Genetic and Horticultural Characterisations of Some Mango Cultivars (*Mangifera indica* L.) Based on Different Markers

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ABSTRACT: Mango (*Mangifera indica* L.) is the most popular fruit crop in the orient particularly in the world. Mango is a diploid fruit tree (2n = 40). The mango is considered as one of the oldest cultivated trees in the world. 28 mango cultivars, different morphological and molecular markers (EST & SSR) were used in the current experiment to identify the genetic relationships with/within cultivars. The results indicated that, high significant variations were observed in the morphological characteristics. Also, the molecular data could be useful tool in calculating the genetic relationship and clustering the recent mango cultivars based on SSR and EST markers. Genetic polymorphism based on different markers were detected.

Key words: Mango, horticulture, molecular, markers

INTRODUCTION

Mango (*Mangifera indica* L.) is one of the most important fruit crops of the Anacardiaceae family (Popenoe, 1920). Mangoes are an important fruit crop in Egypt. Per the latest statistics provided by the Ministry of Agriculture and Land Reclamation of Egypt (20١٥), indicated that, a total of 243028 Feddan is planted by mangoes. Adoption of molecular markers and genomics-based breeding strategies will likely improve predictability and breeding efficiency. In recent years, *Mangifera* germplasm has been collected and analysed using simple sequence repeat (SSR) markers by Duval *et al.* (2006), Schnell *et al*. (2006) and more recently by Dillon *et al*. (2013). The traditional techniques of developing SSR markers are usually time consuming, labor intensive and of low efficiency, Ellis and Burke (2007). However, alternative strategies to identify SSR markers have been developed that use comparative genomics tools such as expressed sequence tags (ESTs) (Wöhrmann and Weising 2011). It is hypothesized that the highly repetitive nature of SSRs makes slippage during replication a common event, leading to the high levels of polymorphism found between populations. A key advantage of EST-SSRs is that they are often more transferable across closely related genera compared to anonymous SSRs from untranslated regions (UTRs) or non-coding sequences e.g., (Pashley *et al*., 2006). This is due to the primer target sequences residing in the expressed DNA regions expected to be relatively well conserved, thereby increasing the chance of marker transferability across species boundaries (Varshney *et al*. 2005). Despite their potential to represent selectively deleterious frame-shift mutations in coding regions, EST-SSRs appear to reveal equivalent levels of polymorphisms compared to SSRs located in UTRs, most likely due to an evolutionary trend towards tri-nucleotide repeats in these coding regions, (Ellis and

Burke, 2007). EST-SSRs are physically linked to expressed genes and therefore represent potentially functional markers. Evaluation of genetic variation within cultivated crop species is central to plant breeding strategies and genetic resource conservation (Dean *et al*., 1999).

One of the many interesting applications of ESTs database (dbEST) is gene discovery where many new genes can be found by querying the dbEST with a protein or DNA sequence. Twenty-two mango cultivars were examined for 40 simple sequence repeat (SSR) anchored primers of 15–18 oligonucleotides which screened by Eiadthonga *et al.* (2005). Microsatellite markers were developed and characterized to assess the genetic diversity among mango cultivars and to test their amplification in closely related species by Kundapura *et al.* (2011). Polymorphic information content values ranged from 0.185 to 0.920 with a mean of 0.687. Dillon *et al.* (2013) a collection of 24,840 expressed sequence tags (ESTs) generated from five mango cDNA libraries was mined for EST-based simple sequence repeat (SSR) markers. Results showed that over 1,000 ESTs with SSR motifs were detected from more than 24,000 EST sequences with di- and tri-nucleotide repeat motifs the most abundant. Twenty-four of the 25 EST-SSR markers exhibited polymorphisms, identifying a total of 86 alleles with an average of 5.38 alleles per locus, and distinguished between all *Mangifera* selections. Private alleles were identified for *Mangifera* species.

Recently, Kundapura *et al*. (2011) studied genetic diversity and population structure of mango cultivars by employing fourteen simple sequence repeat markers, with high polymorphic information content. A set of 387 mango cultivars from different regions of India was used. The main objectives of the present research are to study the molecular and horticultural characterization of some mango cultivars in Egypt from different localities.

MATERIALS AND METHODS

The present experiments were carried out at the Agricultural Botany Department, Faculty of Agriculture, Saba Basha, Alexandria University, Egypt. These studies were conducted during 2014 up to 2016. Twenty eight Mango *(Mangifera Indica* L.) cultivars growing in Egypt have been used for morphological and molecular markers analyses, all of the cultivars were obtained kindly from the Agricultural Research Center, Horticulture Research Institute, (HRI), Giza, Egypt i.e. Shelly, Kensington Bride, Yasmina, Succari, Hindi Besennara, Golek, Alphonso, Piva, R2E2, Zebda, Sabre, Heidi, Osteen, Langra Benersi, Maya, Nam Doc Mai, Princess, Hindi Mloki, Fajri Kalan, Sidik, Joa, Sensation, Tommy Atkins, Kent, Haden, Naomi, Palmer and Lilly.

Eight morphological characters were measured at maturity and harvest stage such as fruit lengths (cm), fruit width (cm), fruit weight (g), peel (%), pulp (%),

fiber length (mm), shelf life (days) and fruit shape. Genomic DNA was isolated from leaves of all varieties using CTAB modified method per Dellaporta *et al.,* (1983). Six SSR specific markers were selected for SSR analysis per the literature of Hameedunnisa *et al*. (2012) (Table 1).

The PCR amplification reactions were performed in 17 µl reaction volume containing 50 ng of DNA, 12.5 µl of Dream Taq master mix (Fermentas co.) and 0.5 µ moles of each primer. The primary program was 6 cycles at 94°C for 1 min, 45°C for 50 seconds decreasing 1°C in every cycle, and 72°C for 1 min, followed by 28 cycles at 94°C for 1 min, 40°C for 1 min and 72°C for 1 min. The previous programs were preceded by a denaturation step at 94°C for 4 minutes and followed by an extension step at 72°C for 7 minutes. The PCR products were separated on 1.5% agarose gel electrophoresis. Seven EST common specific markers (Table 1) were selected to carry out the EST analysis for *Mangifera Indica* L varieties per Dillon *et al*. (2013).

The primary program was carried out for: 7 cycles at 94°C for 1 min, 47°C for 50 seconds decreasing 1°C in every cycle, and 72°C for 1 min. The main programs were carried out for 28 cycles at 94°C for 1 min, 42°C for 1 min and 72°C for 1 min. The previous programs were preceded by a denaturation step at 94°C for 4 minutes and followed by an extension step at 72°C for 7 minutes. The PCR products were separated on 1.5% agarose gel electrophoresis. Morphological data were subjected to analysis of variance (ANOVA) to determine variation among the varieties using SPSS 14 (Statistical Package for the Social Sciences). DNA bands of PCR product were visualized on UV Transilluminator gel documentation system and photographed.

The gel pictures were manipulated using Adope Photoshop 8. The gels were scored for band presence or absence as (1) or (0), respectively. The total number of bands generated from each primer as well as the polymorphic bands number generated from each primer was calculated. The polymorphism percentage of each primer as well as the polymorphic information content (PIC) was also calculated. Similarity coefficient matrices were calculated using the Jaccard similarity algorithm (Jaccard, 1908).

Table (1). Marker names, sequences for SSR and EST used in the current study

Marker	Marker name	Forward and Reverse sequence
SSR	SSR-16	'5-AGCGATGGTGCTCATGCTTA-3' 3'-TCTCTCACGGAATCACATCTT-'5
	SSR-19	'5-TTTCAGCAAACTAGAACCAA-3' 3'-GGCATTCAGTTTTTACCTTGT-'5
	SSR-52	'5-AAAAACCTTACATAAGTGAATC-3' 3'-GAACAGTTGTTTCGTGTCGTA-'5
	SSR-59	'5-GATGTTGTTGGTGTTGTTTA-3' 3'-CAATTAGGAGCAAAATCAGA-'5
	SSR-65	'5-GGTTTTGAATAGAAATGCAA-3' 3'-AAGATGTGTCAATATTGTTTT-'5
	SSR-83	'5-GGCTATTGTCACGAACAAAT-3' 3'-GATTCAGACCCGGATACATT-'5
EST	QGMI-001	'5-GAAAGGCTTGCAGAGACAGG-3' 3'-GTTTCTTCTGTTCGGTGATGGAGGAGT-'5
	QGMI-003	'5-CAGGAATCTTCCCAAACGAA-3' 3'-GTTTCTTTGCCAGTGTCTTCACCTTCA-'5
	QGMI-004	'5-TTCACAACGAGAAGACATGGA-3' 3'-GTTTCTTGGGACCTATTCGATCCCACT-'5
	QGMI-005	'5-TGGAGGAATTGAACCGATTG-3' 3'-GTTTCTTCAGTATCGGAGGCGTCAGTC-'5
	QGMI-010	'5-GGTTTGAGCTTCCAAATTGC-3' 3'-GTTTCTTCCTGGGAAAGTCAACAGCAG-'5
	QGMI-020	'5-GCTCTGACGCGGAGATTC-3' 3'-GTTTCTTGTTGTTTTCCTGGCTGCAAT-'5

RESULTS AND DISCUSSION

a. Morphological variations of *Mangifera Indica* cultivars

Regrading to the data in Table (2) for fruit length (cm) in 28 Mango cultivars, data showed that the highest accession was Fajri Kalan by 16.5 cm and the lowest one was Succari by 9.0 cm. The general average was 12.11 cm for fruit length. Significant variations were observed between the current cultivars with L.S.D.0.05= 2.30. Five cultivars from 28 detected fruit length less than 10 cm such as Alphonso (9.2 cm), Maya (9.5 cm), Princess (9.6 cm), Sensation (9.5 cm) and Haden (10 cm). these values were less than the overall and nearly to the minimum values (Table, 2).Data for fruit width (cm) recorded in Table (1), detected that, the fruit width ranged from 6.3 to 11.5 cm by general average was 10.6 cm. The highest value recorded to R2E3 and the lowest fruit width recorded to Sabre by 6.3 cm. Data showed the different in morphological variations between the 28 mango cultivars with significant values L.S.D.0.05= 3.10. No significant variations were

observed between the maximum and minimum values, while between cultivars there were significantly difference in relation to fruit width (cm).

Concerning to fruit weight (g) high significant variation was observed between all the cultivars (Table, 2). The highest fruit weight was 650 g (Piva accession) followed by 625 g (Hindi mloki accession) then Tommy (615 g). The lowest value was 225 g was recorded to Zebda accession. The general mean was 416. 4 g between thee 28 cultivars with L.S.D.0.05= 114.30. Three different categories were observed for fruit weight, the first group was over than 600 g such as Piva (650 g), Hindi moloki (626 g), Tommy Atkins (615 g). the second group was from 300 to 600 g and this one includes 17 cultivars. Finally, the last one was less than 300 g and that includes 7 cultivars such as Yasmina, Succori, Hindi Besenara, Golek, Zebda, Maya and Joa. Concerning to peel percentage in different mango cultivars, data in Table showed that Succari detect the lowest percent (14%) and it was the shortest fruit also. On the other hand, Tommy Atlins showed the highest peel percentage (34%) flowered by Hindi Mloki by (33%) and it was also the highest fruit weight. While, for pulp %, the data ranged from 16 to 46% the general mean was 23.2%. The highest one was Hindi Besennara (46%) and the lowest one was Tommy (16%) although the fruit weight was high (615 g) as shown in Table 2.

For fiber length (mm), data in Table (2) showed that, values ranged from 6 to 23 mm by general mean 10.9 mm. The lowest cultivars were Princess achieved 6 mm while, the highest was Sabre with 23 mm and the last one showed the lowest fruit width also. Data showed relationship between the fruit width and pulp percentage. Finally, the shelf life for the current accession ranged from 5 to 7 day and the general mean was 6.1 day. Yasmina, Alphonso and Nam Doc Mai showed the lowest values comparing with other cultivars (Table, 2). For fruit shape, data in Table 2 showed different shapes such as cordate, ovate, Cylindrical, Obliqueovate, fusiform, Cylindrical oblique, Rectangular oblique and Oval roundish. Results showed the different morphological variation between the twenty-eight Mano cultivars. The previous data could be reference for the researchers in the future when worked on the mango cultivars in Egypt.

The present results are in consonance with those of Singh *et al*. (2009) who detected prominent variation in the mango cultivar ‘Banganapalli’ based on morphological analysis of 17 fruit characters. The present findings are also in agreement with those of Bally *et al*. (1996), who also observed phenotypic variation in the type of fruit in 15 cultivars of 'Kensington Pride', a polyembryonic cultivar of mango. Conventionally also, the intracultivar heterogeneity of mango has been characterized mostly at the morphological level by several researchers (Gan *et al*., 1981; Naik, 1948; Pandey, 1998; Singh *et al.,* 2009).

Table (2). Morphological characters of twenty-eight mango cultivars

	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Peel (%)	Pulp (%)	Fiber length (mm)	Shelf life (days)	Fruit shape
Shelly	12.5	11.0	425.0	25.0	33.0	8.0	6.0	cordate
Kensington Bride	12.6	9.8	400.0	18.0	42.3	11.0	7.0	cordate
Yasmina	11.5	6.7	275.0	17.0	35.0	7.0	5.0	ovate
Succari	9.0	6.5	275.0	14.0	44.0	12.0	6.0	cordate
Hindi Besennara	12.0	6.7	300.0	20.0	46.0	13.0	6.0	Cylindrical
Golek	11.0	7.0	250.0	18.0	29.0	11.0	6.0	Cylindrical
Alphonso	9.2	7.8	500.0	30.0	41.0	7.0	7.0	cordate
Piva	13.7	8.8	650.0	28.0	38.0	8.0	5.0	Obliqueovate
R2E2	13.5	11.5	500.0	23.0	18.0	12.0	7.0	cordate
Zebda	12.5	9.0	225.0	17.0	33.0	13.0	6.0	ovate
Sabre	12.2	6.3	375.0	27.0	39.0	23.0	7.0	Cylindrical
Heidi	11.4	9.5	575.0	17.0	22.0	7.0	7.0	cordate
Osteen	12.9	8.0	400.0	22.0	21.0	16.0	7.0	Cylindrical
Langra Benersi	10.7	8.1	325.0	26.0	28.0	7.0	6.0	ovate
Maya	9.5	8.0	300.0	18.0	25.0	9.0	6.0	cordate
Nam Doc Mai	13.6	7.2	425.0	28.0	21.0	9.0	5.0	fusiform
Princess	9.6	6.9	375.0	24.0	36.0	6.0	5.0	cordate
Hindi Mloki	12.4	7.0	625.0	33.0	33.0	8.0	6.0	Cylindrical
Fajri Kalan	16.5	8.0	500.0	25.0	24.0	8.0	6.0	Cylindrical
Sidik	16.4	7.3	425.0	19.0	28.0	16.0	7.0	Cylindrical
Joa	12.5	7.5	300.0	22.0	35.0	8.0	7.0	Rectangular
Sensation	9.5	7.3	480.0	28.0	41.0	22.0	6.0	Rectangular
Tommy Atkins	12.1	8.8	615.0	34.0	16.0	9.0	5.0	Oval roundish
Kent	11.9	9.7	310.0	22.0	26.0	10.0	6.0	cordate
Haden	10.0	8.5	505.0	26.0	21.0	11.0	6.0	cordate
Naomi	13.5	9.1	455.0	23.0	28.0	8.0	7.0	Rectangular
Palmer	13.0	7.0	490.0	28.0	22.0	15.0	5.0	Cylindrical
Lilly	12.5	8.6	380.0	18.0	18.0	12.0	6.0	ovate oblique
Average	**12.1**	**10.6**	**416.4**	**23.2**	**30.1**	**10.9**	**6.1**	**--**
Maximum	**16.5**	**11.5**	**650.0**	**34.0**	**46.0**	**23.0**	**7.0**	**--**
Minimum	**9.0**	**6.3**	**225.0**	**14.0**	**16.0**	**6.0**	**5.0**	**--**
L.S.D=0.05	**2.30**	**3.1**	**114.30**	**10.50**	**8.2**	**11.5**	**1.6**	**--**

The prime advantages of morphological traits are simplicity and rapid, inexpensive assays, even from herbarium specimens and other dead tissues. Although morphological traits are very useful, they have several disadvantages. They are often limited in number. They suffer from lack of decisiveness. They face heritability problems as they may be controlled by epistatic and pleiotropic gene effects. Morphological characterizations are error prone due to environmental variations affecting expression of these characteristics. In addition, these observations are time consuming and this mode of identification is slow because of long juvenile periods. Thus, these morphological characters may not adequately represent the genetic heterogeneity among cultivars of a cultivar. Hence, characterization of intravarietal heterogeneity based on morphological traits needs complementation with molecular markers as they can contribute greatly to the

utilization of intravarietal heterogeneity through descriptive information of structure of genotypes, analyses of relatedness, the study of identity and location diversity. Assessment of intracultivar diversity of mango has traditionally been made through morphological traits by several researchers such as Naik (1948); Singh *et al*. (2009), where in intracultivar variability was found. Here also, analysis of 8 quantitative fruit traits following descriptive statistics indicated significant variability in fruit morpho-physiology among 28 cultivars of mango under study. In addition, the data on 8 qualitative fruit traits also revealed considerable variation among total sample under study. Overall, morphological analysis indicated considerable variability among the mango trees grown in Egypt. However, assessment of genetic variability based on phenotype has certain limitations, since most of the morphological characters of economic importance are often limited in number; have complex inheritance and dramatically influenced by environmental factors (Tanksley, 1992). These results are suggesting both to focus our attention on the effects of the environment on the genotype and to consider, as a practical consequence, the importance of preserving these cultivars found in different areas to truly preserve the richness of the germplasm of a cultivar.

b. Molecular studies of *Mangifera indica* L.

During the current research thirteen specific markers were used (SSR and EST-PCR) to calculate the genetic variations between 28 mangos (*Mangifera indica)* cultivars. Data in Table (3) and Figure (1) for simple sequence repeat (SSR), the SSR-16 marker produced two alleles and the allele size ranged from 169 to 235 bp. The second marker SSR-19 detected also two alleles by molecular weight ranged from 137 to 173 bp, while SSR-52 and SSR-65 detect one allele with 199 and 154 bp, in respect. Finally, SSR-59 and SSR-83 recorded two alleles with the molecular weight range 145-168 and 157-183 bp, respectively. For SSR markers, the annealing temperature ranged from 52:59 ˚C. The genetic polymorphism (PIC%) ranged from 0.71 to 100% based on the different markers. The data for SSR-52 AND 65 showed 100 PIC flowered by SSR59 by 0.87, SSR19 by 0.83, SSR16 by 0.77 and finally SSR83 by 0.71%. At present, SSRs are the most preferred marker types because they are highly polymorphic even between closely related lines, require low amounts of DNA, can be easily automated and allow high throughput screening, can be exchanged between laboratories and are highly transferable between populations. SSR markers are efficient, time consuming and cost-effective approaches for diversity analysis. Molecular marker analysis is an efficient method of assessing genetic heterogeneity within the cultivars of mango and PCR-based genomic polymorphism has been detected in several cultivars of mango (Bally *et al*., 1996; De Souza and Lima, 2004; Diaz-Matallana *et al*., 2009 and Rocha *et al*., 2012). Intra cultivars study of genomes from different locations can confirm whether there are any genetic differences among the location-specific cultivars or not. In the present study with SSR markers, a total of 190 amplification fragments, ranging from 137-235 bp in length,

were detected at the two microsatellite loci validated in the cultivars. overall, larger intra cultivars variation and significant differentiation in different accession pairs was observed at several loci. SSR analysis is performed by using pairs of specific primers flanking tandem arrays of microsatellite repeats. Microsatellites are abundant in plant systems (Condit and Hubbel, 1991). The first report of length polymorphisms of microsatellites in soybean (Akkaya *et al*., 1992) opened a new source of PCR-based molecular markers for other plant genomes. Microsatellite markers are consistently found to be highly polymorphic, easily visualized, stable, and codominant (McCouch *et al.,* 1997 and Powell *et al.,* 1996). In addition, they have hyper-variability, wide genomic distribution, reproducibility, multiallelic nature, and chromosome specific location. Our results are agreeing with Manchekar (2008) who reported the level of polymorphism present in the microsatellites was variable ranging from 2 alleles (SSR-18, SSR-23 etc.) to 4 alleles (SSR-81) with an average of 2.48 alleles per SSR. The analysis of 23 SSRs revealed that the PCR product size (bp) ranged from 100 (SSR-52) to 310 (SSR20) in 31 cultivars. Polymorphic information content (PIC) value is the reflection of allele diversity and frequency among the cultivars, and varied greatly for all the SSR loci tested and these results were agreeing with our results that showed the PIC values varied widely among loci and ranged from 0.77 (SSR-16) to 100.0 (SSR-52 & 65) with an average of 86.33 per locus (Table 3). These results are in a line with Manchekar (2008) reported that the microsatellites with high PIC values in mango “Beneshan” were (SSR-80, SSR-87, SSR-28, and SSR-89) were found to be more useful in differentiating the ‘Beneshan’ cultivars. Over all, these data extend the knowledge of SSR application as a molecular tool in intravarietal improvement of mango as reported by Bally *et al*. (1996), De Souza and Lima (2004), Diaz-Matallana *et al.* (2009) and Rocha *et al*. (2012), they have used ISSR and RAPD markers for molecular characterization of intravarietal heterogeneity in different cultivars of mango. The present work provides evidence that the SSRs appear to be effective to explore the molecular polymorphism in the mango cultivars.Data in Table (4) and Figure (2) for EST markers showed that all EST markers detect one specific allele except QGMI-001 recorded three alleles with size ranged from 161 to 253 bp. The other primers showed different allele size i.g. 172, 227, 315, 240, 110 and 140 for the flowing primers: QGMI-003, QGMI-004, QGMI-005, QGMI-0010, QGMI-020 and QGMI-023, respectively. Concerning to EST-PCR markers used in our experiment as observed in Table (4) different specific genes were selected to identify he genetic diversity between 28 mangos (*Mangifera indica)* cultivars. The first one was QGMI-001 and the homology traits for this gene were short vegetative phase (controlling flowering time) or floral development. This marker produced three alleles with size range 161 to 253 bp with genetic polymorphism 0.82%; the next six markers gave just one allele and related to different homology traits such as disease resistance gene (defence response), cis epoxy carotenoid dioxygenase 5 (abscisic acid biosynthesis); stress response, WRKY40 (transcription factor); defence response, Carotenoid cleavage dioxygenase 1 (carotenoid biosynthesis), IAA-leucine resistant 3 (transcription factor) and Phytochrome-associated protein 2

(plant development). The alleles size ranged from 110 to 240 bp. Data in Table (4) showed the present and absent amplified fragments for both SSR and EST-PCR markers for 28 mangoes cultivars. Dendrogram illustrating genetic relationships of 28 mango cultivars was generated using an unweighted pair-group method with arithmetic averages (UPGMA) and Jaccard's similarity coefficient. A cluster analysis based on genetic similarity estimates is shown in Figure 3. The dendrogram constructed from the matrix of simple matching coefficients revealed two major clusters with genetic similarity 46%. The first major bifurcation in the dendrogram (Figure 3) separated the 26 cultivars into two major clusters (56%). Cluster-I divided into sub-clusters (74%) includes Shelly, Golek (100%), Succari (87%), Alphonso (82%), Piva & Princess (87%). Cluster II (65%) divided into sub-clusters includes Nam Doc Mai and Sidik in separate sub-cluster (87%), Kent (80%), Hindi Besennara, R2E2, Tommy Atkins, Naomi (88%) and the other sub-cluster (80%) includes Zebda, Fajri Kalan (87%) and Heidi, Joa, Sensation, Lilly (87%). The third sub-cluster (68%) includes Sabre, Haden and Langra Benersi (81%) and Osteen, Maya, Hindi Mloki, Palmer (87%). While Kensington Bride and Yasmina were in separate cluster (74%).

Table (3). Primers, Annealing Temperature, allele's size and polymorphic microsatellite primers used in this study

No.	Primer	Annealing Temperature(℃)	No.of alleles	Allele size range (bp)	PIC
1	SSR- 16	54	2	169-235	0.77
2	SSR- 19	54	2	137-173	0.83
3	SSR- 52	52	1	199	100.0
4	SSR- 59	59	2	145-168	0.87
5	SSR- 65	53	1	154	100.0
6	SSR -83	57	2	157-183	0.71

Table (4). Characteristics of seven EST-SSR markers screened across 28 of *M. Mangifera cultivars*

Marker	GenBank Accession No	Repeat Motif	Homology	No. Alleles	Size Range	PIC
QGMI-001	JZ532296	(CCTTT)5	(floral development)	3	161-253	100
QGMI-003	JZ532319	(CTT)6	(defence response)	1	172	0.89
QGMI-004	JZ532302	(AAG)5	(abscisic acid biosynthesis; stress response)	1	227	0.88
QGMI-005	JZ532303	(AAC)8	(defence response)	1	315	0.75
QGMI-010	JZ532309	(AGG)4	(carotenoid biosynthesis)	1	240	0.80
QGMI-020	JZ532301	(CT)7	IAA-leucine resistant 3	1	110	0.82
QGMI-0023	JZ532311	(AAC)7	Phytochrome-associated protein 2	1	140	0.77

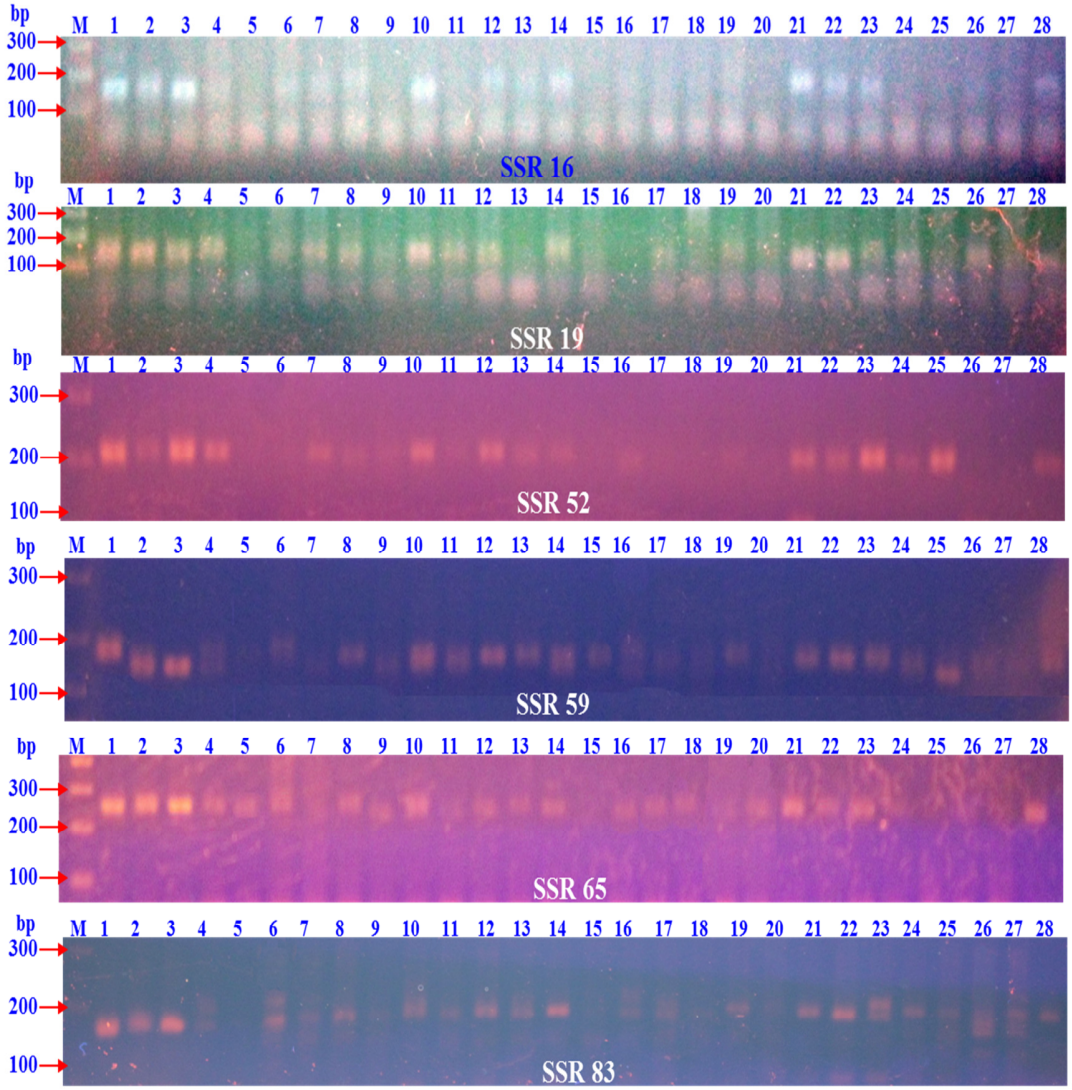

Figure (1). Amplification pattern of 28 mango cultivars generated by SSR-16, 19, 52, 59, 65 and 83 primers. M: Molecular weight marker (200 base pair DNA ladder in left).

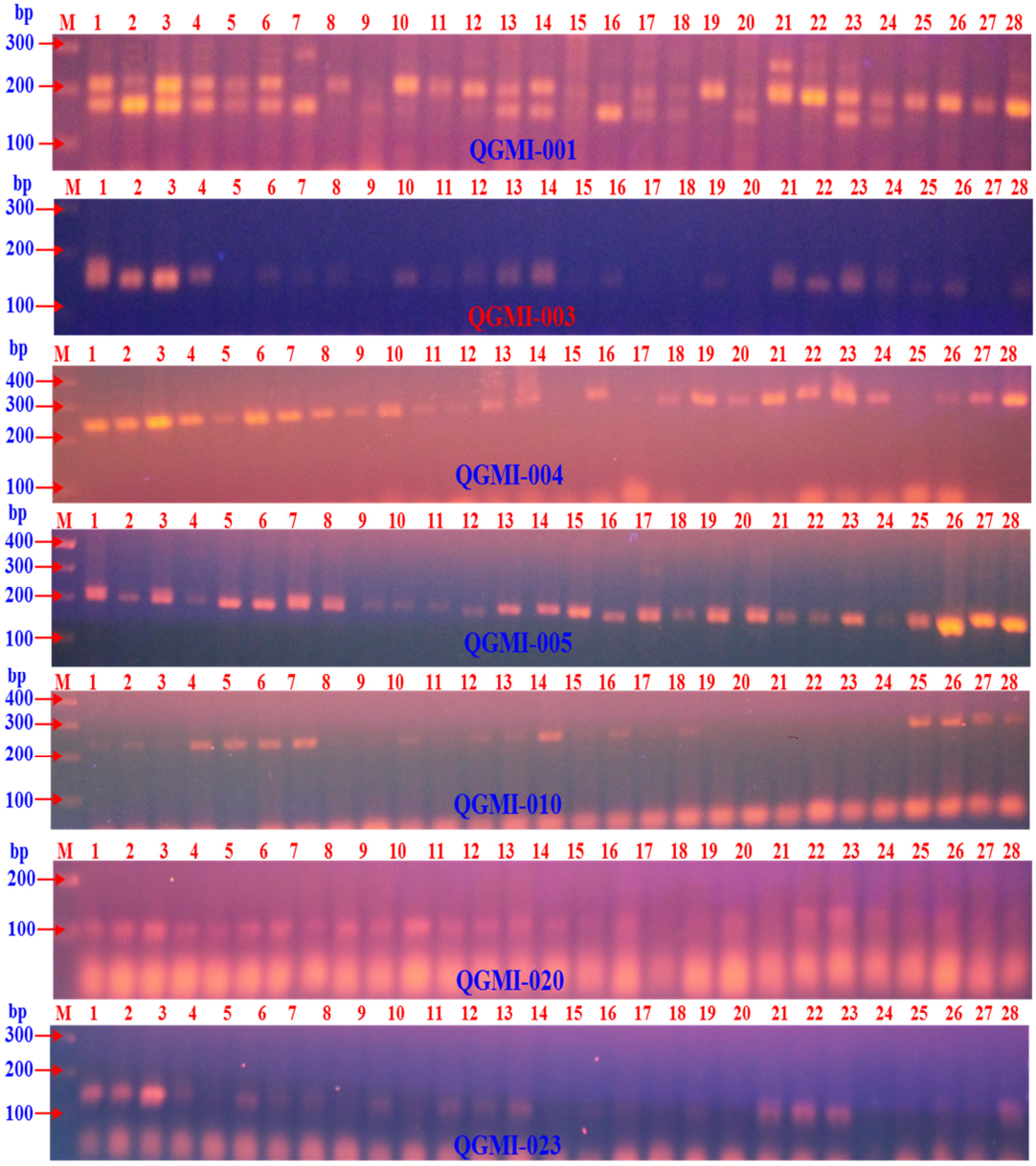

Figure (2). Amplification pattern of 28 mango cultivars generated by EST-01, 03, 04, 05, 10, 20 and 23 primers. M: Molecular weight marker (200 base pair DNA ladder in left).

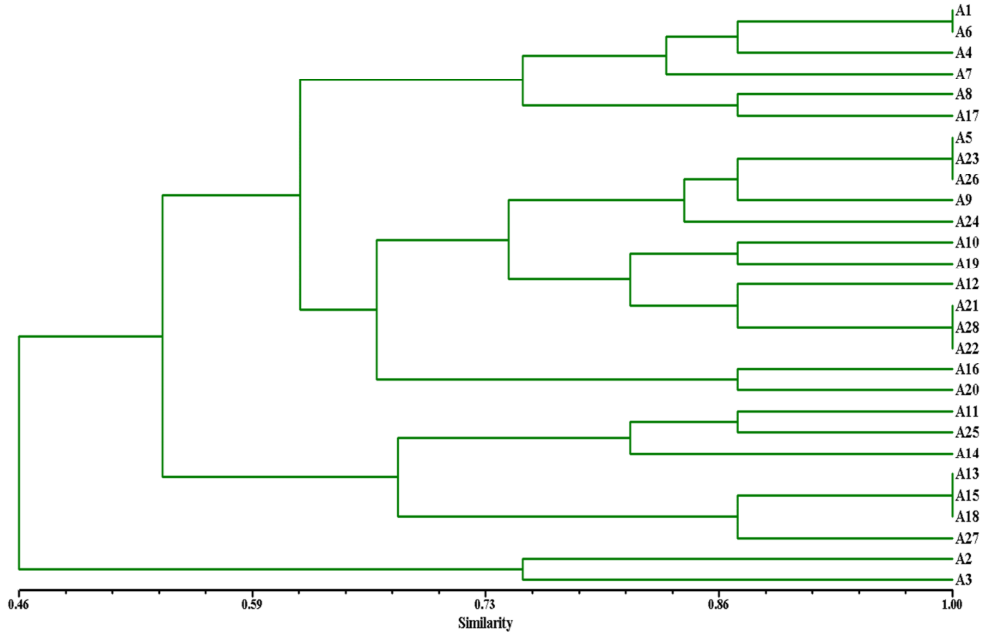

Figure (3). Dendrogram of mango cultivars obtained by UPGMA cluster analysis based on SSR and EST markers

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الملخص العربى

التوصيف الوراثى والبستانى لبعض اصناف المانجو اعتمادا على بعض الواسمات المختلفة

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تعتبر المانجو واحدة من أهم اشجار الفاكهة المنتشرة على مستوى العالم لما تتمتع بة من خصائص عالية وتقبل لدى المستهلك. وتحتوى المانجو على ٢٠ كروموسوم. فى الأونة الاخيرة إنتشرت الأنواع العديدة من المانجو المنزرعة حيث يوجد فى مصر حوالى ثمانية وعشرون نوع مانجو منزرع وذات جودة عالية وعلية كان الهدف من هذة الدراسة وهو دراسة الخصائص البستانية والجزيئية لتلك الانواع المنزرعة فى مصر بغرض إستخدامها فى برامج التربية المستقبلية. استخدمت فى هذة الدراسة ثمان صفات بستانية هامة مثل طول وعرض الثمار ووزن الثمار ونسبة اللب والقشرة وشكل الثمرة كما استخدم ثلاثة عشر واسمة متخصصة من المعلمات المتخصصة وهى SSR & EST لتوضيح مدى التقارب والبعد الوراثى بين تلك الانواع المستخدمة. اوضحت النتائج ان هناك اختلاف معنوى واضح بين تلك الأنواع موضوع الدراسة اعتمادا على خصائصها البستانية كما اظهرت النتائج ان هناك تعدد فى الاشكال المظهرية اعتمادا على معلمات تكرار التراكيب البسيطة والمتخصصة تراوحت من ٧١.٠ الى ١٠٠ %.

الكلمات الدالة: المانجو – الخصائص البستانية – التنوع الوراثى- البصمة الوراثية- الواسمات المتخصصة.