Study of Genetic variation in *Mangifera indica* L. using SSR marker in Vindhyan region of Madhya Pradesh

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Abstract:

Mango (*Mangifera indica* L.) is the most important commercial fruit of India and belongs to the family anacardiaceae. The morphological and physico-chemical traits such as tree, leaf, and inflorescence and fruit characteristics are influenced by environmental factors and caused numerous synonyms. The DNA fingerprints, resembling barcodes, are unique to the individual and hence can be utilized in much the same way as conventional fingerprints to identify individuals with absolute certainty. Fingerprinting a vast number of mango cultivars is a significant contribution to mango cultivation, as presently several mango cultivars have many synonyms in different regions, which make identification difficult and create confusion. Simple Sequence Repeat (SSR) markers, also known as microsatellites, are tandemly repeated motifs of 1-6 nucleotides found in all prokaryotic and eukaryotic genomes.

Similarity coefficients for the 16 mango accessions based on 10 SSR markers. Pair-wise association among 16 mango accessions, showed the highest Distance value 1.51 and the lowest Distance value 0.612. The Cophenetic Correlation among 16 mango verities is 0.7167. The highest polymorphism 90% was observed in primer L7. The dendrogram showing the genetic relationships among 16 accessions based on SSR markers is presented in NCSS dendrogram report. The dendrogram showed four major clusters A, B, C and D. The highest similarity index is 0.875 between AbAPSU1 and Bombai. Dendrogram revealed that the genotypes could be grouped into four clusters. The dendrogram showed four clusters in which A and B at 16.7% similarity. Whereas cluster C and D similar as 37.5%. The measurement of similarity index of mango germplasm, ranged from 0.111 to 0.875 according to the genetic affinity were generated by Jaccard's coefficient.

Keywords: *Mangifera indica* L., SSR, Jaccard's coefficient, Genetic diversity.

Introduction:

Mango (*Mangifera indica* L.) is the choicest fruit of India and occupies a prominent place among the best fruits of the world. It is widely grown in the tropical and subtropical regions world over. India has rich mango varietal wealth and the country has the richest wealth of mango germplasm in Southeast Asia. Reportedly, there are over 1,000 varieties of mango found in India. However, there is a lot of confusion in nomenclature of the mango cultivars noted that lack of systematic approach in naming of mango cultivars in the past has resulted in a great confusion in their nomenclature due to many synonyms and duplication of names in

the absence of any rules governing nomenclature ***(Mukherjee SK, 1951; Singh AK, 1996; Kaur M, et. al. 2014).***

The traditional commercial mango varieties of India suffer from notable drawbacks like alternate bearing, mango malformation, spongy tissue and poor shelf-life which impose limitations on their profitable cultivation. So as to conquer these obstructions, different focuses in India started mango reproducing projects to create unrivaled high yielding half and halves free from the above deformities. Mukherjee SK, et al. were the first to escribe between varietal hybridization in mango with 1.45 percent achievement. These cross breeds have numerous attractive highlights, for example, intelligence, productive and customary bearing, better keeping quality and diminutive person plant stature ***(Singh AK, 1996).*** Amrapali has risen as the excellent selection of farmers in the nation especially in the eastern states. Additionally, mango half and half Mallika is ending up exceptionally famous among the ranchers in Karnataka and Maharashtra ***(Mukherjee SK et al. 1961; Singh AK, 1996).***

A striking component of Indian mango indusry is the unimportant nearness of Indian exporters in world mango showcase. Noticed that in spite of the fact that the global exchange mango was expanding quickly, India kept on lingering behind in complete mango sends out when contrasted with other trading nations like Mexico, Philippines and Venezuela. In spite of the fact that there is an immense potential for fare to western nations, imperatives like reasonableness of a couple of assortments for fare, nuisances and illness issues have limited the extension of the fares from India. Evacuation of a portion of the imperatives will build the potential for fares to USA and Japan ***(Campbell RJ and Zill G, 2009; Ganogpichayagrai A et. al. 2016).***

The DNA fingerprints, looking like scanner tags, are one of a kind to the individual and subsequently can be used similarly as regular fingerprints to distinguish people with outright assurance. Fingerprinting an immense number of mango cultivars is a huge commitment to mango development, as by and by a few mango cultivars have numerous equivalent words in various districts, which make recognizable proof troublesome and make perplexity. Simple Sequence Repeat (SSR) markers, also known as microsatellites, are tandemly repeated motifs of 1-6 nucleotides found in all prokaryotic and eukaryotic genomes ***(Zane L et al., 2002).*** Microsatellites, with a polymorphism dependent on various quantities of rehashed themes at a given locus, are getting to be markers of decision in many organic product reproducing programs since they are multi-allelic and agreeable to mechanization. Notwithstanding their value in mapping and rearing, have turned into the markers of decision for fingerprinting purposes in most plant species ***(Gupta MN and Varshney RS, 2000),*** because of their high polymorphism, co-dominance and reproducibility. Of the different sub-atomic methods that are utilized for fingerprinting, microsatellite or Simple Sequence Repeat (SSR) markers are generally utilized in numerous regions of harvest improvement on account of the high fluctuation in the quantity of rehash units. These markers have a few focal points over other hereditary markers since they can be scored unambiguously and results are profoundly reproducible (***Zane L et al., 2012; Gupta MN and Varshney RS, 2000; Kumar M et. al., 2015).***

Mango (Mangifera indica L.) is the most important commercial fruit of India and belongs to the family anacardiaceae. The morphological and physico-chemical traits such as tree, leaf, and inflorescence and fruit characteristics are influenced by environmental factors. It is most imperative to characterize the promotions into their homogeneous gatherings based on multivariate parameters as opposed to utilizing univariate strategy to

recognize the nature and structure of assortments and to stay away from duplicacy of increases. A significant method to expand efficiency in any organic product yield is to initially choose alluring cultivars from existing variety and to utilize the unrivaled sorts for crop improvement programs. In this way, Therefore, Qualitative attributes, Genetic Variability and Character Association are fundamental for better utilization of assortments/genotypes in crop improvement program ***(Krishnapillai, N and Wijeratnam WRS, 2016; Singh A. et. al. 2016; Rao CR et. al. 1964).***

Mango (Mangifera indica L.) is known as the 'ruler of natural products' for its rich taste, season, shading, generation volume and differing end use. It has a place with plant family Anacardiaceae and has a little genome size of 439 Mb (2n = 40). Antiquated writing demonstrates source of developed mango in India. Albeit wild types of variety Mangifera are appropriated all through South and South-East Asia, recuperation of Paleocene mango leaf fossils close Damalgiri, West Garo Hills, Meghalaya point to the source of class in peninsular India before joining of the Indian and Asian mainland plates. India delivers in excess of 50% of the world's mango and develops in excess of thousand assortments. In spite of its tremendous financial criticalness genomic assets for mango are restricted and hereditary qualities of valuable plant attributes are ineffectively comprehended. Here we present a short record of our ongoing endeavors to create genomic assets for mango and its utilization in the investigation of hereditary decent variety and populace structure of mango cultivars ***(Aliyu, OM 2014; Ahman, M L, et. al. 2014).***

Materials & Methods:

The experiment on ‘‘Classification of different varieties and new accessions of mango (*Mangifera indica* L.) based on qualitative traits and assessment of genetic diversity’’ was carried out at Centre for Biotechnology studies, A.P.S. University Rewa (M.P.) and Department of Horticulture, College of Agriculture, Rewa (M.P.). The experimental material comprised of 16 well known varieties. The grouping of mango varieties/accessions by using assessment of genetic diversity.

Experimental Materials:

The experimental materials for present investigation were comprised of 16 mango varieties including new accessions, which are being maintained at Centre for Biotechnology studies, A.P.S. University Rewa (M.P.) and Department of Horticulture, College of Agriculture, Rewa (M.P.). The list of varieties including new accessions considered for present investigation during the years 2014 to 2018 has been given in Table No.1.

Table No. 1:

List of varieties including new accessions of mango considered for experiment

S.No.	Varieties/accessions	S.No.	Varieties/accessions
1.	Bombai	9.	Alphanso
2.	AbAPSU-1	10.	Chousa
3.	Dashehari	11.	AbAPSU-3
4.	Dalma	12.	Neeludin
5.	Langra	13.	AbAPSU-4
6.	Baramasia	14.	Sabri
7.	AbAPSU-2	15.	AbAPSU-5
8.	Vanraj	16.	Fajri

The investigation was carried out during 2014-2018 at Experimental Field of Horticulture department at Centre for Biotechnology studies, A.P.S. University Rewa and Department of Horticulture, Govt. Agriculture college Rewa (M.P.). The experiment consisted of 24 treatments i.e., Bombai, AbAPSU-1, Dashehari, Dalma,

Langra, Baramasia, AbAPSU-2, Vanraj, Alphanso, Chousa, AbAPSU-3, Neeludin, AbAPSU-4, Sabri, AbAPSU-5, Fajri. The site enjoys an average annual rainfall 34.9 mm. The mean maximum and minimum temperature are 31.08 0C and 17.34 0C, respectively. The soils were classified as slightly alkaline with 7.65 pH. Data were collected on morphological (qualitative) characters using character descriptors.

Genetic Variability:

Accumulation and handling of leaf material:

For every genotype, 5 g of flushing, delicate and sound leaves from single tree of each increase were culled, placed into named polyethylene packs and put in a refrigerator. On arriving at the research facility, leaves were washed under faucet water and cleaned with tissue paper. The midribs and thick veins of the leaves were evacuated. Tests were enveloped by aluminum foil, marked appropriately, fixed by plunging quickly in fluid nitrogen and put away at – 80 0C till DNA extraction.

DNA separation:

Genomic DNA was removed by the cetylhexadecyl-trimethyl ammonium bromide (CTAB) technique (Saghai-Maroof et al., 1984) with minor alterations (Porebski et al. 1997; Khanuja et al. 1999). Basically, the extraction cradle organization was 4% w/v C TAB, 1.4M NaCl, 100mM Tris-HCl (pH-8), 20mM EDTA, I% PVP w/v and 0.2% â mercaptoethanol. The arrangements, officials and instruments utilized are depicted in Annexure I. Leaf tests were ground to fine powder in pre-cooled mortar and pestle in fluid itrogen. Powdered leaf material was immediately moved to axis cylinders containing 20 ml pre-warmed CTAB extraction cradle and vortexed to scatter the tissue powder. The cylinders were then brooded at 65^0C for 60 minutes, with irregular shaking. Toward the finish of the hatching, tubes were cooled to room temperature and 15 ml chloroform: isoamyl liquor (24:1) was included, after which blending of substance by reversal was completed for around 10 minutes. The examples were then centrifuged at 250C for 15 minutes at 12,000 rpm. The supernatant fluid stage, containing nucleic acids was pipetted out into crisp rotator tubes. Nucleic acids were encouraged by including half volume of NaCl (Porebski et al., 1997) and one volume of chilled isopropanol (Khanuja et al., 1999) and giving it a chance to represent a couple of hours at 4 0C (Porebski et al., 1997). To help the precipitation, the cylinders were spun at 10 0C for 10 minutes at 10,000 rpm. The subsequent supernatant was disposed of and DNA pellet was given two 70% ethanol washes and a last wash with outright ethanol. The fluid part was emptied and the pellet was dried free of ethanol. The DNA was broken up in 1 ml TE cradle.

DNA purification:

The disintegrated DNA was moved to 2ml eppendorf tubes; 2µl of RNase A (25 mg/ml) was included and brooded for 1 hour at 37 0C. In this manner, DNA was treated with an equivalent volume of phenol: chloroform: isoamyl liquor (25:24:1 blend) and blended the substance by delicate twirling for 5 minutes. The cylinders were centrifuged at 10,000 rpm for 5 minutes and the supernatant was gathered in a crisp cylinder. This was trailed by two extractions with chloroform: Isoamyl liquor (24:1). Without rna, refined DNA was hastened by including 0.1 volume sodium acetic acid derivation and 2.5 volumes chilled isopropanol to the

watery stage and afterward gathered by turning at 12,000 rpm for 15 minutes. The accelerate was washed twice with 70 % ethanol, air-dried and broke down in TE cushion and put away at - 20 0C.

DNA measurement:

For DNA measurement, the secluded DNA was kept running in 0.8% agarose gel. Agarose gel was set up by liquefying 0.8 g of agarose in 100 ml of 1X TBE. After cooling, ethidium bromide was included at the pace of 0.5 µg/ml and the substance weregently twirled and poured in a gel throwing plate with an appropriately put brush. Polymerization of gel was took into consideration 30 minutes, after which the brush was taken out cautiously with no harm to the wells. The gel was moved to an electrophoresis tank having proper amount of 1X TBE cushion. Two µl of stacking color 1 x was added to each example tube after consummation of filtration. The sanitized DNA tests were stacked into the gel wells with phage DNA as a control. Electrophoresis was completed in 1 x TBE cushion at 50 V for 60 minutes, for example till the bromophenol blue color voyaged under 2/3 of the gel length. The gel envisioned under UV light on an UV-transilluminator and shot by utilizing Polaroid Gelcam and Digital DC-40. The amount of DNA evaluated in the example by its examination with the control phage DNA by visual judgment. Minimized band at the relating position to phage DNA showed tallness and weight of DNA.

SSR Analysis:

Determination of Primer:

The groundworks utilized for the examination were 15 microsatellites loci from mango detailed by Schnell et al. (2005) and 10 microsatellites by Viruel et al. (2006). Rundown of groundworks utilized alongside their groupings are given in Table 3.2. The preliminary was given by the maker in a lyophilized structure. In light of the sub-atomic load of a given preliminary, a stock arrangement of 100 M was set up by including the necessary measure of TE support and the stock was kept at – 20oC. From the stock arrangement, a working example was set up by including 5µl groundwork arrangement and 95 µl autoclaved refined water.

Streamlining of PCR conditions for Simple Sequence Repeats (SSRs):

Variety in format DNA groundwork, MgCl2 and Taq DNA polymerase affected DNA enhancement. To decide ideal enhancement response conditions, a factorial investigation was led wherein PCR was completed at two groupings of MgCl2 (1µl and 2 µl), two centralizations of Taq DNA polymerase (0.5 U and 0.75 U), three convergences of layout DNA (10 ng, 25 ng and 50 ng) and 2.5 µl preliminary (forward and switch each) in a volume of 15 µl at various toughening temperatures. PCR was completed in Perkin Elmer 9,600 Thermocycler (USA). 25 ng of layout DNA per response blend was found to yield ideal enhancement for SSR groundworks. In light of the consistency of groups, the ideal centralization of PCR parts was institutionalized.

PCR amplification:

Following the analyses for improvement of part fixations, PCR enhancement was done with 25 ng of genomic DNA, 2µl MgCl2, 0.75 U Taq DNA olymerase, 1x PCR cushion without MgCl2, 1.25 µl of every one of preliminaries and 200 µM of dNTPs. The volume was made up to 15 µl with sterile refined water. PCR cylinders containing the above parts were topped and centrifuged at 10,000 rpm for 2 minutes to permit

legitimate settling of response blend. Thermocycling was done in a PE-Thermocycler. Thermocycling conditions were as per the following:

1. Denaturation at 950C for 5 minutes.
2. Denaturation (35 cycles) at 940C for 1 moment, preliminary toughening at 550C for 1 moment and groundwork augmentation at 720C for 2 minutes.
3. Last augmentation step at 720C for 10 minutes at 40C.

Gel electrophoresis:

Gel planning:

PCR intensified items were kept running in 4% high goals agarose (Metaphor) gels. Fitting amount of agarose and 1X TBE cushion were blended altogether and bubbled for around 2 minutes to break down the substance. The blend was cooled to 500C and 2µl ethidium bromide 1mg/ml arrangement) was included per 100 ml gel. Liquid gel was thrown in a gel plate with proper brush. Polymerization of the gel was took into consideration 30 minutes after which the brush was taken out cautiously. The gel was moved to an electrophoresis tank having a proper amount of 1X TBE cradle.

Electrophoresis:

Two µl stacking color (Annexure I) was added to each PCR cylinder containing intensified items and stacked in the openings of the representation agarose gel. 2.5 µl GeneRulerTM (100 bp stepping stool) was stacked in the main path of each gel to decide sizes of distinguished groups. Electrophoresis was completed at 5 V/cm for 2.5 hours. The gels were captured on an UV transilluminator utilizing a Polaroid camera.

Information scoring and investigation:

Each band was treated as one SSR marker. Scoring of groups was done from the photos. Homology of groups depended on their movement separation in the gel. The nearness of a band was scored as '1', nonattendance of a band as '0' and missing datum was indicated by '9'.

Jaccard's closeness coefficient (J):

The Jaccard's closeness coefficient (J) was utilized to compute the similitude between pair's promotions (Jaccard, 1968).

$J = y/n – d$

Where,

y = Number of groups regular to test an and b

n = Total number of groups present in all examples

d = Number of groups not present in an or b, however present in different examples

The hereditary relationship between promotions were assessed by ascertaining the Jaccard's comparability coefficient for pair savvy correlations dependent on the extent of shared groups delivered by the preliminaries.

3.22. Heterozygosity (H):

Heterozygosity is the widely used measure of the allelic diversity or informativeness of a genetic marker. The informativeness of a genetic marker increases as the heterozygosity increases. In outbred populations, heterozygosity estimates the probability that a randomly sampled individual is heterozygous.

3.23. Polymorphism information content (PIC):

The basic information that determines their application in genetic mapping of both the marker system was calculated for each marker by using the PIC (Lynch and Walsh, 1998).

Result:

SSR Fingerprinting:

Analysis of 16 mango hybrids with 10 SSR primer pairs identified. The fingerprint pattern of the 16 mango hybrids based on the present and absent of SSR markers is illustrated in table no.2. We analyzed distinguished unambiguously using the combined molecular profiles from 10 primer pairs. Number of fingerprints generated, number of unique fingerprints and probability of identity of SSR markers are presented in the Table no. 11. The fingerprints generated by individual SSR primers ranged from 2 to 12. Highest PIC value was generated by primer **L7**.

Table No. 2

Selected Primer sequence and their PIC of Locus

Locus	Primer Sequence	Heterozygosity (H)	Polymorphic Information Content (PIC)
L1	F: TAACAGCTTTGCTTGCCTCC R: TCCGCCGATAAACATCAGAC	**0.044**	**0.073**
L2	F: AAACGAGGAAACAGAGCAC R: CAAGTACCTGCTGCAACTAG	**0.256**	**0.144**
L3	F: AGGTCTTTTATCTTCGGCCC R: AAACGAAAAAGCAGCCCA	**0.313**	**0.265**
L4	F: CAACTTGGCAACATAGAC R: ATACAGGAATCCAGCTTC	**0.042**	**0.041**
L5	F: AGAATAAAGGGGACACCAGAC R: CCATCATCGCCCACTCAG	**0.238**	**0.171**
L6	F: TTGATGCAACTTTCTGCC R: ATGTGATTGTTAGAATGAACTT	**0.440**	**0.251**
L7	F:CGAGGAAGAGGAAGATTATGAC R: CGAATACCATCCAGCAAAATAC	**0.321**	**0.298**
L8	F:CGAGGAAGAGGAAGATTATGAC	**0.067**	**0.042**

	R: CGAATACCATCCAGCAAAATAC		
L9	F: CTCGCATTTCTCGCAGTC R: TCCCTCCATTTAACCCTCC	**0.484**	**0.249**
L10	F: GAACGAGAAATCGGGAAC R: GCAGCCATTGAATACAGAG	**0.117**	**0.023**

Agaroge gel electrophoresis analysis reveals locus of SSR primer (L1 to L10). Four maximum PIC value containing primers L7, L3, L6 and L9 are highly polymorphic (depicted in Figure No. 7, 8, 9 and 10). L7 locus shows 200 bp bands in 12 mango varieties. Thus all selected primer for specific SSR marker give amplified bands help to make dendrogram graph generated by Jaccard's coefficient.

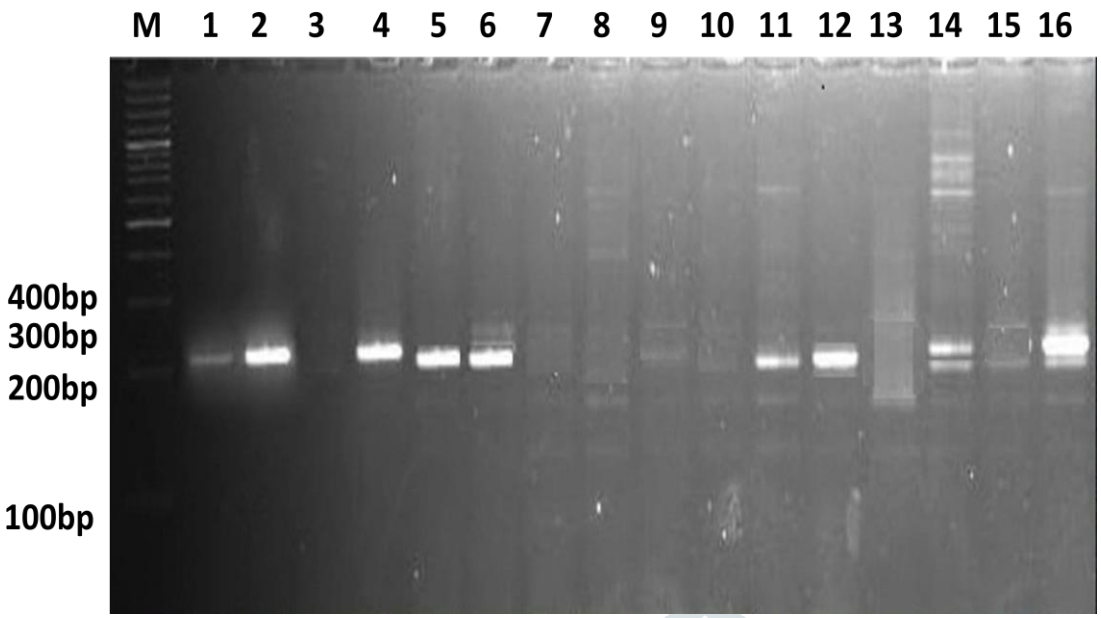


Figure No. 1: Amplification profile of mango hybrids using the primer **L3.**

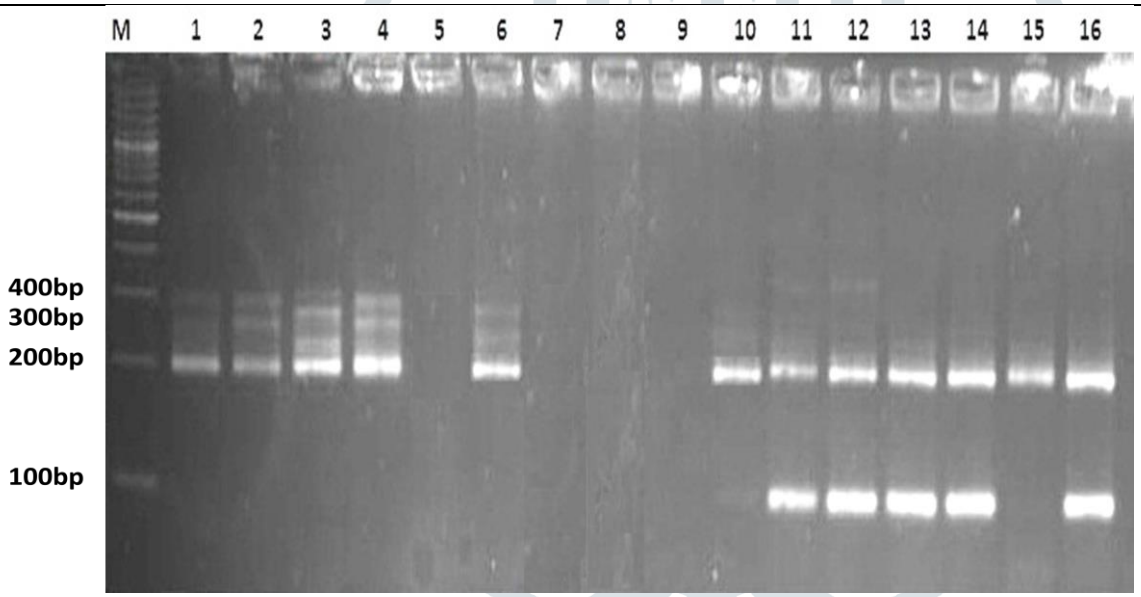


Figure No. 2: Amplification profile of mango hybrids using the primer **L7.**

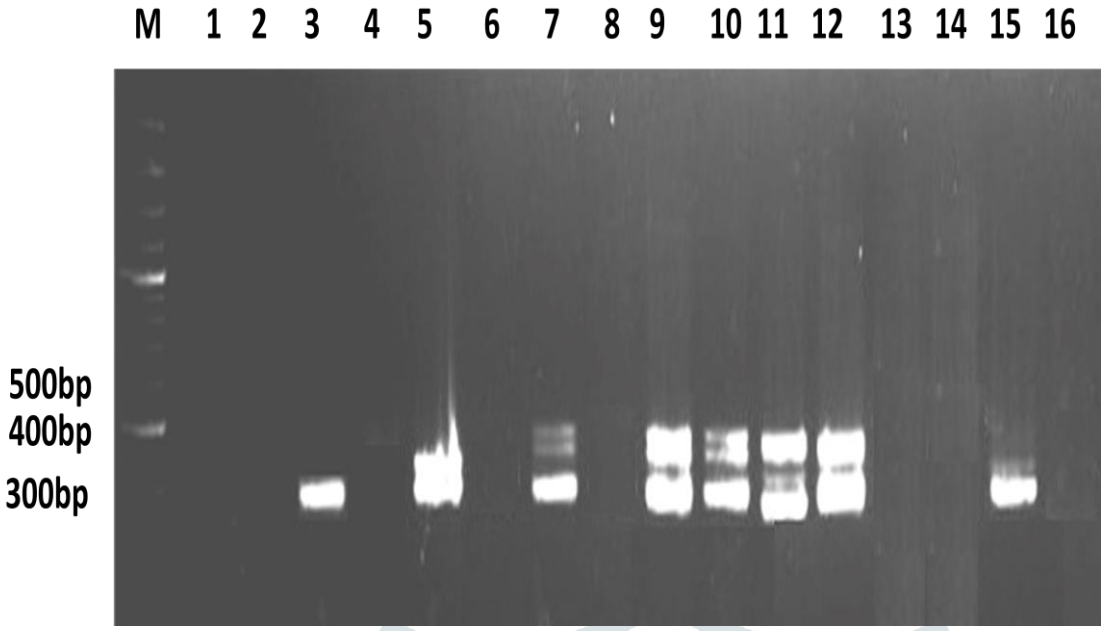


Figure No. 3: Amplification profile of mango hybrids using the primer **L6.**

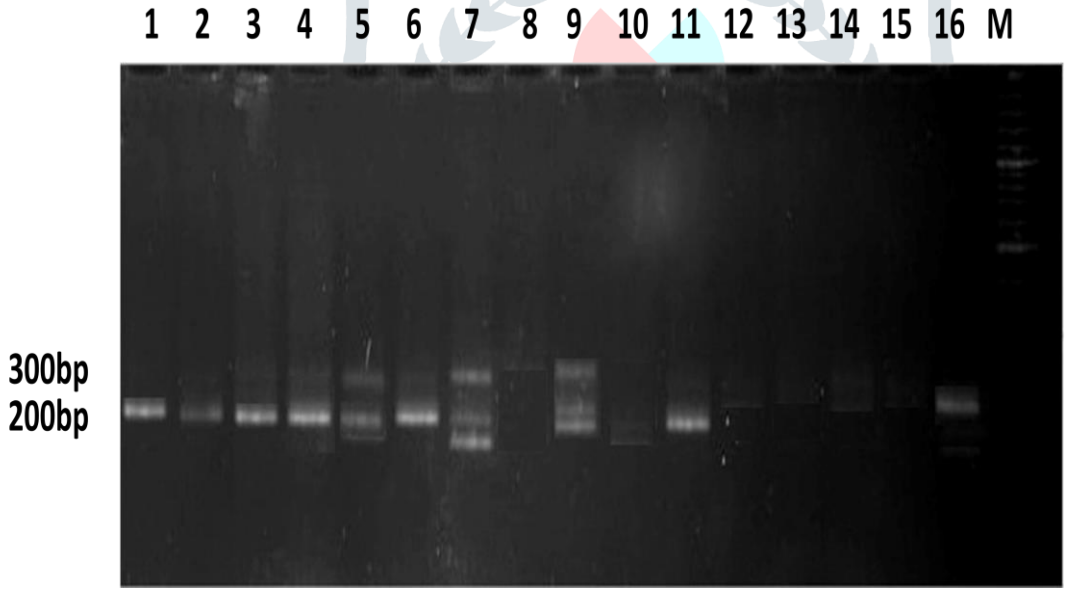


Figure No. 4: Amplification profile of mango hybrids using the primer **L9.**

Table No. 3

Selected locus present in mango varieties:

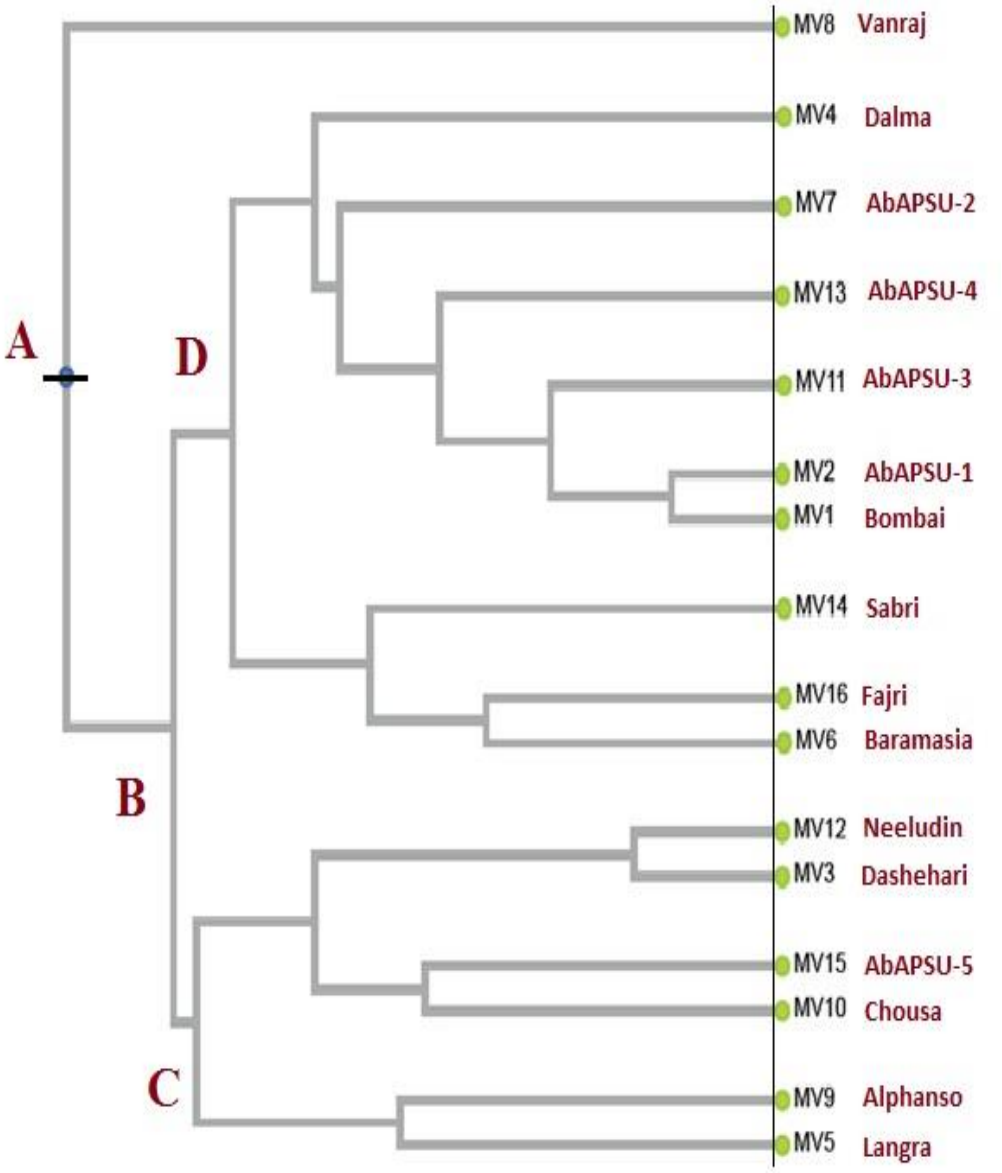
S.No.	Variety	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10
MV1	Bombai	0	1	1	0	1	0	1	1	1	1
MV2	AbAPSU-1	1	1	1	0	1	0	1	1	1	1
MV3	Dashehari	1	0	1	0	0	1	1	0	1	1
MV4	Dalma	0	1	0	0	0	0	1	0	1	1
MV5	Langra	1	0	1	1	1	1	0	0	1	0
MV6	Baramasia	0	0	1	1	1	0	1	0	1	1
MV7	AbAPSU-2	0	1	0	1	0	1	0	1	1	1
MV8	Vanraj	0	1	0	0	1	0	0	1	0	0
MV9	Alphanso	1	0	0	1	0	1	0	1	1	0
MV10	Chousa	1	0	0	0	0	1	1	0	0	0
MV11	AbAPSU-3	0	1	1	1	1	1	1	1	1	1
MV12	Neeludin	1	0	1	0	0	1	1	0	0	1
MV13	AbAPSU-4	0	1	0	1	1	0	1	1	0	1
MV14	Sabri	1	0	1	1	1	0	1	0	0	0
MV15	AbAPSU-5	1	1	0	0	1	1	1	0	0	0
MV16	Fajri	0	0	1	1	0	0	1	0	1	0

1= Locus present, 0= Locus Absent

Table No. 4

Similarity Index

	MV1	MV2	MV3	MV4	MV5	MV6	MV7	MV8	MV9	MV10	MV11	MV12	MV13	MV14	MV15	MV16
MV1	1	0.875	0.444	0.571	0.300	0.625	0.444	0.429	0.200	0.111	0.778	0.333	0.625	0.333	0.333	0.375
MV2		1	0.556	0.500	0.400	0.556	0.400	0.375	0.300	0.222	0.700	0.444	0.556	0.444	0.444	0.333
MV3			1	0.429	0.500	0.500	0.333	0.000	0.375	0.500	0.500	0.833	0.200	0.375	0.375	0.429
MV4				1	0.111	0.429	0.429	0.167	0.125	0.167	0.444	0.286	0.429	0.125	0.286	0.333
MV5					1	0.500	0.333	0.125	0.571	0.286	0.500	0.375	0.200	0.571	0.375	0.429
MV6						1	0.333	0.125	0.222	0.125	0.667	0.375	0.500	0.571	0.222	0.667
MV7							1	0.286	0.571	0.125	0.667	0.222	0.500	0.100	0.222	0.250
MV8								1	0.143	0.000	0.333	0.000	0.500	0.143	0.333	0.000
MV9									1	0.333	0.400	0.250	0.222	0.250	0.250	0.286
MV10										1	0.200	0.600	0.125	0.333	0.600	0.167
MV11											1	0.400	0.667	0.400	0.400	0.444
MV12												1	0.222	0.429	0.429	0.286
MV13													1	0.375	0.375	0.250
MV14														1	0.429	0.500
MV15															1	0.125
MV16																1
	Cophenetic Correlation Coefficient = 0.7167															



Graph No. 1: UPGMA dendrogram of aonla germplasm based on RAPD primers

The UPGMA is the simplest method of tree construction. It was originally developed for constructing taxonomic phenograms, i.e. trees that reflect the genotypic similarities between OTUs, but it can also be used to construct phylogenetic trees if the rates of evolution are approximately constant among the different lineages. For this purpose the number of observed nucleotide or amino-acid substitutions can be used. UPGMA employs a sequential clustering algorithm, in which local topological relationships are identified in order of similarity, and the phylogenetic tree, is build in a stepwise manner. We first identify from among all the OTUs the two OTUs that are most similar to each other and then treat these as a new single OTU. Such an OTU is referred to as a composite OTU. Subsequently from among the new group of OTUs we identify the pair with the highest similarity, and so on, until we are left with only two UTUs.

Similarity coefficients for the 16 mango accessions based on 10 SSR markers. Pair-wise association among 16 mango accessions, showed the highest Distance value 1.51 and the lowest Distance value 0.612. The Cophenetic Correlation among 16 mango verities are 0.7167. The highest polymorphism 90% was observed in primer L7. The dendrogram showing the genetic relationships among 16 accessions based on SSR markers is presented in NCSS dendrogram report. The dendrogram showed four major clusters A, B, C and D. The highest similarity index is 0.875 between AbAPSU1 and Bombai.

Dendrogram revealed that the genotypes could be grouped into four clusters. The dendrogram showed four clusters in which A and B at 16.7% similarity. Whereas cluster C and D similar as 37.5% (Graph No. 1). The similarities amid germplasm from altered regions could be due to introductions from assorted added regions. Whereas absorption of accessions from altered bounded regions calm can be explained by the common barter alteration of genetic material. The measurement of similarity index of mango germplasm, ranged from 0.111 to 0.875 according to the genetic affinity were generated by Jaccard's coefficient, (Table No.4), suggesting an actual top genetic abject amid the mango germplasm.

Discussion:

Our NCSS 2019 report revealed Similarity coefficients for the 16 mango accessions based on 10 SSR markers. Pair-wise association among 16 mango accessions, showed the highest Distance value 1.51 and the lowest Distance value 0.612. The Cophenetic Correlation among 16 mango verities are 0.7167. The highest polymorphism 90% was observed in primer L7. The dendrogram showing the genetic relationships among 16 accessions based on SSR markers is presented in NCSS dendrogram report. The dendrogram showed four major clusters A, B, C and D. The highest similarity index is 0.875 between AbAPSU1 and Bombai. Dendrogram revealed that the genotypes could be grouped into four clusters. The dendrogram showed four clusters in which A and B at 16.7% similarity. Whereas cluster C and D similar as 37.5% (Graph No. 8). The similarities amid germplasm from altered regions could be due to introductions from assorted added regions. Whereas absorption of accessions from altered bounded regions calm can be explained by the common barter alteration of genetic material. The measurement of similarity index of mango germplasm, ranged from 0.111 to 0.875 according to the genetic affinity were generated by Jaccard's coefficient, (Table

No.2), suggesting an actual top genetic abject amid the mango germplasm.

Assessment of physical and synthetic attributes of organic product harvests has been effectively utilized for determination of improved cultivars for reproducing programs. The examination was directed at common subtropical conditions in North-West India for assessing the changeability of mango germplasm to preserve the world class ones and recognize the unrivaled genotypes dependent on organic product quality for duplication and for future harvest improvement ***(Neguse TB, et. al. 2019).*** Fourteen genotypes were tried for their physiological and compound qualities. Randomized total square structure was utilized and basic distinction was utilized to think about quality attributes of fourteen mango genotypes. Greatest organic product weight was found in Chausa though most extreme lessening and absolute sugars were seen in Malda. Dashehari positioned first in regard of yield per tree, that is, 148.90 kg/tree. Nearby Selection-I was the soonest to develop. Among all genotypes Chausa, Kala Gola, Hundel and Gola demonstrated propensity towards normal bearing. The Alphonso, Malda and Chausa was distinguished for unrivaled attributes like absolute solvent solids/corrosive proportion (TSS/corrosive proportion); Chausa and Langra Banarasi for high mash rate and mash stone proportion; Rattaul for astounding flavor; 'Neighborhood ***(Kaur M, et. al. 2014).***

The appraisal of hereditary decent variety is basic for the preservation and rearing purposes. This examination meant to survey and assess the hereditary assorted variety of 116 promotions of mango (Mangifera indica) germplasm utilizing microsatellite markers. The DNA was extricated from youthful crisp leaf before genotyping utilizing microsatellites to decide the allele size. The UPGMA dendrogram demonstrated that the increases were isolated into two significant bunches, which were separated into a few sub-groups dependent on their hereditary separation lattice esteems. A few promotions were profoundly like one another, presumably because of the duplication of gathered increases or inadequate microsatellite markers to separate them ***(Bhamini K, et. al. 2018).***The examination of the populace structure of the people additionally demonstrated two subpopulations, proposing that the increases could be isolated into two gatherings, which bolstered the produced dendrogram. The discoveries of this examination encourage improved protection the board of the germplasm and help to discover methodologies for future reproducing exercises ***(Razak SA, et. al. 2019).***

Our findings stabilize morphological, biochemical and genetic diversity of mango in vindhyan region of Madhya Pradesh. This work suggest all about quality and quantity of mango fruits. As we know about mango is a king of fruits. It is fruit of common man that fulfil the nutrients. So we need improve its quality and quantity. Diversity among mango plant in vidhyan region reveals a clue for new variety development. Genetic makeup of mango provides also tolerance properties to stress and pathogenic disease. Our works also help in grafting and commercial production of mango.

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