



## Molecular Techniques to ascertain the Genetic Strategies in some Malvaceae *s.l.* species



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**F**AMILY Malvaceae has been traditionally subjected to several taxonomic approaches regarding their taxon relationships and divisions. With the rapid advancement of PCR-based methods and DNA sequence information, taxonomists now have the opportunity to shift from traditional systems of classification to more recent systems. Molecular studies of Malvaceous taxa have provided new opinions about the grouping and phylogeny of these taxa. This work involved molecular analyses of twenty-three Malvaceae species. Three molecular techniques were used, namely, inter simple sequence repeat (ISSR), sequence-related amplified polymorphism (SRAP), and internal transcribed spacer (ITS), to investigate the relationships between the studied taxa. Phylogenetic relationships were constructed using Molecular Evolutionary Genetics Analysis and Phylogenetic Analysis Using Parsimony (MEGA and PAUP) software. The results of this investigation revealed 301 molecular characteristics (78 ISSR and 223 SRAP bands) between the taxa. These data support the taxonomic view of the Malvaceae *s.l.* subfamilies in the Angiosperm Phylogeny Group system of plant classification (APG systems).

**Keywords:** Classification, ISSR, ITS, Malvaceae *s.l.*, Phylogeny, SRAP.

### Introduction

Malvaceae *s.l.* originated from the Latin word mallow. This name was first used by Pliny the Elder (Simpson, 2010). It is a worldwide, diverse, large, and economically important family with approximately 246 genera and 4225 species (Kew Science, 2021). The diversification centers are in tropical and temperate areas of both hemispheres (Cvetkovi'c et al., 2021). In Egypt, this family includes 10 genera and 32 species (Taeckholm, 1974; Boulos, 1995 & 2009). The native range of this species is the Nile region, the Oases region, the Mediterranean coast, all deserts of Egypt, the Red Sea coast, Gebel Elba and the entire Sinai Peninsula (Boulos, 2009). The circumscription of the Malvaceae *s.l.* is controversial and faces many taxonomic suggestions. Previous studies (Cronquist, 1988; Thorne, 1992; Takhtajan, 1997; Kubitziki, 2003; Judd et al., 2008) considered the four families

Bombacaceae, Sterculiaceae, Tiliaceae and Malvaceae as the "core Malvales". These four families were found to be closely related since the time of Linnaeus (1753) and are still affirmed by morphological, anatomical, chemical, and molecular studies (Chase et al., 1993; Judd & Manchester, 1997; Alverson et al., 1998; Bayer et al., 1999; Nyffeler et al., 2005; Péchon and Gigord, 2014). The vast development of PCR-based techniques and DNA sequence information has allowed taxonomists to break away from the classical systems of classification and given birth to the APG systems (Angiosperm Phylogeny Group system, I, II, III & IV, 1998-2016).

A previous study treated both Bombacoideae and Malvoideae as separate families rather than combined as subfamilies under Malvatheca. Additionally, these findings supported the identification of Sterculiaceae

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Received: 22/12/2023; Accepted: 19/02/2024

ORCID ID: 0000-0003-1164-9158

DOI: 10.21608/ejbo.2024.257350.2624

Edited by: Prof. Dr. Reda Gaafar, Botany and Microbiology Department, Faculty of Science, Tanta University, Tanta, Egypt  
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and Tiliaceae and pointed to the great difference in opinion given that Tiliaceae and Sterculiaceae are distinct families. Furthermore, these findings suggested that Dombeyaceae should be treated at the family level. In addition, *Abutilon* spp. with *Sida* spp. were placed in one tribe (Abutilae) (Shamso & Khattab, 2016).

In the present study, the position of the taxa within Malvaceae *s.l.* was unclear, and the grouping lacked a well-resolved framework using morphological characteristics only. Thus, Weising et al. (2006) recommended the use of specific molecular parameters for clear-cut Malvaceae *s.l.* to detect variability among closely related species. Therefore, this study aimed to assess the validity of the APG classification systems for Malvaceae *s.l.* through the use of different molecular markers; Inter Simple Sequence Repeat (ISSR), Sequence-Related Amplified Polymorphism (SRAP), and Internal Transcribed Spacer (ITS). This is done to evaluate the phylogenetic relationships among the studied species and obtain a more detailed phylogenetic classification.

## Materials and Methods

### *Sample collections*

A total of 23 species were used in this study as representative genera of Malvaceae in Egypt. Nineteen fresh specimens were collected from the Shehab Mazhar Botanical Garden in Baragil, Giza, Egypt, as well as from the botanical gardens of the Faculty of Science and Agriculture, Alexandria University. The remaining 4 dry specimens were obtained from the herbaria of Alexandria University, Tanta University, and Loutfy Boulous. Voucher specimens of the fresh samples were deposited in the Alex Herbarium, Alexandria, Egypt. The locations of the collected specimens and their related information are presented in Table 1. Unfortunately, Egyptian *Pavonia arabica* was not represented in the Egyptian herbaria, and to represent the genus in the study, the only available herbarium sample was collected from the United Arab Emirates.

The extraction of DNA from Malvaceae *s.l.* species was more problematic, especially for fresh specimens, than for herbarium specimens due to the presence of a large amount of polysaccharides and mucilage in their leaves. Therefore, molecular studies were conducted on the specimens by applying the

modified extraction method of Dellaporta et al. (1983) to obtain good extraction and purification results.

### *ISSR analysis*

A set of 10 primers obtained from Sigma was used to prescreen the species under investigation for polymorphisms. Only five primers produced clear scorable bands with good reproducibility and amplification patterns. The primers selected for PCR amplification were described by Celka et al. (2012) and Vanijajiva (2012) (Table 2). The nucleotide sequences with a GC content of 33-80% were selected to generate the DNA fingerprint profiles of all the genotypes. The selected primers had di-, tri- or pentanucleotide repeats anchored or not anchored at 3'. The annealing temperatures were optimized for those primers before performing the experiments.

### *SRAP analysis*

Several combinations of 6 forward primers (Me1, Me2, Me3, Me4, Me7 and Me8) and 5 reverse primers (Em1, Em2, Em4, Em6 and Em10) were used. The abovementioned primers and their 11 combinations were selected according to Li & Quiros (2001) and Badrakhani et al. (2014) based on the maximum number of polymorphic bands obtained in their study (Table 3).

### *PCR amplification, cloning and sequencing of the ITS region*

The entire ITS region (ITS1, 5.8S and ITS2) was sequenced following PCR amplification from the genomic DNA. The primers used were 5' TCCGTAGGTGAACCTGCGG 3' for ITS1 and 5' TCCTCCGCTTATTGATATGC 3' for ITS4. PCR amplification was carried out according to Tate et al. (2005). The DNA products obtained after electrophoresis were cut, weighed, recovered and purified according to the protocol of the MEG Aquick-spin total fragment DNA purification kit (iNtRON Biotechnology, Inc., South Korea).

Aliquots of each amplified product were run on a 2% agarose gel with ethidium bromide, visualized on a UV transilluminator, and photographed by a gel documentation system. A one kilo base pair DNA ladder (Sigma) was used as a DNA fragment size marker.

TABLE 1. Samples collected with their families, locations and dates of collection. (Families as proposed by the APG systems; 1998-2016).

Family	Code	Taxa	Site	Date		
Tiliaceae s.s.	1	** <i>Corechorus olitorius</i> L. <sup>6</sup>	Cultivated area, Nile Delta	October 2019		
	2	<i>Grewia pondoensis</i> Burret. <sup>6</sup>	Shehab Mazhar botanic garden Giza, Egypt	June 2019		
	3*	<i>Triumfetta flavescens</i> Hochst. ex A. Rich. <sup>6</sup>	Gebel Elba	March 1997		
Sterculiaceae s.s.	4	** <i>Brachychiton discolor</i> F. Muell. <sup>3</sup>	Shehab Mazhar botanic garden, Giza, Egypt	June 2019		
	5	<i>Dombeya walltchii</i> (Lindl.) Benth. ex Baill. <sup>4</sup>	Shehab Mazhar botanical garden, Giza, Egypt	June 2019		
	6	<i>Guazuma ulmifolia</i> Lam. <sup>5</sup>	Shehab Mazhar botanic garden, Giza, Egypt	June 2019		
	7*	<i>Melhania denhamii</i> R. Br. <sup>4</sup>	Gebel Elba, Wadi Eikwan upstream, southeast of Halaieb. N. 22 00' 00" E. 36 39' 21". Code 18750	March 1998		
	8	<i>Pterospermum acerifolium</i> (L.) Willd. <sup>4</sup>	Shehab Mazhar botanic garden, Giza, Egypt	June 2019		
Bombacaceae s.s.	9	** <i>Bombax. ceiba</i> L. <sup>1</sup>	Faculty of Agriculture botanic garden, Alex. University	March 2020		
	10	** <i>Ceiba pentandra</i> (L.) Gaertn. <sup>1</sup>	Shehab Mazhar botanic garden, Giza, Egypt	June 2019		
	11	<i>Ceiba speciosa</i> (A.St.-Hil., A.Juss. & Cambess.) <sup>1</sup> Ravenna	Faculty of Science botanic garden, Alex. University.	May 2018		
	12	<i>Pseudobombax ellipticum</i> (Kunth) Dugand <sup>1</sup>	Shehab Mazhar Botanic garden, Giza, Egypt	June 2019		
	13	** <i>Abelmoschus esculentus</i> (L.) Moench 2	<i>Shehab Mazhar botanic garden, Giza, Egypt.</i>	June 2019		
	14	** <i>Abutilon hirtum</i> (Lam.) Sweet. 2	<i>Shehab Mazhar botanic garden, Giza, Egypt.</i>	June 2018		
	15	<i>Alcea rosea</i> L. 2	<i>Faculty of science botanic garden, Alex. University</i>	May 2018		
	16	** <i>Gossypium herbaceum</i> L. 2	<i>Shehab Mazhar botanic garden, Giza, Egypt.</i>	June 2019		
	17	** <i>Hibiscus syriacus</i> L. 2	<i>Shehab Mazhar botanic garden, Giza, Egypt</i>	June 2019		
	18	<i>Lagunaria patersonia</i> (Andrews) G.Don	<i>Faculty of science botanic garden, Alex. University</i>	May 2018		
Malvaceae s.s.	19	** <i>Malva parviflora</i> L. 2	<i>Alexandria Burg El-Arab coastal road</i>	April 2019		
	20	<i>Malva viscus arboreus</i> Dill ex Cav. 2	<i>Shehab Mazhar botanic garden, Giza, Egypt</i>	June 2019		
	21*	<i>Pavonia arabica</i> Hochst & Steud. 2 ex Boiss.	<i>Headland of beach north of oceanic hotel, Khor Fakkan, United Arab Emirates. Code 3696</i>	May 1998		
	22*	<i>Sida alba</i> L. 2	<i>Wadi Feiran (St. 123)</i> <i>N. 28 45' 48" E. 33 23' 448" A. 242 m. Code 19123</i>	May 2005		
	23	** <i>Thespesia populnea</i> (L.) Sol. ex Corrêa. 2	<i>Shehab Mazhar botanic garden, Giza, Egypt</i>	June 2019		
		<sup>2</sup> Malvoideae	<sup>3</sup> Sterculioideae	<sup>4</sup> Dombeyoideae	<sup>5</sup> Byttnerioideae	<sup>6</sup> Grewioideae

<sup>1</sup> Bombacoideae <sup>2</sup> Malvoideae <sup>3</sup> Sterculioideae <sup>4</sup> Dombeyoideae <sup>5</sup> Byttnerioideae <sup>6</sup> Grewioideae

\* Samples obtained from herbarium sheets, \*\* Samples used in sequence analysis.

**TABLE 2. Primer sequences, Repeat motif, GC% and T<sub>m</sub> used in the ISSR analysis.**

Primer	Sequence 5' → 3'	Repeat motif	GC%	T <sub>m</sub> (°C)
ISSR3	AG AG AG AG AG AG AG T	(AG) <sub>7</sub>	47	44
IS810	GA GA GA GA GA GA GA T	(GA) <sub>8</sub>	47	50
IS813	CT CT CT CT CT CT CT T	(CT) <sub>8</sub>	47	50
IS834	ATG ATG ATG ATG AT G	(ATG) <sub>5</sub>	33	40
IS846	GGGT GGGGT GGGGT G	(GGGGT) <sub>2</sub>	80	54

**TABLE 3. Primer sequences and their combinations employed in the SRAP analysis.**

Forward Primers	Forward Sequence 5' → 3'	Reverse Primers	Reverse Sequence 5' → 3'
Me1	TGAGTCCAAACCGGATA	Em1	GACTGCGTACGAATTAAT
Me2	TGAGTCCAAACCGGAGC	Em2	GACTGCGTACGAATTTGC
Me3	TGAGTCCAAACCGGAAT	Em4	GACTGCGTACGAATTTGA
Me4	TGAGTCCAAACCGGACC	Em6	GACTGCGTACGAATTGCA
Me7	TGAGTCCAAACCGGTTG	Em10	GACTGCGTACGAATTTAG
Me8	TGAGTCCAAACCGGTGT		
Primer Combinations			
Me1-Em2	Me3-Em1	Me4-Em2	Me8-Em1
Me2-Em1	Me3-Em2	Me4-Em6	Me8-Em2
Me2-Em6	Me3-Em4	Me7-Em10	

#### Statistical analyses

The ISSR and SRAP gels were analyzed through TotalLab image analysis software (version 1.1.4301, 26877). Only intensely stained unambiguous bands were used in the analysis. The bands were scored as binary characters: absent (0) or present (1). Six different parameters and indices were used to characterize the efficiency of each marker and primer to detect polymorphisms among the different species used. The percentage of polymorphisms (pb%) was calculated. The Polymorphic Information Content (PIC), Resolving Power (Rp) and Marker Index (MI) were subsequently evaluated according to De Riek et al. (2001), Sorkheh et al. (2007), and Prevost & Wilkinson (1999), respectively. The Effective Multiplex Ratio (EMR) and Multiplex Ratio (MR) were calculated according to Powell et al. (1996). The data were obtained by scoring the ISSR and SRAP profiles with different primers, individually and collectively, and subsequently constructing a similarity matrix using Jaccard's coefficients (Jaccard, 1908). The similarity values used for Cluster analysis were calculated by using the Unweighted Pair Group Method with the Arithmetic means (UPGMA) algorithm, and dendrogram

construction was performed with the PAST program v.3 (Hammer et al., 2001).

#### Phylogenetic data

Purified DNA from 10 out of the 23 studied species was sequenced by Macrogen Company (South Korea; Table 1). *Elaeocarpus nitenifolius* Merr. & Chun was chosen as an outgroup (Judd & Manchester, 1997). The sequences were subjected to pairwise and multiple sequence alignment using CLUSTAL W version 2 (Thompson et al., 1997). Phylogenetic relationships were constructed using MEGA version 11 (Tamura et al., 2021) and another software package, PAUP version 4 (Swofford, 2002), to assess the phylogenetic relationships. In MEGA software, aligned sequences were analyzed by *p*-distance and UPGMA methods of sorting. In PAUP software, aligned sequences were evaluated by the Wagner parsimony method using 'branch & bound', 'heuristic' and the parsimony method of likelihood. Moreover, the software generated a phylogenetic tree based on transition/transversion ratios, the consistency index (CI) and the homoplasy index (HI) Farris (1989 a, 1989 b).

**Results**

**ISSR analysis**

Five primers out of ten ISSR with di-, tri- and pentanucleotides were used to screen 23 species of Malvaceae *s.l.* These primers produced clear, reproducible bands of genomic DNA, as represented by ISSR34 (Figure 1 & S1). The total and specific

number of bands as well as the percentage of polymorphisms are presented in Table 4. The generated bands were variable in size and number depending upon their sequence repeat motifs in different species. The polymorphic amplicon size ranged from 100 to 1000 bp, with 100% polymorphism.

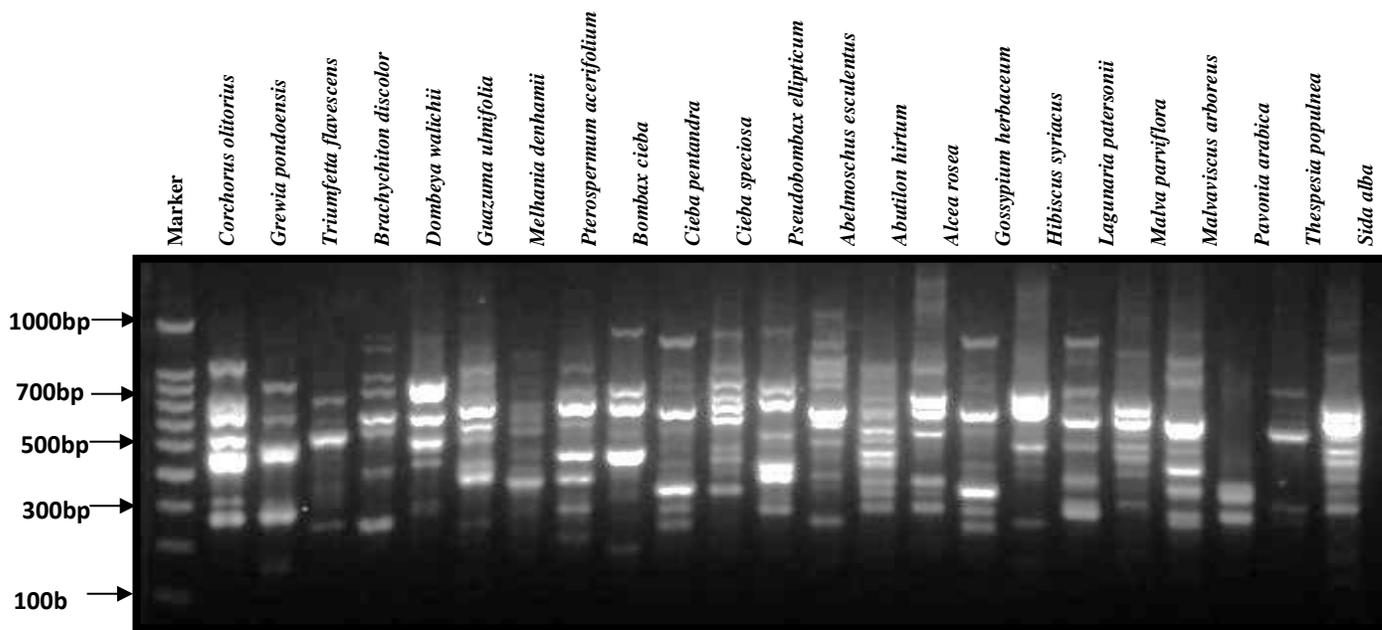


Fig. 1. Bands produced by using ISSR34 primer.

TABLE 4. Indices amplified with the 5 ISSR primers for the examined species of Malvaceae *s.l.*

Primer Combination	TB <sup>1</sup>	PB <sup>2</sup>	MB <sup>3</sup>	% PB <sup>4</sup>	SB <sup>5</sup>	PIC <sup>6</sup>	MI <sup>7</sup>	RP <sup>8</sup>	EMR <sup>9</sup>
ISSR3	18	18	0		2	0.75	55.44	8.22	74
ISSR10	16	17	0		1	0.59	74.60	15.75	126
ISSR13	14	15	0	100%	2	0.55	48.66	12.57	88
ISSR34	19	19	0		1	0.72	99.76	14.63	139
ISSR46	11	11	0		0	0.39	54.08	17.64	139
<b>Total</b>	<b>78</b>	<b>78</b>	<b>0</b>		<b>7</b>	<b>3.00</b>	<b>332.55</b>	<b>68.81</b>	<b>566.00</b>
<b>Mean</b>	-	-	-	-	-	0.60	66.51	13.76	113.20

<sup>1</sup>Total number of bands, <sup>2</sup>Polymorphic bands, <sup>3</sup>Monomorphic bands, <sup>4</sup>Percentage of polymorphism, <sup>5</sup>Specific bands, <sup>6</sup>Polymorphic information content, <sup>7</sup>Marker index, <sup>8</sup>Resolution power, <sup>9</sup>Effective multiplex ratio.

The use of ISSR primers was highly productive and polymorphic, with a total of 78 bands and seven specific bands within the examined species. The number of amplified amplicons ranged from 11 to 19, with a mean of 15.6 amplicons per primer. *Abutilon hirtum* (Lam.) Sweet produced the greatest number of bands and the highest percentage of polymorphisms (33 and 42.37%, respectively). However, *Pavonia arabica* Hochst. & Steud. ex Boiss. amplified the least number of bands and percentage polymorphism

(4 and 5.17%, respectively). For each primer, 3 specific bands were from ISSR3, 2 from ISSR13, and 1 from both ISSR10 and ISSR34; however, no specific bands were from ISSR46. *A. hirtum* and *Cieba speciosa* (A.St.-Hil., A.Juss. & Cambess.) Ravenna gave the maximum number of specific bands (2 bands). While each of *Lagunaria patersonii* (Andrews) G. Don, *Malva parviflora* L. and *Malvaviscus arboreus* Dill. ex Cav. produced the minimum values (1 band) (Table 4, 5).



The efficiency of the ISSR primers slightly differed, as shown in Table 4. The PIC ranged from 0.39 (ISSR46) to 0.75 (ISSR3), with an average of 0.60, and the MI varied from 48.66 (ISSR13) to 74.60 (ISSR10), with an average of 66.51. The average RP values were 13.76, which ranged from 8.22 (ISSR3) to 17.64 (ISSR46), with an average of 13.76. Additionally, the primer ISSR46 appeared to be the most efficient for assessing genetic diversity, as indicated by the high rate of RP. All primers showed

100% polymorphism with a high effective multiplex ratio (EMR), which varied from 88 (ISSR 13) to 139 (ISSR 34, ISSR 46), with a mean value of 113.

**SRAP analysis**

Using 11 primer combinations, clear, reproducible bands were produced, as represented by SRAP Me4-Em6 (Fig. 2 & S1). The total and specific bands as well as the percentages of polymorphisms are shown in Table 6.

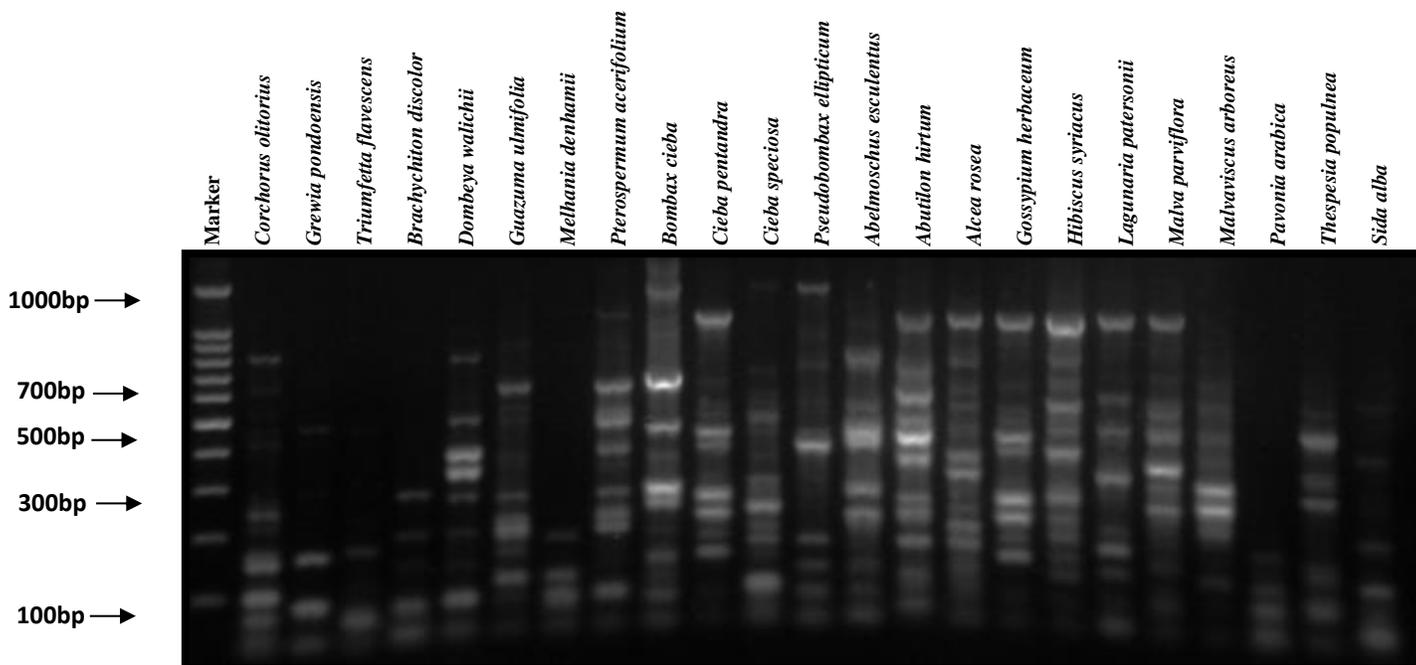


Fig. 2. SRAP of the primer combination Me4-Em6.

TABLE 6. Indices amplified with the examined species of Malvaceae *s.l.* by the 11 SRAP primer combinations.

Primer Combinations	TB <sup>1</sup>	PB <sup>2</sup>	MB <sup>3</sup>	% PB <sup>4</sup>	SB <sup>5</sup>	PIC <sup>6</sup>	MI <sup>7</sup>	RP <sup>8</sup>	EMR <sup>9</sup>
Me1-Em2	21	20	1	95%	2	0.763	127.38	16.00	166.99
Me2-Em1	21	21	0	100%	5	0.786	113.20	13.71	144.00
Me2-Em6	17	16	1	94%	2	0.65	66.33	12.12	102.00
Me3-Em1	17	16	1	94%	0	0.647	70.51	12.94	109.00
Me3-Em2	18	18	0	100%	0	0.669	95.73	15.89	143.00
Me3-Em4	22	22	0	100%	2	0.841	126.97	13.73	151.00
Me4-Em2	17	16	1	94%	0	0.61	85.45	16.59	140.00
Me4-Em6	25	25	0	100%	1	0.957	167.51	14.00	175.00
Me7-Em10	20	19	1	95%	5	0.776	87.71	13.40	113.00
Me8-Em1	23	23	0	100%	5	0.91	110.13	10.52	121.00
Me8-Em2	22	21	1	95.5%	1	0.809	137.47	15.55	170.00
<b>Total</b>	<b>223</b>	<b>217</b>	<b>6</b>	<b>97.3%</b>	<b>23</b>	<b>0.842</b>	<b>1188.40</b>	<b>154.44</b>	<b>1534.99</b>
<b>Mean</b>	-	-	-	-	-	<b>0.77</b>	<b>108.04</b>	<b>14.04</b>	<b>139.54</b>

<sup>1</sup>Total number of bands, <sup>2</sup>Polymorphic bands, <sup>3</sup>Monomorphic bands, <sup>4</sup>Percentage of polymorphism, <sup>5</sup>Specific bands, <sup>6</sup>Polymorphic information content, <sup>7</sup>Marker index, <sup>8</sup>Resolution power, <sup>9</sup>Effective multiplex ratio.

Two hundred and seventeen out of 223 bands were polymorphic, with a few common bands (6), as shown in Table 6. *Hibiscus syriacus* L. achieved the maximum number of bands (90), while *P. arabica* produced the minimum number (25). Consequently, the percentage of polymorphisms ranged from 38.11% to 8.15 %, respectively. The studied taxa revealed a total of 23 specific bands were detected: 5 in *Bombax ceiba* L., 4 in *Pterospermum acerifolium* (L.) Willd., 3 in *Ceiba pentandra* (L.) Gaertn., 2 in both *Corchorus olitorius* L. and *Grewia pondoensis* Burret, and 1 in *Triumfetta flavescens* Hochst ex A.Rich., *Guazuma ulmifolia* Lam., *C. speciosa*, *Pseudobombax ellipticum* (Kunth) Dugand, *Gossypium herbaceum* L., *H. syriacus* and *Sida alba* L. The detected bands ranged from 1000 to 50bp with a high percentage of polymorphism ranging from 94% (the Me2-Em6, Me3-Em1 and Me4-Em2 primer combinations) to 100% (the Me2-Em1, Me3-Em2, Me3-Em4, Me4-Em6 and Me8-Em1 primer combinations). There were 5 specific bands corresponding to Me2-Em1, Me7-Em10 and Me8-Em1; 2 corresponding to Me1-Em2, Me2-Em6 and Me3-Em4; and 1 corresponding to Me4-Em6 and Me8-Em2 (Table 7).

The efficacy of the 11 primer combinations based on the SRAP-PCR analysis (Table 6) was high, which was also reflected in the MR data (20.2). The PIC was 0.77, with values ranging from 0.61 (primer Me4-Em2) to 0.91 (primer Me8-Em1). The mean MI was 137.47, which varied from 66.3 (primer Me2-Em6) to 167.51 (primer Me4-Em6). The RP values ranged from 10.52 (primer Me8-Em1) to 16.95 (primer Me4-Em2), with an average of 14.04. The mean EMR value was 170, which varied from 102 to 175 for the primers Me2-Em6 and Me4-Em6, respectively.

The dendrogram based on the banding patterns for each of the ISSR and SRAP analyses did not show good clustering, and therefore, a combined dendrogram was constructed according to Ward's method using the Jaccard coefficient (Fig. 3). It is distinguished into two major clades; I and II. Clade 'I' included five species of (Malvaceae s.s. which are *Abelmoschus esculentus* L.Moench, *P. arabica*, *H. syriacus*, *M. arboreus* and *Alcea rosea* L.), while Clade 'II' included the remaining eighteen species with intermingled families (Tiliaceae s.s., Sterculiaceae s.s. and Bombacaceae s.s.) in several subclades.

### ITS polymorphisms

In the present study, ten species were selected for the ITS sequence technique: *C. olitorius*, *Brachychiton discolor* F. Muell., *B. ceiba*, *C. pentandra*, *A. esculentus*, *Abutilon hirtum*, *G. herbaceum*, *H.*

*syriacus*, *M. parviflora* and *Thespesia populnea* (L.) Sol. ex Correa. These species represented the distinct subclades of the combined dendrogram, in addition to the problematic Malvaceae s.s species. The ITS sequences produced a single band at a size of 700 bp (Fig. 4). The sequence data of the ten species were aligned pairwise using CLUSTAL W software (S2), and the alignment results are summarized in Table (8). The length of the ITS region varied from 677 bp in *A. hirtum* to 798 bp in *C. olitorius*, with a mean of 727 bp. The 'G+C' content for the entire spacer region ranged from 54.06% (*A. hirtum*) to 67.23% (*B. ceiba*), with a mean of 60.95%. The numbers of conserved and variable sites within the sequences were 287 and 511, respectively. The sequencing data for all the examined ten species have been deposited in GenBank/NCBI under the accession numbers OQ302173-OQ302182.

### ITS phylogenetic analysis

The phylogenetic relationship was constructed using MEGA and PAUP software, and the simulation analysis was carried out by choosing the ITS sequence of *E. nitentifolius* as an outgroup from the GenBank/NCBI sequence database (GenBank: KP093062.1). The constructed phylogenetic trees achieved the same topology. In this study, the ten Malvaceae s.l. species were classified as subfamilies or tribes rather than at the family level. With the PAUP software, the ITS dataset was analyzed via the parsimony method (using the likelihood and pairwise comparisons of nucleotide substitutions), which revealed that transversions were more common than transitions (Table 9, Fig. 5). In the dendrogram and phylogenetic tree, two major clades were distinguished: 'I' and 'II'. The major clade 'I' contained the outgroup (*E. nitentifolius*), and the major clade 'II' contained *C. olitorius* (Grewioideae) in clade 'A' from the rest of the species in clade 'B'. Clade 'B' is distinguished into two groups: 'a' and 'b'. Bombacoideae (*B. ceiba* and *C. pentandra*) were assembled in group 'a', and both Sterculioideae and Malvoideae were assembled in group 'b', with 2 branches, '1' and '2'. The four tribes were distinct in Malvoideae, Abutilae (*A. hirtum*), Gossypie (*G. herbaceum* and *Thespesia populnea*), Hibiscie (*A. esculentus* and *H. syriacus*) and Malvie (*M. parviflora*). The transition/transversion (Ti/Tv) ratios ranged from 0.82 in *C. olitorius* (Grewioideae) to 1.158 in *T. populnea* (Malvoideae, tribe Gossypie).

Parsimony analysis with accelerated transformation character state optimization (ACCTRAN) yielded a tree length of 1132 steps. After excluding the uninformative characters, the consistency index (CI) was 0.671, and the homoplasy index (HI) was 0.329.





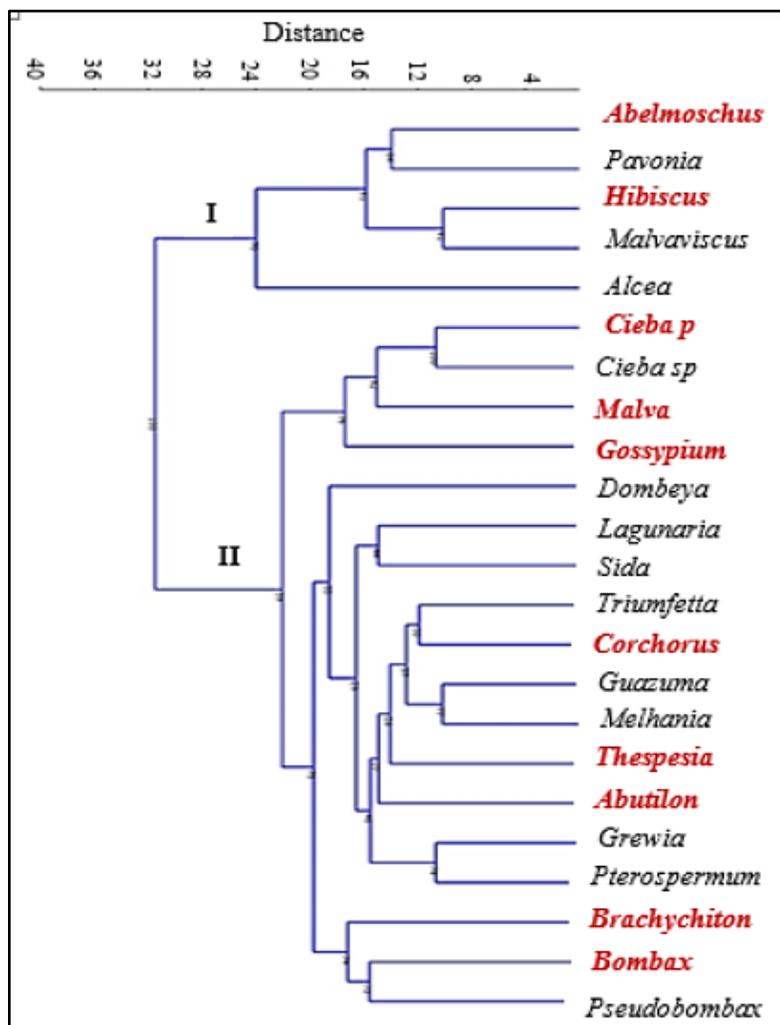


Fig. 3. Ward's dendrogram using Jaccard coefficient of Malvaceae *s.l.* species based on combined molecular markers (ISSR and SRAP).

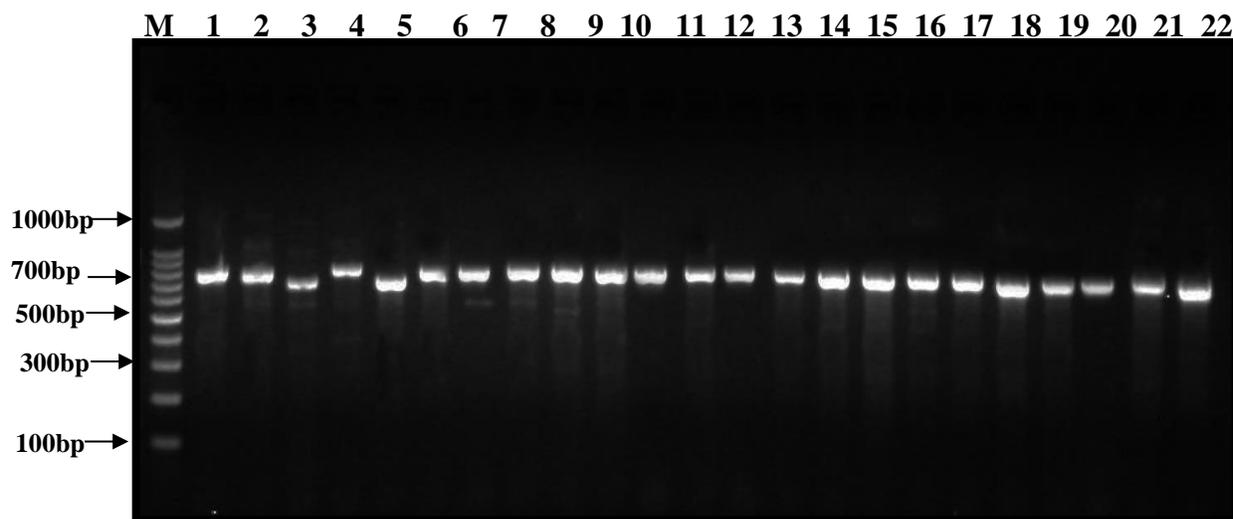


Fig. 4. The amplified product of the ITS region (approx. 700 bp) for 23 Malvaceae *s.l.* M: 1 kbp marker/ladder.

**TABLE 8.** The number of private segregating sites and the number of shared polymorphisms among different species of the 10 selected Malvaceae *s.l.* species.

Species	Length (bp)	A	T	C	G	G+C content (%)
<i>Corchorus olitorius</i>	798	163 (20%)	162 (21%)	233 (29%)	240 (30%)	59.27
<i>Brachychiton discolor</i>	745	155 (20%)	134 (20%)	208 (27%)	248 (33%)	61.21
<i>Bombax ceiba</i>	711	117 (16%)	116 (17%)	235 (33%)	243 (34%)	67.23
<i>Ceiba pentandra</i>	706	128 (18%)	117 (18%)	221 (31%)	240 (33%)	65.30
<i>Abelmoschus esculentus</i>	735	152 (20%)	126 (19%)	218 (29%)	239 (32%)	62.18
<i>Abutilon hirtum</i>	677	155 (22%)	156 (25%)	181 (26%)	185 (27%)	54.06
<i>Gossypium herbaceum</i>	705	143 (20%)	137 (21%)	203 (28%)	222 (31%)	60.28
<i>Hibiscus syriacus</i>	727	151 (20%)	153 (23%)	209 (28%)	214 (29%)	58.18
<i>Malva parviflora</i>	714	140 (19%)	134 (20%)	218 (30%)	222 (31%)	61.62
<i>Thespesia populnea</i>	755	153 (20%)	148 (20%)	219 (29%)	235 (31%)	60.13
<b>Mean</b>	<b>727</b>	<b>145 (19.5%)</b>	<b>138.8 (20.4%)</b>	<b>214 (29%)</b>	<b>228 (31.1%)</b>	<b>60.95%</b>
<b>Number of Variable Site</b>	<b>511</b>					

**TABLE 9.** Transition/transversion (Ti/Tv) ratios obtained by PAUP software according to the aligned sequence of ITS for the ten selected species of Malvaceae *s.l.*

Species	<i>Corchorus olitorius</i>	<i>Brachychiton discolor</i>	<i>Bombax ceiba</i>	<i>Ceiba pentandra</i>	<i>Abelmoschus esculentus</i>	<i>Abutilon hirtum</i>	<i>Gossypium herbaceum</i>	<i>Hibiscus syriacus</i>	<i>Malva parviflora</i>	<i>Thespesia populnea</i>	Mean
<i>Corchorus olitorius</i>		0.86	0.78	0.80	0.90	0.91	0.79	0.86	0.73	0.75	<b>0.82</b>
<i>Brachychiton discolor</i>	80/93		0.91	0.87	0.74	0.91	0.79	0.81	0.67	0.86	<b>0.824</b>
<i>Bombax ceiba</i>	77/99	92/101		0.83	1.07	1.90	0.88	1.21	0.96	0.86	<b>1.04</b>
<i>Ceiba pentandra</i>	80/99	90/103	40/48		1.04	1.29	0.75	1.01	0.84	0.79	<b>0.913</b>
<i>Abelmoschus esculentus</i>	71/79	64/87	76/71	70/76		1.11	0.99	1.30	0.94	1.00	<b>1.01</b>
<i>Abutilon hirtum</i>	79/87	86/95	106/56	90/70	70/63		0.83	0.90	1.10	0.82	<b>1.086</b>
<i>Gossypium herbaceum</i>	79/100	78/99	91/104	83/111	71/72	71/86		0.84	0.74	3.69	<b>1.144</b>
<i>Hibiscus syriacus</i>	71/83	79/97	95/78	83/82	51/39	64/71	72/86		0.89	0.89	<b>0.968</b>
<i>Malva parviflora</i>	72/99	69/103	87/91	83/99	66/70	77/70	67/90	71/80		0.76	<b>0.848</b>
<i>Thespesia populnea</i>	77/103	81/94	89/104	84/107	72/72	70/85	48/13	72/84	68/89		<b>1.158</b>

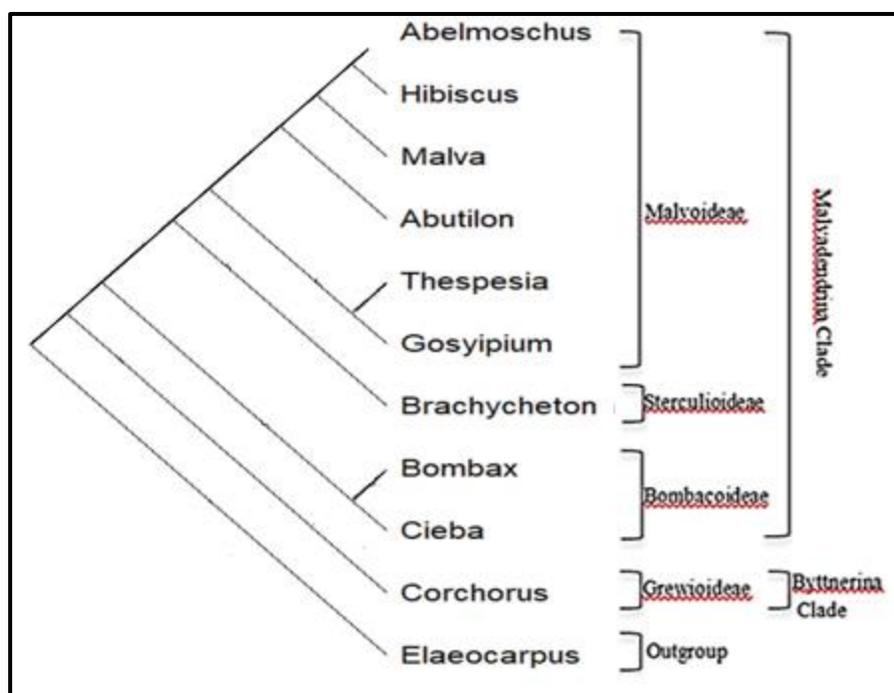


Fig. 5. UPGMA phylogenetic tree based on ITS sequencing of 10 Malvaceae *s.l.* species generated by MEGA software with the outgroup.

### Discussion

Molecular data, improvements in DNA sequencing and computational power allowed the construction of phylogenetic relationships and provided an enhanced understanding of evolutionary processes (Besse, 2014, El-Sherif et al., 2020). Based on molecular analyses, Malvaceae was placed in the subclass Dilleniidae. According to Bayer et al. (1999), Malvaceae *s.l.* was divided into nine subfamilies: Bombacoideae, Brownlowioideae, Byttnerioideae, Dombeyoideae, Grewioideae, Helicteroideae, Malvoideae, Sterculioideae and Tilioideae. Baum et al. (1998), Kubitzki & Chase (2003), Baum et al. (2004) and Wilkie et al. (2006) claimed that groups within Malvaceae *s.l.* require extensive review to provide accommodation for its molecular-based subfamilies. Weising et al. (2006) supported the use of molecular markers to detect variability among closely related taxa. The present study aimed to clarify the debate between classical and modern circumscription of Malvaceae *s.l.* through molecular analyses. Molecular analyses were performed by using 301 molecular characteristics (78 ISSR and 223 SRAP bands) and highlighting the phylogenetic relationships among the studied taxa.

The inter-simple sequence repeats (ISSR) is a dominant marker that have been successfully used in genetic diversity and evolutionary studies in Malvaceae *s.l.* (Celka et al., 2012; Vanijajiva, 2012). Similarly, sequence-related amplified polymorphism

(SRAP) is a codominant molecular marker introduced by Li & Queros (2001) that targets coding regions within the genome and is frequently used for gene tagging and genetic diversity (Badrakhani et al., 2014). The primer ISSR34 had the maximum number of amplified bands (19), while ISSR3 had the greatest number of specific bands (3). From an efficiency point of view, ISSR34 attained the maximum values for the PIC, MI, RP and EMR indices, followed by the ISSR3 primer. The present study recommends the use of these two primers, especially ISSR34, for the distinctiveness among taxa of Malvaceae *s.l.* *A. hirtum* amplified the maximum number of bands (33) and consequently the largest polymorphism percentage (42.37%). While *P. arabica* produced the lowest band and polymorphism percentage values (4 and 5.17%, respectively). Both *A. hirtum* and *C. speciosa* share the maximum number of specific bands (2). Using the SRAP technique, the percentage of polymorphisms revealed by the six primer combinations ranged from 94-95.5%, with one common band per primer. Therefore, the study suggested the use of these primer combinations for the identification of Malvaceae *s.l.* taxa. Five primer combinations generated 100% polymorphism without any common bands. These primers can be used as distinctive markers among taxa. The primer combination Me4-Em6 achieved the maximum number of bands (25) and the highest values for the PIC, MI, RP and EMR indices. The combinations of Me2-Em1, Me7-Em10 and Me8-Em1 generated the

most specific bands (5 bands each). *H. syriacus* was characterized by the highest number of bands (90) and percentage polymorphism (38.11%); on the other hand, *P. arabica* had the lowest number of bands (25) and percentage polymorphism (8.15%). A comparison of the taxa revealed one (*T. flavescens*, *G. ulmifolia*, *C. speciosa*, *P. ellipticum*, *G. herbaceum*, *H. syriacus* and *S. alba*), two (*C. olitorius* and *G. pondoensis*), three (*C. pentandra*), four (*P. acerifolium*) and five (*B. ceiba*) specific bands, while the remaining examined taxa lacked specific bands. These findings are in agreement with those of Badrakhani et al. (2014), who reported that the SRAP technique is powerful for identifying genetic distance among species of Malvaceae *s.l.* and could be explained by the detection of polymorphisms in coding regions that are conserved among closely related taxa.

Generally, both ISSR and SRAP are valuable as distinctive techniques for identifying Malvaceae *s.l.* taxa (Ghafoor & Hamarashid, 2022; Meerza et al., 2023). Both techniques achieve high PIC values (> 0.5), which is attributed to their ability to serve as a distinctive identification marker (Badrakhani et al., 2014). In comparison to the two DNA techniques, SRAP analysis yielded more MR than ISSR which indicated the efficiency of SRAP because of its greater ratio of the total number of bands. The dendrograms obtained by ISSR and SRAP are noninformative and unclear enough to show the positioning of Malvaceae *s.l.* species. The species are mixed in different clades that do not follow any of the proposed systems of classification of Malvaceae.

Several factors make the ITS region valuable for use in phylogenetic analyses (Álvarez, & Wendel, 2003). First, the ITS region is highly repeated in plant nuclear genomes, along with other components of the nrDNA multigene family, including a highly variable region between the ribosomal repeats, the intergenic spacer. The high copy number of the nrDNA repeat facilitates the amplification and sequencing of the nrDNA. Second, the nrDNA multigene family has undergone rapid concerted evolution (Baldwin et al., 1995). This property of the ITS region is most important from a phylogenetic standpoint and promotes the accurate reconstruction of species relationships by sequencing (Slotta, 2000). ITS sequencing clearly distinguished three tribes: Gossypie (705- 755 bp), Hibiscie (727-735 bp) and Malvie (677-714 bp). This conclusion is supported by Takhtjan (2009), Reveal (2012) and APG (2016). In phylogenetic analyses based on the sequencing of the ITS region, *E. nitentifolius* (Elaeocarpaceae) was used as an outgroup. It was considered to be closely

related to the core Malvales (Cronquist, 1988; Judd & Manchester, 1997).

The obtained phylogenetic tree based on ITS sequencing using PAUP software attained a relatively high consistency index (CI) of 0.671 as an assessment of the strength of the phylogenetic signal. Farris (1989a) determines the value of '1' for a perfect fit to the value '0' for the poorest fit. Sanderson and Hufford (1996) mentioned CI as a parameter of the goodness of fit of a dataset to a hierarchical tree structure. Moreover, the homoplasy index (HI) is relatively low (0.329), which indicates low homoplasy; i.e., the similarity between species is attributed to common ancestry and is a result of divergent evolution (Cvetković et al., 2021). For a more reliable construction of the phylogenetic tree, the ratio of transversions to transitions (Ti/Tv) was determined, which ranged from 0.67 to 3.64 in the studied taxa. Taxa with a greater number of transversions (lower Ti/Tv values) would be older, diverging early in the history of evolution (Saha et al., 2013). The obtained phylogenetic tree distinguished three clades (A, B and C). Clade A represents the outgroup (*E. nitentifolius*), while Clades B and C represent Byttnerina and Malvadendrina, respectively. The subfamily Grewioideae (Tiliaceae), which is represented by *C. olitorius*, is considered the most primitive taxon (Edlin, 1935; Cronquist, 1981& 1988; Takhtajan, 1980& 1997; Thorne, 1992& 2000) and treats Tiliaceae as the most primitive family in core Malvales. This is supported by the low mean value of Ti/Tv (0.82), which implies the primitiveness of this subfamily. Cvetković et al. (2021) placed Grewioideae in a separate clade based on the plastome dataset. On the other hand, Warming (1895) and Rao (1952) noted Sterculiaceae as the most primitive group. Jones and Good (2016), Johnson et al. (2019) and Stijik et al. (2020) mentioned that the ranking and phylogenetic relationships of a clade are crucial steps in evolutionary analyses of this complex group. Clade C assembles the Malvadendrina clade with three subfamilies: 1, 2 and 3 of Bombacoideae, Sterculioideae and Malvoideae, respectively. Bombacoideae and Malvoideae together form a well-supported clade, Malvatheca, as supported previously by many authors by molecular analysis (Alverson et al. 1998; Bayer et al. 1999; Nyffeler et al. 2005). The sequencing data treat Bombacoideae as a more primitive subfamily than Sterculioideae, with an average Tv/Ti of 0.976. This finding contradicts the findings of Edlin (1935), Cronquist (1981& 1988), Takhtajan (1980& 1997), and Thorne (1992& 2000), who considered Sterculioideae (Sterculiaceae) the primitive subfamily. The phylogenetic data suggest the inclusion of Sterculioideae within Malvadendrina,

this conclusion was previously remarked as an unclear opinion described by Wilkie et al. (2006) and Hernández-Gutiérrez & Magallon (2019). Malvoideae (Malvaceae *s.s.*) is by far the largest subfamily in Malvaceae *s.l.* (c. 1800 species). It acquired the highest average Tv/Ti (1.036), which was attributed to the advanced placement in the tree. This study was well supported by all the previous authors. The dendrogram of the ITS sequencing data revealed three tribes within Malvoideae: the Gossypie, Hibiscie and Malvie tribes. However, the phylogenetic tree discriminates four tribes: Abutilae, Gossypie, Hibiscie and Malvie. This finding agrees with the classical tribal system of Hutchinson (1967) and contradicts those of Shultz-Motel (1974), Takhtjan (2009) and the APG (2016). The tribe Abutilae (*A. hirtum*) was distinguished by the highest number of total and specific bands produced in ISSR, while in SRAP, it had a high percentage of polymorphisms. Phylogenetically, the present study suggested the tribal level of Abutilae.

The study indicated that the use of ISSR and SRAP as two powerful distinctive molecular techniques especially SRAP was proven more efficient. Both techniques were more successful at accessing a natural classification, with special referrals to sequencing techniques. The present study disagrees with the view of the traditional four families included in the classical systems of classification, and it agrees with the APG IV system of the nine subfamilies classification within two clades. However, the infrastructures of those clades were unclear, especially with the limits between Sterculioideae and Dombeyoideae, as well as between Malvoideae and Bombacoideae. Additionally, most of the tribal systems for both Malvoideae and Bombacoideae were confirmed.

**Dedication:** To Professor El-Sadek Laila, who passed away before we edited this work; God Bless you and thank you for all you have done.

**Acknowledgments:** The authors appreciate the editorial and reviewers' comments for their valuable suggestions.

**Competing interests:** No conflicts of interest have been declared.

**Authors' contributions:** Conceptualization W. K. T.; Methodology N. H. A.; Formal analysis and investigation performed by A. M. H.; Data interpretation, Writing of the original draft preparation, critical revision and editing of the final version of the article prior to journal submission G. E. B. Prior advice L. M. S. All the authors agreed with the published version of the manuscript.

**Ethics Approval:** Not applicable.

### Supplementary Information:

Supplementary file 1 (S1): ISSR and SRAP Amplifications.

Supplementary file 2 (S2): Sequence alignment of the ITS region.

### References

- Álvarez, I., Wendel, J.F. (2003) Ribosomal ITS sequences and plant phylogenetic inference. *Molecular Phylogenetics and Evolution*, **29**(3), 417-434. [https://doi.org/10.1016/S1055-7903\(03\)00208-2](https://doi.org/10.1016/S1055-7903(03)00208-2)
- Alverson, W.S., Karol, K.G., Baum, D.A., Chase, M.W., Swensen, S.M., McCourt R., Sytsma, K.J. (1998) Circumscription of the Malvales and relationships to other rosidae: evidence from rbcL sequence data. *American Journal of Botany*, **85**, 876-887. <https://pubmed.ncbi.nlm.nih.gov/21684971/>
- APG I (1998) An ordinal classification for the families of flowering plants. *Annals of the Missouri Botanical Garden*, **85**, 531-553. DOI: 10.2307/2992015
- APG II (2003) An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG II. *Botanical Journal of the Linnean Society*, **141**, 399-436. <https://doi.org/10.1046/j.1095-8339.2003.t01-1-00158.x>
- APG III (2009) An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG III. *Botanical Journal of the Linnean Society*, **161**(2), 105-121. <https://doi.org/10.1111/j.1095-8339.2009.00996.x>
- APG IV (2016) An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG IV. *Botanical Journal of the Linnean Society*, **181**, 1-20. <https://doi.org/10.1111/boj.12385>
- Badrkhani, N., Rahmani, F., Larti, M. (2014) Evaluation of Genetic Diversity in *Alcea* (Malvaceae) Using SRAP Markers. *Botanical Sciences*, **92**(3), 433-439. DOI: <https://doi.org/10.17129/botsoci.98>
- Baldwin, B.G., Sanderson, M.J., Porter, J.M., Wojciechowski, M.F., Campbell, C.S., Donoghue, M.J. (1995) The ITS region of nuclear ribosomal DNA: a valuable source of evidence on angiosperm phylogeny. *Annals of the Missouri Botanical Garden*, **82**(2), 247-277. <https://doi.org/10.2307/2399880>
- Baum, D.A., William A.S., Nyffeler, R. (1998) A Durian by any other name: taxonomy and nomenclature of the core Malvales. *Harvard Papers in Botany*, **3**(2), 315-330. <https://www.jstor.org/stable/41761576>
- Baum, D.A., Smith, S., Yen, A., Alverson, W.S., Nyffeler, R., Whitlock, B.A., Oldham, R.L. (2004) Phylogenetic relationships of Malvatheca (Bombacoideae and Malvoideae; Malvaceae *s.l.*) as inferred from plastid

- DNA sequences. *American Journal of Botany*, **91**(11), 1863-1871. DOI: 10.3732/ajb.91.11.1863
- Bayer, C., Fay, M.F., Bruijn, A.Y., Savolainen, V., Morton, C.M., Kubitzki K., Alverson, W.S., Chase, M.W. (1999) Support for an expanded family concept of Malvaceae within a recircumscribed order Malvales: a combined analysis of plastid atpB and rbcL DNA sequences. *Botanical Journal of the Linnean Society*, **129**(4), 267-303. DOI: 10.1006/bojl.1998.0226
- Besse, P. (2014) In “*Molecular Plant Taxonomy, Methods and Protocols*” MIMB, 1115. Springer Science, New York. <https://link.springer.com/book/10.1007/978-1-62703-767-9#about-this-book>
- Boulos, L. (1995) “*Flora of Egypt checklist*”. Al Hadara Publishing, Cairo.p283.
- Boulos, L. (2009) *Flora of Egypt checklist. Revised Annotated Edition*. Al Hadara Publishing, Cairo.p283.
- Celka, Z., Szczecinska, M., Sawicki, J., Shevera, M.V. (2012) Molecular studies did not support the distinctiveness of *Malva alcea* and *M. excisa* (Malvaceae) in Central and Eastern Europe. *Biologia*, **67**, 1088-1098. <https://doi.org/10.2478/s11756-012-0107-9>
- Chase, M.W., Douglas, E.S., Olmstead, R., Albert, V.A. (1993) Phylogenetics of seed plants – an analysis of nucleotide sequences from the plastid gene rbcL. *Annals of the Missouri Botanical Garden*, **80**, 528-580. <https://scholarworks.boisestate.edu/cgi/viewcontent.cgi?article=1045&context=biofacpubs>
- Cronquist, A. (1981) In “*An integrated system of classification of flowering plants*”. Angiosperms, 1262 pages, Columbia University Press.
- Cronquist, A. (1988) In “*The Evolution and Classification of Flowering Plants*”. The New York Botanical Garden, New York. 555 pages.
- Cvetković, T., Areces-Berazain, F., Hinsinger, D.D., Thomas, D.C., Wieringa, J.J., Ganesan, S.K., Strijk, J.S. (2021) Phylogenomics resolves deep subfamilial relationships in Malvaceae *s.l.* G3 (Bethesda) **11** jkab136. <https://doi.org/10.1093/g3journal/jkab136>
- Dellaporta, S.L., Wood, J., Hicks, J.B. (1983) A plant DNA miniprep: Version II. *Plant Molecular Biology Reporter*, **1**, 19-21. <https://doi.org/10.1007/BF02712670>
- De Riek, J., Clsyn, E. Everaert, I., Van Bockstaele, E. (2001) AFLP-based alternatives for the assessment of distinctiveness, uniformity and stability of sugar beet varieties. *Theoretical and Applied Genetics*, **103**, 1254-1265. DOI: 10.1007/s001220100710
- Edlin, H.L. (1935) A critical revision of certain taxonomic groups of the Malvales. *New Phytol*, **34**, 1-20. <https://doi.org/10.1111/j.1469-8137.1935.tb06824.x>
- El-Sherif, N., Ibrahim, M. (2020) Implications of rbcL and rpoC1 DNA Barcoding in Phylogenetic Relationships of some Egyptian *Medicago sativa* L. Cultivars. *Egyptian Journal of Botany*, **60**(2), 451-460. doi: 10.21608/ejbo.2020.20028.1399.
- Farris, J.S. (1989 a) The retention index and the rescaled consistency index. *Cladistics*, **5**(4), 417-419. DOI: 10.1111/j.1096-0031.1989.tb00573.x
- Farris, J.S. (1989 b) The retention index and homoplasy excess. *Systematic Biology*, **38**(4), 406-407. <https://doi.org/10.2307/2992406>
- Ghafoor, B.S., Hamarashid, S.H. (2022) Genetic Diversity and Relationships Among Medicinal Species of Malva L. (Malvaceae) Based on Issr Markers. *Bangladesh Journal of Plant Taxonomy*, **29**(2):193-202. DOI: 10.3329/bjpt.v29i2.63526
- Hammer, O., Harper, D.A.T., Ryan, P.D. (2001) PAST Palynological Statistics Software package for education and Data analysis. *Palaeontologia Electronica*, **4**(1), art. 4: 9pp. [http://paleo-electronica.org/2001\\_1/past/issue1\\_01.htm](http://paleo-electronica.org/2001_1/past/issue1_01.htm)
- Hernández-Gutiérrez, R., Magallon, S. (2019) Data for The timing of Malvales evolution: incorporating its extensive fossil record to inform about lineage diversification. Mendeley Data V1. <https://doi.org/10.17632/2ftkfv8gdd.1>
- Hutchinson, J. (1967) “*The genera of flowering plants*”. (Angiospermoe). Vol. 2, Clarendon Press, Oxford. 659 pages.
- Jaccard, P. (1908) Nouvelles recherches sur la distribution florale. *Bulletin de la Société Vaudoise des Sciences naturelles*, **44**, 223-270.
- Johnson, M.G., Pokorny, L., Dodsworth, S., Botigue, L.R., Cowan, R.S., Devault, A., Eiserhardt, W.L., Epitawalage, F., Forest, J.T. Kim, J.T., Leebens-Mack, J.H., Leitch, I.J., Maurin O., Soltis, D.E., Soltis, P.S., Wong, G.K., Baker, W.J. Wickett, N.J. (2019) A universal probe set for targeted sequencing of 353 nuclear genes from any flowering plant designed using k-medoids clustering. *Systematic Biology*, **68**,594-606. DOI: 10.1093/sysbio/syy086
- Jones, M.R., Good, J.M. (2016) Detecting selection in natural populations: making sense of genome scans and toward alternative solutions, targeted capture in evolutionary and ecological genomics. *Molecular Ecology*, **2**,185-202. DOI: 10.1111/mec.13304
- Judd, W.S., Manchester, R.S. (1997) Circumscription of Malvaceae (Malvales) as determined by a preliminary cladistic analysis of morphological, anatomical, palynological, and chemical characters. *Brittonia*, **49**(3), 384-405. <http://www.jstor.org/stable/2807839>
- Judd, W.S., Campbell, C.S., Kellogg, E.A., Stevens, P.F., Donoghue, M.J. (2008) *Plant Systematics: A Phylogenetic Approach*. Sinauer Associates, Sunderland, Massachusetts. 3rd edn, 611 pp. <https://doi.org/10.1111/j.1096-0031.2008.00212.x>

- Kew Science. (2021) "Plants of the world online". Royal Botanic Gardens, Kew, UK. <http://www.plantsoftheworldonline.org/>
- Kubitzki, K. (2003) "The Families and Genera of Vascular Plants". pp 225-311, Berlin: Springer-Verlag.
- Kubitzki, K., Chase, M.W. (2003) Introduction to Malvales. In. "The Families and Genera of Vascular Plants. Flowering Plants. Dicotyledons: Malvales, Capparales and Nonbetalain Caryophyllales" Kubitzki, K. & Bayer, C. editors, Berlin, Germany: Springer-Verlag, **5**, 12-17.
- Li, G., Quiros, C.F. (2001) Sequence-related amplified polymorphism (SRAP), a new marker system based on a simple PCR reaction: its application to mapping and gene tagging in *Brassica*. *Theoretical and Applied Genetics*, **103**, 455-461. <http://dx.doi.org/10.1007/s001220100570>
- Linnaeus, C. (1753) "Species Plantarum. Holmiae". By Laurentius Salvius, Sweden. 1200 pages.
- Meerza, C., Muhealdin, B.S., Hamarashid, S.H., Qadir, S.A., Juan, Y. (2023) Delimiting species using DNA and morphological variation in some *Alcea* (Malvaceae) species based on SRAP markers. *Caryologia*, **75**(4). DOI: 10.36253/caryologia-1629
- Nyffeler, R., Bayer, C., Alverson, W.S., Yen, A., Whitlock, B.A., Chase, M.W., Baum, D.A. (2005) Phylogenetic analysis of the Malvaceae clade (Malvaceae s.l.) based on plastid DNA sequences. *Organisms Diversity & Evolution*, **5**(2), 109-123. <https://doi.org/10.1016/j.ode.2004.08.001>
- Péchon, T. L. and Gigord, L.D.B. (2014) On the relevance of molecular tools for taxonomic revision in Malvales, Malvaceae s.l., and Dombeyoideae. *Methods in Molecular Biology*, 1115:337-63. DOI: 10.1007/978-1-62703-767-9\_17.
- Powell, W., Morgante, M., Andre, C., Hanafey, M., Voges, J., Tingey, S., Rafalski, A. (1996) A comparison of RFLP, RAPD, AFLP and SSR (microsatellite) markers for germplasm analysis. *Molecular Breeding*, **2**, 225-230. <https://doi.org/10.1007/BF00564200>
- Prevost, A., Wilkinson, M.J. (1999) A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theoretical and Applied Genetics*, **98**, 107-112. <https://doi.org/10.1007/s001220051046>
- Rao, C.V. (1952) Floral anatomy of some Malvales and its bearing on the affinities of families included in the order. *Journal of Indian Botanical Society*, **31**, 171-203.
- Reveal, J.L. (2012) An outline of a classification scheme for extant flowering plants. *Phytoneuron*, **37**, 1-221.
- Saha, J., Gupta, K., Gupta, B. (2013) Phylogenetic analyses and evolutionary relationships of *Saraca asoca* with their allied taxa (Tribe-Detarieae) based on the chloroplast matK gene. *Journal of Plant Biochemistry and Biotechnology*, **24**, 65-74. <https://doi.org/10.1007/s13562-013-0237-3>
- Sanderson, M.J., Hufford, L. (1996) Homoplasy. The recurrence of similarity in evolution. Published by: American Society of Ichthyologists and Herpetologists (ASIH). *Copeia*, **2**, 472-474. <http://www.jstor.org/stable/1447779>
- Schultze-Motel, W. (1974) In H Melchior (ed.). A. Engler's "Syllabus der Pflanzenfamilien". 12th ed, Gebrüder Borntraeger Verlag, Berlin. 233 pages.
- Shamso, E.M., Khattab, A.A. (2016) Phenetic relationship between Malvaceae s.s. and its related families. *Taeckholmia*, **36**, 115-135.
- Simpson, M.G. (2010) "Plant systematics". Burlington: Elsevier Science. 752 pages.
- Slotta, T.A.B. (2000) Phylogenetic Analysis of *Iliamna* (Malvaceae) Using the Internal Transcribed Spacer Region. *Ph.D. Dissertation*, Virginia Polytechnic Institute and State University, USA.
- Sorkkeh, K., Shiran, B., Gradziel, T.M., Epperson, B.K., Martinez-Gomez, P., Asadi, E. (2007) Amplified fragment length polymorphism as a tool for molecular characterization of almond germplasm: genetic diversity among cultivated genotypes and related wild species of almond, and its relationships with agronomic traits. *Euphytica*, **156**, 327-344. DOI: 10.1007/s10681-007-9382-x
- Strijk, J.S., Binh, H.T., Ngoc, N.V., Pereira, J.T., Slik, J.F. (2020) Museomics for reconstructing historical floristic exchanges: divergence of stone oaks across Wallaceae. *PLoS One*, **15**, e0232936. <https://doi.org/10.1371/journal.pone.0232936>
- Swofford, D.L. (2002) PAUP: Phylogenetic Analysis Using Parsimony (and Other Methods), version 4.0b10. Sinauer, Sunderland. DOI: 10.1111/j.0014-3820.2002.tb00191.x
- Taeckholm, V. (1974) Students' flora of Egypt, (ed. 2), Cairo University, Egypt. 888 pages.
- Takhtajan, A. (1980) Classification of Flowering Plants Author(s): Hollis G. Bedell and James L. Reveal Source. *Taxon*, **31**, 211-232.
- Takhtajan, A. (1997) *Diversity and Classification of Flowering Plants*. New York, NY: Columbia University Press, 643. *Brittonia*, **50**, 191-192. <https://doi.org/10.2307/2807851>
- Takhtajan, A. (2009) *Diversity and Classification of Flowering Plants*. New York, NY: Springer Science & Business Media. <https://doi.org/10.1007/978-1-4020-9609-9>
- Tamura, K., Stecher, G., Kumar, S. (2021) MEGA11: Molecular Evolutionary Genetics Analysis Version 11. *Molecular Biology and Evolution*, **38**(7), 3022-3027. <https://doi.org/10.1093/molbev/msab120>
- Tate, J.A., Aguilar, J.F., Wagstaff, S.J., La Duke, J.C., Slotta B.T.A., Simpson, B.B. (2005) Phylogenetic relationships within the tribe Malveae (Malvaceae, subfamily Malvoideae) as inferred from ITS sequence

- data. *American Journal of Botany*, **92**(4), 584-602. DOI: 10.3732/ajb.92.4.584
- Thompson, J.D., Gibson, T.J., Plewniak, F., Jeanmougin, F., Higgins, D.G. (1997) The CLUSTAL\_X Windows interface: Flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research*, **25**, 4876-4882. DOI: 10.1093/nar/25.24.4876
- Thorne, R. (1992) Classification and geography of the flowering plants. *Botanical Review*, **58**(3), 225-348.
- Thorne, R. (2000) The classification and geography of the flowering plants: dicotyledons of the class Angiospermae. *Botanical Review*, **66**, 441-647. <https://www.jstor.org/stable/4354190>
- Vanijajiva, O. (2012) Assessment of genetic diversity and relationships in pineapple cultivars from Thailand using ISSR marker. *Journal of Agricultural Technology*, **8**(5), 1829-1838. <http://www.ijat-aatsea.com>
- Warming, E. (1895) “*Handbook of Systematic Botany*” London, pp. 620.
- Weising, K., Nyborm, H., Wolf, K., Khal, G. (2006) DNA fingerprinting in plants. Principles, methods and applications. *Biologia plantarum*, **50**, 799. <https://doi.org/10.1201/9781420040043>
- Wilkie, P., Clark, A., Pennington, R.T., Cheek, M., Bayer, C., Wilcock, C.C. (2006) Phylogenetic relationships within the subfamily Sterculioideae (Malvaceae/Sterculiaceae- Sterculieae) using the chloroplast gene *ndhF*. *Systematic Botany*, **31**, 160-170. DOI: 10.1600/036364406775971714.

## التقنيات الجزيئية للتأكد من الاستراتيجيات الوراثية في بعض أصناف Malvaceae s.l.

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لقد تعرضت عائلة Malvaceae تقليدياً للعديد من الأساليب التصنيفية فيما يتعلق بعلاقاتها وأقسامها التصنيفية. ومع التقدم السريع في الأساليب المعتمدة على تفاعل البوليميراز المتسلسل ومعلومات تسلسل الحمض النووي، أصبح لدى علماء التصنيف الآن فرصة التحول من أنظمة التصنيف التقليدية إلى أنظمة أحدث. قدمت الدراسات الجزيئية للأصناف Malvaceous آراء جديدة حول تجمع هذه الأصناف وتطورها. تضمن هذا العمل تحليلات جزيئية لثلاثة وعشرين نوعاً من أنواع Malvaceae. تم استخدام ثلاث تقنيات جزيئية، وهي تكرار التسلسل البسيط (ISSR)، وتعدد الأشكال المضخم المرتبط بالتسلسل (SRAP)، والمباعد الداخلي المكتوب (ITS)، لدراسة العلاقات بين الأصناف المدروسة. تم بناء علاقات التطور الوراثي باستخدام تحليل الوراثة التطورية الجزيئية والتحليل الوراثي باستخدام برنامج Parsimony (MEGA و PAUP). كشفت نتائج هذا البحث عن 301 خاصية جزيئية (78 ISSR و 223 نطاق SRAP) بين الأصناف. تدعم هذه البيانات وجهة النظر التصنيفية لعائلات Malvaceae s.l.s الفرعية في نظام Angiosperm Phylogeny Group لتصنيف النباتات (أنظمة APG).