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A HIGH GENETIC SIMILARITY AMONG THE SELECTED MANGO (*MANGIFERA INDICA* L.) GENOTYPES-CULTIVARS DEMONSTRATED BY SSR FINGERPRINTING ASSAY

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ABSTRACT

Mango (*Mangifera indica* L.) is one of the most important fruit crops worldwide. Mango has a long history of cultivation in Indo-Pak region which resulted in the development of novel regional germplasm as well as many famous mango cultivars. For sustaining the mango production especially in the present scenario of changing climate, it is important to characterize and estimate the genetic divergence among the mango genotypes-cultivars germplasm. To the extent of our knowledge, little efforts have been made to explore the magnitude of genetic divergence among the mango genotypes-cultivars. In this study, the genetic diversity assessments among 32 including 25 local and 7 exotic genotype-cultivars have been calculated using thirty-five simple sequence repeat (SSR) markers. The most informative primer was found Micir-6 while the polymorphism information content (PIC) value of all SSRs was found low, *i.e.,* 0.168 - 0.5. Genetic diversity ranged from 15% to 47% among cultivars with a mean value 30%. The dissimilarity coefficients based unweighted pair group of arithmetic means (UPGMA) was used to make clusters. Mostly East Indian, North Indian and Pakistani cultivars were grouped in one cluster while South Indian and Florida cultivars in other according to the dendogram. The present study would help in taking proactive decision to buffer the spread of any epidemics and will also be helpful in initiating marker-assisted breeding program for developing cultivars with excellent genetics.

Keywords: Genetic Diversity, Indo-Pak, *Mangifera indica* L., SSR markers.

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INTRODUCTION

Mango is the significant and prevalent fruit crop and important cash crop produced about 40 Mt in 2012, is mainly grown in subtropical and tropical areas worldwide (Fig. 1). It is an allopolyploid species and a member of family Anacardiaceae (Jha *et al.,* 2010: Yamanaka *et al.,* 2019). Mango is rich in germplasm diversity having approximately 1600 varieties distributed in the world (Panday *et al.,* 1998; Yamanaka *et al.,* 2019). Worldwide, more than 75% mango is produced in China, India, Thailand, Mexico, Pakistan and Indonesia (Viruel *et al.,* 2005; Mitra 2016), while Pakistan is at fifth position in mango production (Maqbool and Malik, 2008; Baloch and Bibi, 2012).

In Pakistan, numerous biotic and abiotic factors resulted in the declined yield of mango. One important and recent risk to the Pakistan mango industry is the mango quick decline (Masood *et al.,* 2011). One of the most important element for helping breeders for making crosses is genetic diversity. Thus it helps breeders for an improved selection of appropriate parents to generate new breeding cultivars. An extended selection output could be attained with a greater information about the range of genetic diversity or genetic similarity inside the germplasm resources (Chowdhury *et al.,* 2002; Majumder *et al.,* 2013). A wider genetic base provides the fruit crops with the ability to produce the high yield under different agro-climatic conditions and also contains the capacity to resist the infectious diseases (Abou-Ellail *et al.,* 2014).

Furthermore, Variation for new assortments can be obtained from a rich germplasm (Rajwana *et al.,* 2008, 2011; Ab Razak *et al.,* 2019). Both categorization and assessment of the genetic diversity among varieties are most important factors to improve the quality of mango and sustainability in its production in the changing climate. In current years, a progressive utility of molecular genetic techniques using DNA-based analysis to depict and calculate genetic diversity and association among various genotypes, cultivars and advanced lines

was observed (Ravishankar *et al.,* 2015). Random amplified polymorphic DNA (RAPD) (Souza *et al.,* 2011; Pruthvish and Chikkaswamy, 2016), restriction fragment length polymorphism (RFLP), inter-simple sequence repeats (Pandit *et al.,* 2007; El Kheshin *et al.,* 2016), simple sequence repeat (SSR) (Kumar *et al.,* 2013; Oloka *et al.,* 2015: Nazish *et al.,* 2017) and amplified fragment length polymorphism (AFLP) (Galvez-Lopez *et al.,* 2009) are the mainly used DNA fingerprinting assays for the evaluation of genetic diversity between plant varieties (Rahman *et al.,* 2002, 2008 and 2012). A number of genetic diversity studies in mango genotypes-cultivars were carried out using RAPD markers (Rajwana *et al.,* 2008; Jena *et al.,* 2010) which are handicapped due to their poor reproducibility. Simple sequence repeats (SSRs) are considered the most promising because of their abundance, reproducibility, informativeness, co-dominance in expression and robustness (Pejic *et al.,* 1998; Hasan *et al.,* 2006: Yamanaka *et al.,* 2019; Ab Razak *et al.,* 2019).

Historically, several important cultivars-genotypes have been evolved in Pakistan. Indo-Pak to the Malay Peninsula in Southeast Asia is considered as area of origin of mango. It is also the center of diversity and evolution of mango because mango has been grown for more than 4000 years in this area (Yamanaka *et al.,* 2019). Preliminary study about genetic diversity among the available gene pools in Pakistan would not only help the mango breeder of Pakistan but would also add useful genetic information for the international mango breeding community. Thus by the use of SSR markers, the current investigation was designed to measure the extent of genetic dissimilarity and or similarity between the different cultivars in Pakistan. The data obtained would pave the way for developing mango cultivars with improved genetics.

MATERIALS AND METHODS

Plant Materials: Total thirty-two commercial mango genotypes-cultivars sourced from various Research |Institutes of Pakistan were included in the study. The morphological traits and geographical origin of genotypes-cultivars used in the current study is presented in Table -1.

Plant DNA Extraction: Two to three days old, fresh leaves grown on the young emerging branches were excised for DNA extraction. The leaves were stored at -70˚C (after washing with distilled water) in freezer until their use. A method (after doing slight modifications) proposed by Doyle and Doyle (1987) was used to extract total genomic DNA from each plant sample. Quality of the extracted genomic DNA was examined on 0.8% (w/v) agarose gel. The quantity of the DNA was measured on NanoDrop-1000 version 3.3.1 spectrophotometer (Nanodrop, USA).

Simple Sequence Repeat (SSR) Analysis: Thirty five SSR primer pairs selected from Micir and Mishrs series (Mishrs-1, Mishrs-4, Mishrs-21, Mishrs-22, Mishrs-39, Mishrs-44, Mishrs-37, Mishrs-34, Mishrs-33, Mishrs-36, Mishrs-48, Micir-1 to 6, Micir-8, Micir-9, Micir-11, Micir-12, Micir-14, Micir-16, Micir-18, Micir-20 to 22, Micir-24, Micir-25, Micir-29, Micir-30, Micir-33, Micir-36, Micir-28, Micir-34) were randomly selected across the mango genome.

The PCR reaction mixture included the reagents (Fermentas) (10 X PCR Buffer ($(NH_4)_2SO_4$+$MgCl_2$), $MgCl_2$ 50 mM, genomic DNA 2.0 µL (30 ηg/µL), 1.5 µL of reverse and forward primer with a concentration of 30 ηg/µL each, 4.5 µL of 0.2 Mm of total $dNTP_s$, and 0.3 µL *Taq* DNA polymerase (5 unit/µL). By adding ddH_2O final volume was kept 20 µL.

Amplification was carried out in Eppendorf Mastercycler (Germany). The sequence of the programme in Mastercycler was as one initial cycle at 94ºC for 5 min, followed by 35 cycles (each cycle was programmed for denaturation for 30 s at 94ºC, annealing for 30 s at 55ºC and extension for 1 min at 72ºC). One final temperature (extension) treatment at 72ºC for 10 min was given, and tubes were immediately removed or hold at 4ºC. PCR amplicons were fractionated on 4.0% (w/v) high resolution metaphor agarose gel and visualized on ultraviolet trans-illuminator. Gel pictures were captured with a gel documentation system.

Data Analysis: Amplicon size was determined by comparing them by running a standard marker (Gene Ruler 100 bp DNA ladder plus, Fermentas, USA). These amplicons were rated '1' if the amplicon was present otherwise '0'. Both types of amplicons *i.e.* reproducible amplicons were counted as polymorphic and monomorphic in the analysis. Some loci were considered as 'null' alleles as they could not be amplified even by repeating PCR reactions thrice in a few genotypes. The extent of diversity (Anderson *et al*.,, 1993) was measured by calculating PIC value for each SSR using the formula "PIC =1- Σ Pij^2". Here, Pij represents the frequency of "jth" allele for the "ith" locus cumulated across all alleles for the locus.

The data was used to measure the extent of genetic similarity using the number of common amplicons (Nei and Li, 1979). The dendrogram of 32 mango genotypes-cultivars was generated using the dissimilarity coefficients by deploying UPGMA.

RESULTS AND DISCUSSION

This study was conducted to investigate inter-varietal genetic diversity among 32 different mango cultivars using SSR markers. All SSRs produced

amplifications in all cultivars-genotypes (Fig 2). Twenty-eight primers (80%) yielded polymorphic bands. Total 1386 amplification products were produced and majority were polymorphic. On average, each SSR produced 38 DNA amplicons. Overall, 11 (39.3%) showed polymorphism because of amplification of alleles of diverse sizes, while 17 (60.7%) were polymorphic because they produced null alleles in few genotypes.

On average 38 amplicons per primer were produced. In another study, relatively few amplicons were reported while using 16 primer pairs on 28 mango genotypes (Viruel and Hormaza, 2004). Twenty-eight (80%) SSRs out of 35 were polymorphic depicting a high rate of polymorphism was similar to the findings of Kumar *et al.,* (2013). The higher ratio of polymorphic primers can be attributed to hyper variable nature of the SSR markers (Zhang *et al.,* 2014).

The range of PIC value was 0.5 (Micir 6) to 0.168 (Micir 16) with an average of 0.50. Micir 6 was the only highly informative marker with PIC value (0.5, Table 3). Ab Razak *et al.* (2019) found average PIC value 0.4585 during a study of genetic diversity of 116 mango genotypes using 20 polymorphic SSRs. The PIC value is an important factor which helps in choosing SSR markers to evaluate germplasm and gene tagging (Peng and Lapitan, 2004). Most informative SSRs can be selected with the help of PIC values and it is done by reducing the amount of SSR markers to calculate the genetic diversity (Tabassam *et al*., 2014), and can also enhance the potential of breeders for estimating the magnitude of genetic diversity and identification of varieties (Masi *et al.,* 2013: Jain *et al.,* 2004; Rajwana *et al.,* 2008).

The inconsistency in PIC values for different SSR primers is primarily because of number of repeat units and length of the SSR locus, and nature of germplasm under investigation (Tabassam *et al.,* 2014; Kebede *et al.,* 2007; Liu *et al.,* 2000a; Kalivas *et al.,* 2011). Also the bottleneck in evolution—contributed largely by the selection imposed by the farmers and breeders is another reason for finding low PIC value for the SSR loci (Thuillet *et al.,* 2004; Vigouroux *et al.,* 2005; Tabassam *et al.,* 2014) and the kind of DNA markers (Liu *et al.,* 2000b; Gutierrez *et al.,* 2002). Results of this study revealed a low PIC values [0.168 (Micir-16) to 0.5 (Micir-6)] for the markers used. The mean PIC value for Mishr and Micir primer series was 0.403 and 0.347 respectively, which was lesser than previous reports (Shareefa, 2000; Nayak, 2010). Particularly in Florida mango cultivars a minimum to medium PIC values of SSR markers were observed (Schnell, 2006). The lower PIC values can be one reason of low genetic diversity displayed in the used cultivars (Kumar *et al.,* 2013).

The range of variation in the genetic dissimilarity coefficients amid different cultivars-genotypes was from 0.15 to 0.47 with an average value of 0.30. Alphonso and Pope were found most genetically similar (85%) while Chaunsa and New Sindhri were least similar (53%) having 0.47 dissimilarity coefficient. In the whole experiment, Pope emerged as the maximum genetically similar genotype, showing 75% similarity with all cultivars-genotypes whereas the most diverse genotype was Sufaid Chaunsa (35% dissimilar or 65% genetically similar to the other genotypes-cultivars, Table 2). This study revealed a relatively great degree of genetic relatedness among the mango genotypes studied. The distribution and the geographical origin of the cultivars may be the one reason of this high level (70% on average) of genetic similarity. There is intense need to expand the genetic base of germplasm to overcome this similarity (Bally *et al.,* 1996). This high degree of genetic relatedness can be attributed to the convenience and usage of Chaunsa stones to develop nursery plants and further preferably unplanned seedling selection from the population. Furthermore, various cultivars like Sufaid Chaunsa and Kala Chaunsa are offshoots of Chaunsa because Chaunsa has been used as parent to develop new cultivars (Ahmad, 2007). Breeding programmes intensely need to have broad genetic base to minimize the dilemma of genetic similarity, which can be achieved by harnessing new cultivars in breeding programmes and amalgamation of local germplasm with exotic germplasm.

In current study, the minimum dissimilarity observed among the local cultivar Faiz Kareem and Taimuria is contrary to the earlier reports using RAPD assay (Rajwana *et al.,* 2008) which supported that Faiz Kareem is a derivative of Anwar Ratole and Chaunsa. Type of markers to assess the genetic diversity can be responsible for this disagreement as SSR markers are more robust than RAPDs (Garcia *et al.,* 2004). Moreover, validation of genealogy of Faiz Kareem need further extensive studies.

The dissimilarity matrix coefficients generated in the present study were used to develop a dendrogram using UPGMA cluster analysis (Fig. 3). The 32 genotypes-cultivars were grouped into two major clusters, 'A' and 'B'. The cluster A was further comprised of two sub-clusters 'A_1' and 'A_2'. Eight cultivars including Taimooria, Faiz Kareem, Sobhey de Ting, Late Ratole No.12, Anwar Ratole, Sufaid Chaunsa, S.B. Chaunsa (known as Chaunsa commonly), and Kala Chaunsa were included in sub-cluster A_1. While eight cultivars including Alphonso, Sindhri, Pope, Fajri, Sensation, Langra, Malda, and Lahootia were present in sub-cluster A_2.

Next major cluster, 'B', was further divided into two sub-clusters 'B_1' and 'B_2'. Sub-cluster 'B_1' included eight cultivars Sanglakhi, Neelum, Kensington Pride, Haden, Maya, Yakta, Totapari and Collector. Seven cultivars in sub-cluster 'B_2', including Dusehri, Tommy Atkins, Haider Shah, Began Palli, Zardalu, New Sindhri

and Keitt showed a sister group relationship. Another cultivar Swarnarekha was also grouped in Cluster B, which was genetically distinct from the genotypes-cultivars grouped in sub-clusters 'B_1' and 'B_2'.

In each sub-clusters of the cluster 'A', mango genotypes evolved in Pakistan, Northern Indian and North Eastern Indian origins grouped together. However, few Pakistani and Indian genotypes distributed in both the sub-clusters, indicating that these genotypes shared a common genetic origin. Sensation and Pope which are exotic cultivars were also grouped in cluster 'A' and is opposite to earlier studies (Rajwana *et al*., 2008) which indicates that these genotypes share common ancestry with the South Asian cultivars.

Majorly Florida and South Indian cultivars were included in Cluster 'B'. Keitt developed a sister group with Tommy Atkins in the sub-cluster B2 which can be attributed to their common geographical origin from Florida and depicts sharing a common ancestor of these cultivars. Uniqueness of South Indian cultivars from other Indian cutivars was also illustrated by the finding that Swarnarekha a South Indian cultivar occupied distinct place in cluster B. Presence of cultivars of Florida (Haden, Keitt and Tommy Atkins) in the same group with Indian cultivars validate the previous findings (Schnell *et al*., 2006). Presence of Maya and Haden in a close sister group confirms the development of Maya from the Haden's seedling (Viruel *et al*., 2005). New Sindhri cultivar (Khan Garh, Pakistan) which is thought to be a variant of Sindhri (Tharparker, Pakistan) was grouped in cluster B, interestingly. Among the morphological features, the genotypes that produce Oblong or Ovate shaped fruit clustered in A. While in cluster B, mostly the genotypes-cultivars produce round or ovate-shaped, while other traits are not showing a clear trend in grouping.

Table-1. Mango cultivars used for SSR analysis and their morphological characters.

Sr. No	Cultivar	Geographic origin	NLC	AFW	FS	Fiber	TSS
1	**Faiz Kareem**	**Multan, Pakistan**	**Yellowish green**	**290**	**Ovate Oblong**	**Absent**	**25–26**
2	Anwar Ratole	Northern India	Yellowish green	185	Round Ovate	Scanty	24–26
3	Chaunsa	Northern India	Yellowish green	350	Oblong Ovate	Medium	25–27
4	Taimooria	Northern India	Yellowish green	180	Oblong	Scanty	22–24
5	Kala Chaunsa	Multan, Pakistan	Light brown	300	Oblong	Much	25–27
6	Sanglakhi	Northern India	Light brown	400	Round Ovate	Absent	17–20
7	Sufaid Chaunsa	Multan, Pakistan	Yellowish green	500	Oblong Ovate	Scanty	24–26
8	Neelum	Southern India	Light Green	250	Ovate	Low	12-14
9	Late Ratole No 12	Multan, Pakistan	Dark green	200	Ovate	Medium	16-17
10	Alphonso	Western India	Medium green	200	Ovate to Cordate	Scanty	21-23
11	Langra	Northern India	Light Green	350	Ovate	Scanty	20-21
12	Yakta	Sindh, Pakistan	Lush Green	400	Ovalish oblong	Low	19-20
13	Dusehri	Northern India	Yellowish green	190	Oblong	Absent	24–26
14	Sindhri	Tharparker, Pakistan	Light brown	450	Oblong Ovate	Absent	17–20
15	Fajri	North Eastern India	Yellowish green	550	Oblong	Scanty	24–26
16	New Sindhri	Khan Garh, Pakistan	Light green with brownish ting	400	Narrowly ecliptic	Absent	14-17
17	Lahootia	Northern India	Yellowish green	220	Oblong Ovate	Scanty	24–25
18	Sobhey de Ting	Muzaffargarh, Pakistan	Yellowish green	125	Ovate Oblong	Scanty	18–20
19	Began Palli	Southern India	Light brown	500	Round Ovate	Scanty	20–22
20	Keitt	Florida, USA	Greenish	300	Round Ovate	Scanty	17–19
21	Tommy Atkins	Florida, USA	Light brown	400	Round Ovate	Scanty	17–19
22	Kensington Pride	Australia	Greenish	345	Round Ovate	Scanty	18–20
23	Maya	Israel	Greenish	335	Round Ovate	Scanty	20–21
24	Swarnarekha	Southern India	Greenish	500	Round Oblong	Scanty	22–24
25	Haider Shah	Muzaffargarh, Pakistan	Yellowish green	125	Ovate	Scanty	22–24
26	Totapari	Southern India	Medium green	400	Oblongish	Medium	15-16
27	Collector	Northern India	Yellowish green	400	Round Ovate	Medium	17–19
28	Zardalu	Eastern India	Greenish	260	Round Ovate	Scanty	20–21
29	Pope	Hawaii, USA	Brownish	385	Oblong Ovate	Scanty	17–18
30	Sensation	Florida, USA	Brownish green	250	Round Ovate	Scanty	17–18
31	Malda	India	Medium green	250	Broad oblongish	Scanty	12-14
32	Haden	Florida, USA	Medium green	400	Ovate	Low	17-18

Where, NLC = new leaf co
lor; AFW = average fruit weight; FS = fruit shape; TSS = total soluble solids.

Table-2. Dissimilarity matrix of 32 mango genotypes-cultivars using 35 SSR primer pairs.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
1	0																															
2	0.23	0																														
3	0.23	0.33	0																													
4	0.17	0.23	0.23	0																												
5	0.29	0.24	0.24	0.21	0																											
6	0.3	0.29	0.29	0.29	0.29	0																										
7	0.26	0.3	0.21	0.3	0.24	0.29	0																									
8	0.26	0.27	0.33	0.3	0.3	0.29	0.3	0																								
9	0.26	0.18	0.33	0.3	0.3	0.29	0.21	0.21	0																							
10	0.27	0.23	0.32	0.29	0.29	0.27	0.32	0.23	0.26	0																						
11	0.27	0.32	0.29	0.32	0.38	0.33	0.29	0.29	0.29	0.27	0																					
12	0.29	0.21	0.42	0.27	0.24	0.38	0.3	0.27	0.24	0.32	0.32	0																				
13	0.33	0.23	0.35	0.29	0.26	0.36	0.38	0.32	0.29	0.36	0.33	0.26	0																			
14	0.36	0.23	0.38	0.35	0.32	0.3	0.38	0.23	0.26	0.18	0.3	0.26	0.24	0																		
15	0.26	0.3	0.27	0.27	0.33	0.32	0.33	0.24	0.27	0.23	0.26	0.3	0.26	0.26	0																	
16	0.33	0.29	0.47	0.29	0.41	0.39	0.5	0.26	0.32	0.33	0.39	0.32	0.3	0.18	0.29	0																
17	0.45	0.26	0.26	0.38	0.26	0.33	0.38	0.29	0.32	0.3	0.33	0.38	0.3	0.27	0.26	0.36	0															
18	0.3	0.17	0.26	0.29	0.26	0.3	0.32	0.32	0.17	0.3	0.27	0.26	0.24	0.27	0.29	0.33	0.21	0														
19	0.38	0.36	0.36	0.36	0.42	0.29	0.39	0.33	0.39	0.41	0.29	0.42	0.29	0.35	0.3	0.32	0.35	0.32	0													
20	0.32	0.33	0.33	0.33	0.36	0.32	0.39	0.24	0.36	0.29	0.29	0.39	0.29	0.29	0.21	0.29	0.32	0.32	0.21	0												
21	0.41	0.27	0.42	0.27	0.36	0.29	0.42	0.27	0.3	0.35	0.35	0.33	0.26	0.23	0.3	0.29	0.32	0.32	0.27	0.24	0											
22	0.41	0.3	0.36	0.33	0.27	0.2	0.42	0.27	0.3	0.32	0.41	0.3	0.26	0.29	0.33	0.35	0.32	0.23	0.24	0.3	0.24	0										
23	0.39	0.29	0.35	0.29	0.29	0.24	0.32	0.26	0.32	0.33	0.42	0.32	0.3	0.27	0.29	0.27	0.33	0.33	0.32	0.32	0.29	0.29	0									
24	0.42	0.38	0.35	0.41	0.41	0.27	0.32	0.32	0.29	0.39	0.27	0.38	0.36	0.3	0.32	0.3	0.3	0.3	0.26	0.35	0.29	0.32	0.3	0								
25	0.39	0.32	0.35	0.32	0.32	0.36	0.47	0.29	0.32	0.36	0.33	0.35	0.24	0.3	0.29	0.24	0.24	0.21	0.29	0.26	0.26	0.23	0.27	0.3	0							
26	0.42	0.23	0.44	0.32	0.32	0.3	0.41	0.26	0.35	0.3	0.36	0.29	0.33	0.27	0.38	0.33	0.3	0.3	0.32	0.29	0.26	0.26	0.27	0.33	0.3	0						
27	0.35	0.21	0.45	0.33	0.3	0.32	0.42	0.27	0.33	0.29	0.38	0.18	0.32	0.2	0.33	0.23	0.32	0.35	0.33	0.33	0.3	0.27	0.26	0.35	0.29	0.2	0					
28	0.38	0.27	0.3	0.3	0.33	0.32	0.45	0.33	0.39	0.38	0.35	0.3	0.26	0.29	0.36	0.26	0.29	0.26	0.24	0.27	0.24	0.27	0.38	0.32	0.23	0.32	0.27	0				
29	0.33	0.29	0.35	0.35	0.32	0.36	0.35	0.26	0.29	0.15	0.24	0.26	0.3	0.18	0.23	0.27	0.33	0.3	0.38	0.23	0.35	0.38	0.3	0.36	0.27	0.33	0.29	0.29	0			
30	0.35	0.3	0.33	0.33	0.39	0.38	0.39	0.33	0.3	0.26	0.23	0.42	0.35	0.23	0.21	0.32	0.26	0.29	0.36	0.27	0.27	0.39	0.35	0.32	0.26	0.38	0.36	0.36	0.26	0		
31	0.27	0.26	0.35	0.29	0.32	0.36	0.32	0.26	0.2	0.24	0.27	0.2	0.27	0.18	0.17	0.24	0.3	0.21	0.41	0.29	0.26	0.35	0.39	0.3	0.33	0.33	0.32	0.32	0.21	0.26	0	
32	0.36	0.29	0.41	0.29	0.35	0.27	0.41	0.23	0.32	0.36	0.33	0.23	0.3	0.3	0.29	0.3	0.39	0.33	0.26	0.29	0.23	0.2	0.21	0.33	0.3	0.21	0.26	0.29	0.3	0.38	0.3	0

Note: The numbers indicate the mango cultivars as under: 1= Faiz Kareem, 2= Anwar Ratole, 3= Chaunsa, 4= Taimooria, 5= Kala Chaunsa, 6= Sanglakhi, 7= Sufaid Chaunsa, 8= Neelum, 9= Late Ratole No 12, 10= Alphonso, 11= Langra, 12= Yakta, 13= Dusehri, 14= Sindhri, 15= Fajri, 16= New Sindhri, 17= Lahootia, 18= Sobhey de Ting, 19= Began Palli, 20= Keitt, 21= Tommy Atkins, 22= Kensington Pride, 23= Maya, 24= Swarnarekha, 25= Haider Shah, 26= Totapari, 27= Collector, 28= Zardalu, 29= Pope, 30= Sensation, 31= Malda and 32= Haden

Table-3. Number of alleles amplified, allele frequency and PIC values of the selected SSR primer pairs.

Marker	No. of alleles	Allele frequency	PIC value
Micir-5	2	0.719, 0.281	0.404
Micir-6	2	0.5, 0.5	0.5
Micir-14	2	0.25,0.75	0.375
Micir-16	2	0.093, 0.907	0.168
Micir-22	2	0.25,0.75	0.375
Micir-25	2	0.157,0.843	0.265
Micir-33	2	0.219, 0.781	0.342
Mishrs-48	2	0.219, 0.781	0.342
Mishrs-21	2	0.312,0.688	0.429
Mishrs-22	2	0.75, 0.25	0.375
Mishrs-36	2	0.625,0.375	0.469

Figure-1. Countries (indicated by asterisk) producing substantial mango production worldwide.

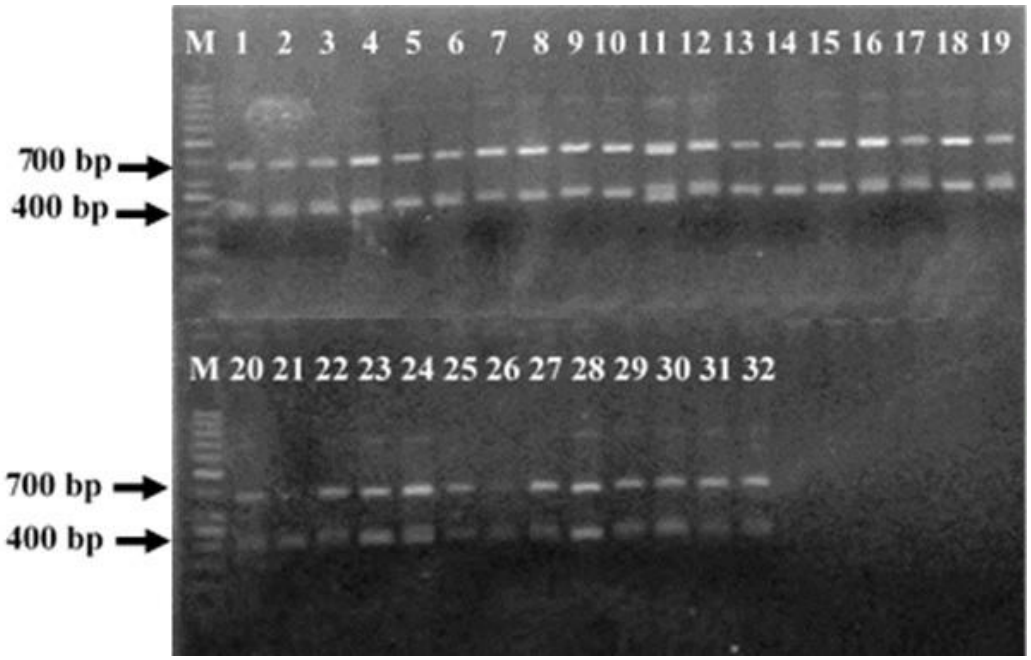

Fig. 2. SSR profile of mango germplasms generated by primer Micir 30 (M=500 bp ladder, 1 to 32 mango genotypes)

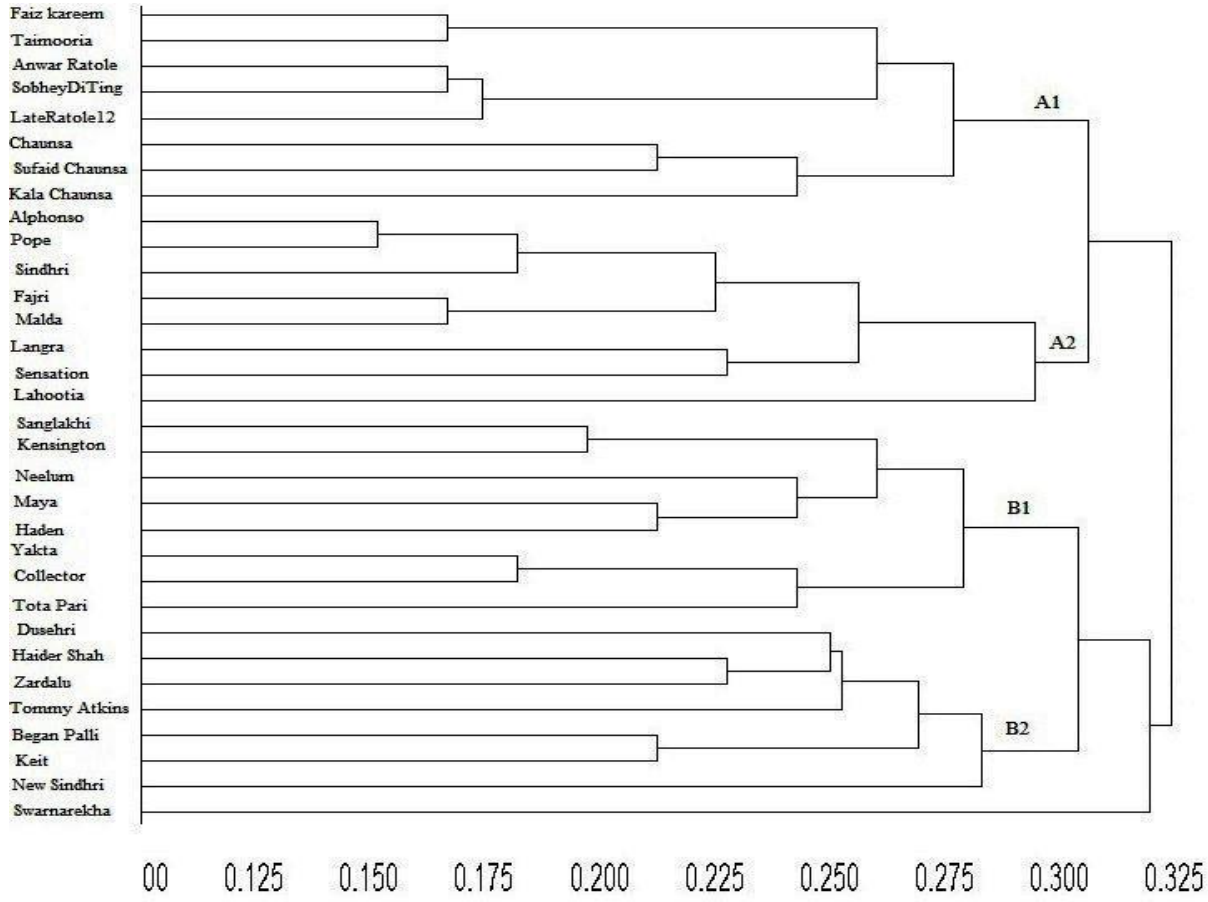

Figure-3. Dendrogram of 32 mango genotypes-cultivars based on UPGMA analysis using Euclidean dissimilarity matrix.

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