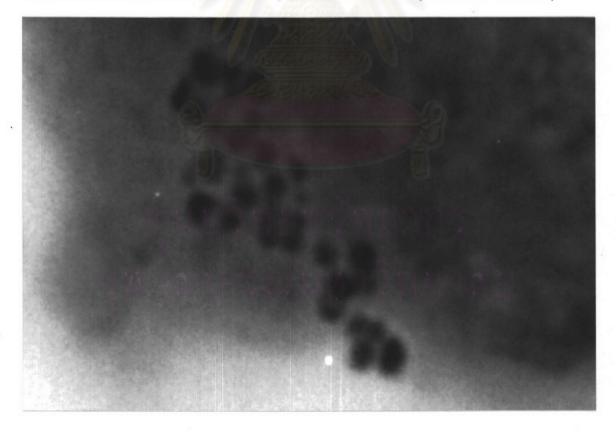


Fig. 42 metaphase I in microsporocyte of *C. surattensis* (estimated 28 bivalent, 2n=56)

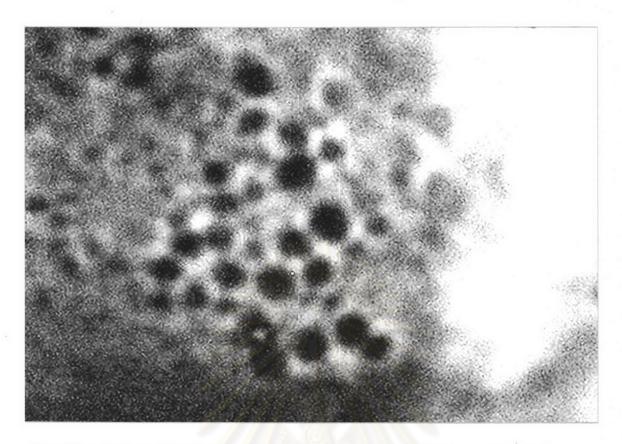


Fig. 43 metaphase I in microsporocyte of *C. tora* (estimated 28 bivalent, 2n=56)



Fig. 44 early metaphase I in microsporocyte of *C. siamea* (estimated 14 bivalent, 2n=28)

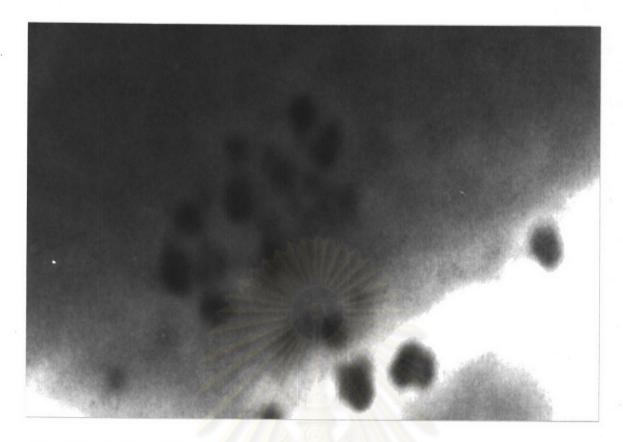


Fig. 45 metaphase I in microsporocyte of *C. garrettiana* (estimated 12-14 bivalent, 2n=24-28)



Fig. 46 late prophase (diakinesis) in microsporocyte of *C. fistula* (estimated 14 bivalent, 2n=28)

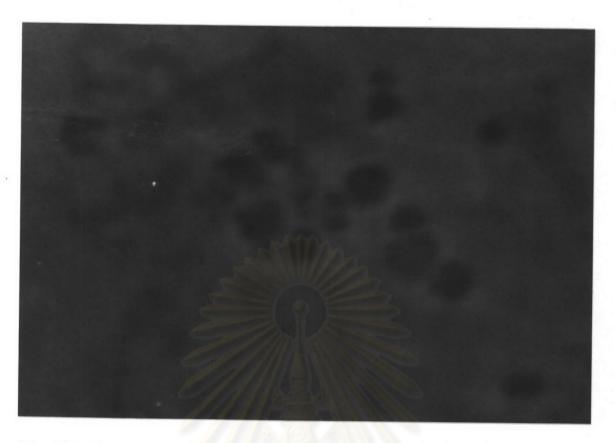


Fig. 47 early metaphase I in microsporocyte of *C. sophera* (estimated 14 bivalent, 2n=28)

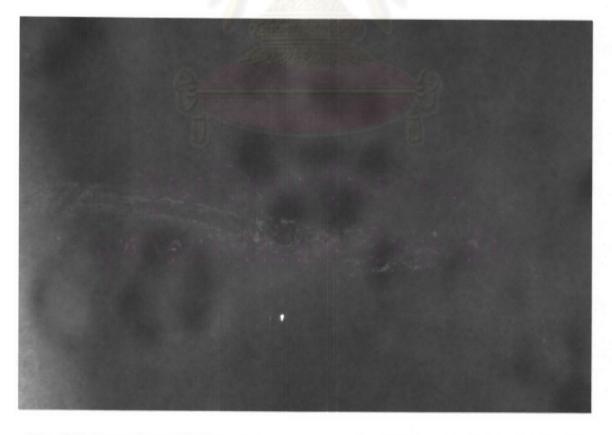


Fig. 48 late prophase (diakinesis) in microsporocyte of *C. javanica* (estimated 13-14 bivalent, 2n=26-28)

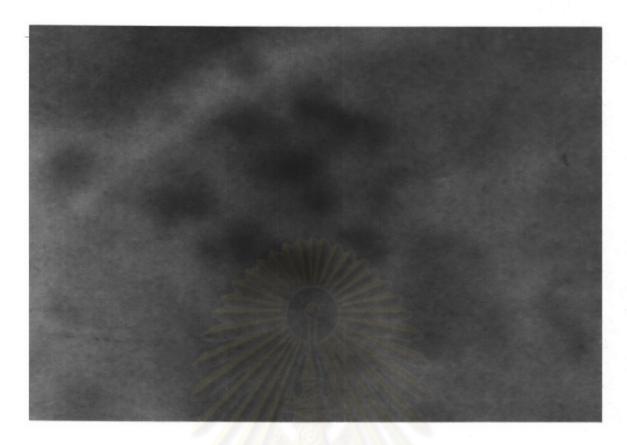


Fig. 49 late prophase (diakinesis) of microsporocyte of *C. spectabilis* (estimated 11-12 bivalent, 2n=22-24)

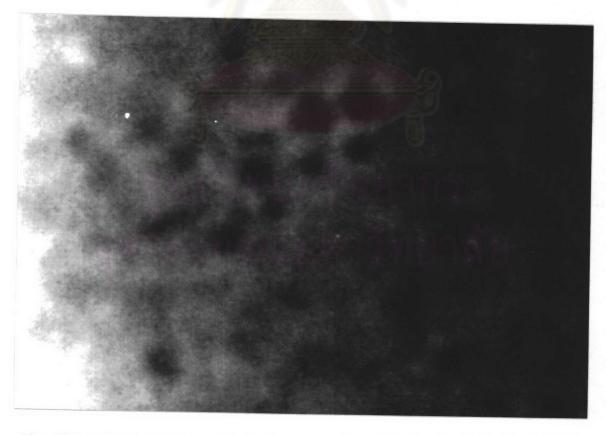


Fig. 50 prophase I (diakinesis) of microsporocyte of *C. timoriensis* (estimated 14 bivalent, 2n=28)