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MORPHO-MOLECULAR DIVERSITY ANALYSIS IN TOMATO (*SOLANUM LYCOPERSICUM* L.)

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ABSTRACT

Genetic diversity of twenty-four genotypes of Tomato was analysed at molecular level using SSR markers. DNA polymorphism was utilized to cluster the genotypes into different clusters based on dissimilarity coefficient. 24 SSR primers were used for divergence studies at molecular level where a total of 41 alleles were detected with an average 1.70 per loci. The maximum number of alleles detected were 3 in primer SL-23. The polymorphic information content value ranged from 0.293 - 0.398 with an average of 0.36. The 24 tomato genotypes showed dissimilarity coefficient values ranging from 0.257 to 0.718. On the basis of SSR analysis, 24 genotypes were grouped into 3 clusters where Cluster I contained 1 genotype, cluster II contained 10 genotypes and cluster III contained 13 genotypes. The highest dissimilarity was observed between EC 914107 in Cluster II and Shopian Sel-1 in Cluster III and EC 164656 in Cluster III and EC 144681 in Cluster II with value of 0.718.

Key words : Tomato, Divergence, SSR markers, Dissimilarity coefficient, Polymorphic information content.

Introduction

Genetic diversity analysis assists in interpreting the genetic background and breeding value of the germplasm. Wide range of variability in shape and size and colour of mature fruits and other character are found within tomato. As a result of its wide diversity in gene pool and consequent improvement in selection and breeding, a large number of cultivars have adapted to different agro-climatic conditions (Villarel *et al.*, 1998). A lot of diversity is also found in growth and development pattern of tomato due to altitudinal variation (Sharma and Singh, 2012). Multivariate technique using D^2 statistics (Mahalanobis, 1928) is a powerful tool in quantifying the degree of divergence among the genotypes which is helpful to screen the genetically diverse parents that are likely to produce high heterotic effects among crosses and also generate large spectrum of variability during segregation and recombination of genes at heterozygous polygenic blocks.

Underutilized extant diversity within and between the tomato species could serve as a valuable resource to enrich the genetic pool of cultivated tomatoes with marginalized alleles that could increase productivity and stress adaptation (Gur *et al.*, 2004). The low genetic diversity of cultivated tomatoes necessitates the use of modern molecular techniques for the discovery of markers able to detect minor variations within tomato germplasm (Foolad and Panthee, 2012).

Different molecular markers have been proved as useful tools for characterizing agricultural crops based on genetic diversity. Researchers have studied genetic variation in tomato landrace and cultivars using various molecular technique, viz. RFLP, AFLP, RAPD and SSR (Bredemeijer *et al.*, 2002). The application of SSR technique to plants depends on the availability of suitable markers. SSR are short (mostly 2-5bp) tandem repeats of DNA sequences and are ideal for diversity assessment due to their high reproducibility, co-dominance and high polymorphism. Several primer sets for SSR analysis are available for tomato. The characterization of much

diversified material with molecular markers offers a unique opportunity to define significant marker trait association of biological and agronomic interest.

Materials and Methods

The present investigation was undertaken at Vegetable Experimental farm of the Division of Vegetable Science, SKUAST-K, Shalimar during *Kharif* 2021. A set of fifty-eight genotypes of tomato (Table 1) were used for the present study. The genotypes were collected from different agro climatic regions and had valuable characteristics for breeding purposes. These genotypes were evaluated for morphological, yield and quality parameters *viz*., plant height (cm), number of primary branches per plant, days to 50 per cent flowering, number of fruits per plant, average fruit weight (g), fruit length (cm), fruit width (cm), days to 1st fruit harvest, fruit yield per plant (kg), pericarp thickness (mm), total soluble solids (°Brix), titratable acidity (%), ascorbic acid content (mg 100^{-1} g), total sugars (%) and lycopene content (mg 100^{-1} g). The experiment was laid out in Randomized Complete Block Design (RCBD). The row to row and plant to plant spacing was maintained at 45 x 30 cm. The experimental field is located at the main campus, Shalimar, Srinagar. Laboratory work was conducted at NSP laboratory, Division of Genetics and Plant Breeding, SKUAST-K Shalimar, during *Kharif* 2022. Molecular characterization was done on 24 genotypes that were selected from 58 genotypes on the basis of maximum intra and inter cluster distances. 24 SSR primer pairs were used. The selected microsatellite markers along with their annealing temperature and amplicon size are presented in Table 2. SSR based analysis was carried out using DARwin software version 6.0 and scoring was done as base pair scoring and binary scoring in which bands were scored as '1' (for presence) and '0' (absence)

Table 1 : Tomato (*Solanum lycopersicum* L.) genotypes used in the present study.

S. no.	Genotype	Source	S. No.	Genotype	Source
1.	**EC 914106**	NBPGR, New Delhi	**30.**	**EC-163711**	NBPGR, New Delhi
2.	**EC 914093**	NBPGR, New Delhi	**31.**	**EC-521067**	NBPGR, New Delhi
3.	**EC 620402**	NBPGR, New Delhi	**32.**	**Shopian Sel-1**	Local
4.	**IARI-7**	IARI, New Delhi	**33.**	**EC-521067-B**	NBPGR, New Delhi
5.	**EC 617047**	NBPGR, New Delhi	**34.**	**EC-367855**	NBPGR, New Delhi
6.	**EC 914114**	NBPGR, New Delhi	**35.**	**EC-159041**	NBPGR, New Delhi
7.	**Kashi Chayan**	IIVR, Varanasi	**36.**	**EC-274122**	NBPGR, New Delhi
8.	**EC 914109**	NBPGR, New Delhi	**37.**	**EC-620389**	NBPGR, New Delhi
9.	**EC 620401**	NBPGR, New Delhi	**38.**	**EC-620372**	NBPGR, New Delhi
10.	**EC 914107**	NBPGR, New Delhi	**39.**	**EC-620373**	NBPGR, New Delhi
11.	**EC 914101**	NBPGR, New Delhi	**40.**	**EC-620775**	NBPGR, New Delhi
12.	**EC 914091**	NBPGR, New Delhi	**41.**	**EC-528368**	NBPGR, New Delhi
13.	**EC 914105**	NBPGR, New Delhi	**42.**	**EC-164625**	NBPGR, New Delhi
14.	**EC-241140**	NBPGR, New Delhi	**43.**	**EC-3176**	NBPGR, New Delhi
15.	**EC-165690**	NBPGR, New Delhi	**44.**	**EC-632943**	NBPGR, New Delhi
16.	**EC-145054**	NBPGR, New Delhi	**45.**	**EC-162516**	NBPGR, New Delhi
17.	**EC-164656**	NBPGR, New Delhi	**46.**	**EC-151568**	NBPGR, New Delhi
18.	**EC-144681**	NBPGR, New Delhi	**47.**	**EC-514109**	NBPGR, New Delhi
19.	**EC-145622**	NBPGR, New Delhi	**48.**	**EC-163605**	NBPGR, New Delhi
20.	**EC-157568**	NBPGR, New Delhi	**49.**	**EC-177343**	NBPGR, New Delhi
21.	**EC-620557**	NBPGR, New Delhi	**50.**	**KSP-5**	PAU, Ludhiana
22.	**EC-162518**	NBPGR, New Delhi	**51.**	**TIH-611**	PAU, Ludhiana
23.	**EC-620395**	NBPGR, New Delhi	**52.**	**TBR-2**	PAU, Ludhiana
24.	**EC-620639**	NBPGR, New Delhi	**53.**	**LVR-7**	PAU, Ludhiana
25.	**EC-249515**	NBPGR, New Delhi	**54.**	**R-ZT-2**	PAU, Ludhiana
26.	**EC-241148**	NBPGR, New Delhi	**55.**	**VN-1**	PAU, Ludhiana
27.	**EC-159053**	NBPGR, New Delhi	**56.**	**CLN-1621-L**	IIVR, Varanasi
28.	**EC-145057**	NBPGR, New Delhi	**57.**	**EC-62038**	NBPGR, New Delhi
29.	**EC-162515**	NBPGR, New Delhi	**58.**	**EC-160194**	NBPGR, New Delhi

Table 2 : Selected SSR primers along with their primer sequence.

S. no.	Primer	Forward primer (5'-3')	Reverse primer (3'-5')	Annealing temperature (°C)	Expected amplicon size (bp)
1	SL-1	CCTTGCAGTTGAGGTGAATT	TCAAGCACCTACAATCAATCA	52.50	100-200
2	SL-2	AGCCACCCATCACAAAGATT	GTCGCACTATCGGTCACGTA	55	150-200
3	SL-3	TTCGGTTTATTCTGCCAACC	GCCTGTAGGATTTTCGCCTA	53.50	50-150
4	SL-4	GAGTCAACAGCATAGTGGAGGAGG	CGTCGCAATTCTCAGGCATG	56.50	150-200
5	SL-5	GCCACGTAGTCATGATATACATAG	GCCTCGGACAATGAATTG	51.50	100-250
6	SL-6	TGAGAACAACGTTTAGAGGAGCTG	CGGGCAGAATCTCGAACTC	55.50	100-150
7	SL-7	AGAATTTTTTCATGAAATTGTCC	TATTGCGTTCCACTCCCTCT	51.50	50-100
8	SL-8	GCTCTGTCCTTACAAATGATACCTCC	CAATGCTGGGACAGAAGATTTAATG	55	150-200
9	SL-9	CGGCGTATTCAAACTCTTGG	GCG69GACCTTTGTTTTGGTAA	53.50	100-150
10	SL-10	CAACAGCATAGTGGAGGAGG	TACATTTCTCTCTCTCCCATGAG	54	100-150
11	SL-11	ACAAACTCAAGATAAGTAAGAGC	GTGAATTGTGTTTTAACATGG	49	100-200
12	SL-12	TGTAGATAACTTCCTAGCGACAATC	ACGGACGGATGGACAAATG	54.50	50-150
13	SL-13	CGATTAGAGAATGTCCCACAG	TTACACATACAAATATACATAGTCTG	50	100-150
14	SL-14	CCCAAATGCTATGCAATACAC	AGTTCAGGATTGGTTTAAGGG	52	150-200
15	SL-15	TTGGTAATTTATGTTCGGGA	TTGAGCCAATTGATTAATAAGTT	48.50	50-100
16	SL-16	GAAGCGACTTCCAAAATCAGA	AAAGGGAGGAATAGAAACCAAAA	52.50	100-150
17	SL-17	TTCTTCCCTTCCATCAGTTCT	TTTGCTGCTATACTGCTGACA	53.50	50-150
18	SL-18	AACGGTGGAAACTATTGAAAGG	CACCACCAAACCCATCGTC	54.50	50-200
19	SL-19	ACCAATCCACCATGTCAATGC	CTCATGGATGGTGTCATTGG	54	50-200
20	SL-20	AGGTTGATGAAAGCTAAATCTGGC	CAACCACCAATGTTCATTACAAGAC	53	150-200
21	SL-21	TAAATACAAAAGCAGGAGTCG	GAGTTGACAGATCCTTCAATG	50.50	200-250
22	SL-22	TCCAGCTGATTGGTTAGGTTG	ATGCGAATCTACTCGTCATGG	54	50-100
23	SL-23	GATGGACACCCTTCAATTTATGGT	TCCAAGTATCAGGCACACCAGC	57	150-250
24	SL-24	ATTGCTCATACATAACCCCC	GGGACAAAATGGTAATCCAT	51	200-250

(Yeh *et al*., 1999).

Results and Discussion

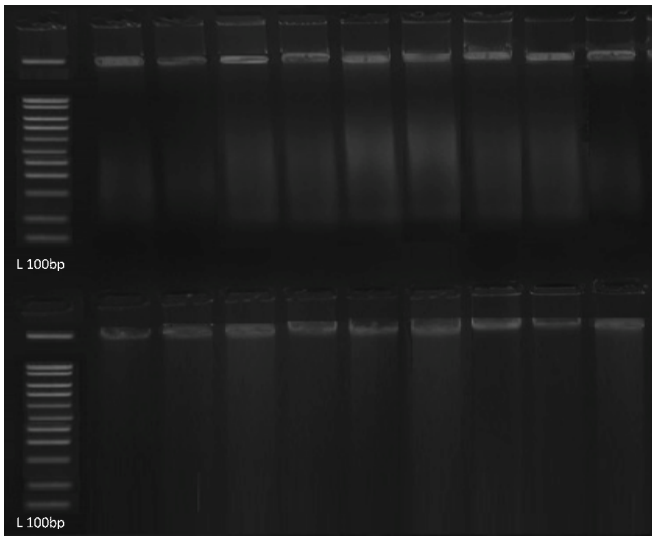
Divergence study at morphological level

In the present study, fifty-eight genotypes of tomato were evaluated to estimate the genetic divergence for identification of potential parents using Mahalanobis D^2 statistics. The genotypes were grouped into twelve clusters. The formation of different clusters with variable number of entries in each cluster indicated diversity among genotypes. The genotypes from different agro- ecological zones were found to be scattered in different clusters, which suggested that a pattern of clustering of accessions was independent of their geographical origin. Maximum number of genotypes fell in cluster I (17). Cluster II consisted of 12 genotypes, cluster III comprised of 10 genotypes, cluster IV consisted of 9 genotypes and cluster XI consisted of 3 genotypes. Cluster V, VI, VII, VIII, IX, X and XII each consisted of single genotypes (Table 3).

Divergence study at molecular level

In this study all the 24 selected SSR primers amplified alleles across the twenty four genotypes with varying degree of polymorphism and revealed clear and consistent amplification profiles in the entire germplasm set.

DNA bands of the genotypes obtained in this study are depicted in Plate 1. The summarized data of 24 polymorphic SSR primers used for identification and evaluation of genetic diversity of twenty four tomato genotypes is presented in Table 4. A total of 41 alleles were amplified by 24 polymorphic SSR loci and the number of alleles ranged from 1 to 3 with an average of 1.70 alleles per locus. The obtained number of alleles per loci is comparable with other findings by He *et al.* (2003); Benor *et al.* (2008); Korir *et al.* (2014) and the average number of alleles per loci was comparable with Todorovska *et al.* (2014) with a value of 1.86. The highest number of alleles i.e, 3 was amplified by SL-23. All these amplified fragments produced different fingerprinting pattern that allowed all the varieties analyzed to be



Top (from left)- EC 162518 (23,) EC 632943(19,) SHOPIAN SEL-1 (5), EC 144681 (10), EC 241140 (15), EC 164625 (17), EC 914107 (6), EC 249515 (22) and EC 159053(18)

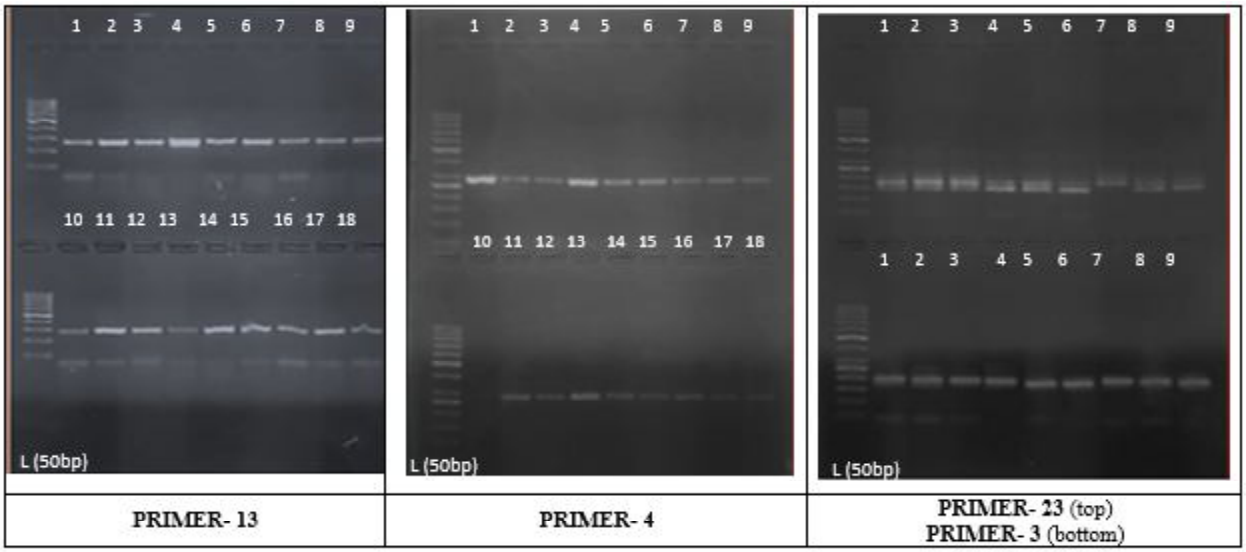
Bottom (from left)- VN-1 (3), TBR 2 (13), KASHI CHAYAN (16), EC 151568 (24), EC 163605 (21), EC 163711 (4), CLN-1621-L (12), EC 157568 (14) and EC 241148 (20)

Plate 1 : DNA Isolation.

closely related genotypes and vice-versa. PIC value ranged from 0.293 (SL-13) to 0.398 (SL-1) with an average value of 0.36 across 24 tomato genotypes indicating that SSR markers are highly informative. Our results were in accordance with results of (He *et al.*, 2003; Benor *et al*., 2008; Korir *et al*., 2014 and Kaushal *et al*., 2017).

Dendrograms are efficient means of summarizing microsatellite data and can reveal relationships including individuals with identical genotypes. The morphological characterization was done on 58 genotypes that produced 12 clusters and from those 12 clusters, 24 genotypes were selected on the basis of maximum intra and inter cluster distances for molecular characterization. Molecular characterization grouped these 24 genotypes into 3 clusters. The cluster dendrogram classified 24 genotypes into 3 clusters (Table 5 and Figs. 1 and 2).

Cluster I consisted of only one genotype namely EC 241140. Cluster II contained 10 genotypes and is further divided into two clusters IIA and IIB. IIA contained 2



From left: KSP-5 (1), IARI 7 (2), VN-1 (3), EC 163711 (4), SHOPIAN SEL-1 (5), EC 914107 (6), EC 914119 (7), EC 164656 (8), EC 160194 (9), EC 144681 (10), EC 3176 (11), CLN-1621-L(12), TBR 2 (13), EC 157568 (14), EC 241140 (15), KASHI CHAYAN (16), EC 164625 (17), EC 159053(18)

Plate 2 : Banding Pattern observed through different primers.

distinguished. Plate 2 depicts the banding pattern of tomato genotypes based on different SSR markers. The variation in number of alleles produced by SSR markers demonstrates heterozygosity in different alleles at a given locus in which the heterozygosity could reflect greatly the state of genetic variability.

The PIC values provide an estimate of discriminating power of markers by taking into account not only the number of alleles at a locus but also relative frequencies of these alleles. Lower PIC value might be a result of

genotypes i.e, namely CLN-1621-L and EC 159053 and IIB contained 8 genotypes i.e, namely VN-1, EC 914107, EC 160194, EC 163605, EC 144681, Kashi Chayan, EC 157568 and EC 249515. Cluster III had maximum number of genotypes i.e 13 and is further divided into two clusters IIIA and IIIB. IIIA contained 5 genotypes i.e, EC 3176, Shopian Sel-1, EC 164656, IARI-7 and EC 241148. IIIB contained 8 genotypes i.e, EC 914119, KSP-5, EC 164625, EC 151568, EC 162518, TBR 2, EC 163711 and EC 632943. The results were in accordance with (Salunke

Table 3 : Distribution of Tomato (*Solanum lycopersicum* L.) genotypes into clusters based on D^2 statistics.

Clusters	Number of genotypes in Cluster	Genotypes included
I	17	IARI-7, EC-620775, EC-274122, EC-367855, EC 617047, EC-620395, EC-620389, EC 914107, EC-163711, EC-145054, EC-620639, Shopian Sel-1, EC-159041, EC-177343, EC-528368, VN-1, KSP-5
II	12	EC 914114, EC-145622, EC-521067, EC-514109, EC 914093, EC-160194, EC-144681, EC-145057, EC 914101, EC-162516, EC 914106, EC-164656
III	10	EC-3176, VN-1, EC-914105, EC-62038, EC-620401, TBR-2, TIH-611, EC 914091, LVR-7, CLN-1621-L
IV	9	EC-157568, EC-521067-B, EC-162515, Kashi Chayan, EC 620402, EC 914109, EC-620557, EC-620373, EC-241140
V	1	EC-164625
VI	1	EC-159053
VII	1	EC-632943
VIII	1	EC-241148
IX	1	EC-163605
X	1	EC-249515
XI	3	EC-165690, EC-162518, EC-620372
XII	1	EC-151568

Table 4 : Allelic variation and polymorphic information content (PIC) for SSR loci across 24 selected tomatoes (*Solanum lycopersicon*) genotypes.

S. no.	Primer	Number of alleles amplified	Expected fragment size (bp)	PIC Value
1	SL-1	2	100-200	0.398
2	SL-2	2	150-200	0.326
3	SL-3	2	50-150	0.356
4	SL-4	1	150-200	0.378
5	SL-5	2	100-250	0.375
6	SL-6	2	100-150	0.367
7	SL-7	2	50-100	0.355
8	SL-8	1	150-200	0.387
9	SL-9	2	100-150	0.363
10	SL-10	1	100-150	0.295
11	SL-11	2	100-200	0.361
12	SL-12	2	50-150	0.382
13	SL-13	1	100-150	0.293
14	SL-14	2	150-200	0.387
15	SL-15	1	50-100	0.362
16	SL-16	1	100-150	0.352
17	SL-17	2	50-150	0.368
18	SL-18	2	50-200	0.334
19	SL-19	2	50-200	0.354
20	SL-20	1	150-200	0.381
21	SL-21	1	200-250	0.383
22	SL-22	2	50-100	0.385
23	SL-23	3	150-250	0.357
24	SL-24	2	200-250	0.384
	Total	41		8.683
	Average	1.70		0.36

Table 4 continued...

Table 4 continued...

et al., 2012; Ayenan *et al*., 2021) and almost comparable to Kaushal *et al.* (2017), where only 2 clusters were formed. The dendrogram shows that there is considerable amount of genetic variation among the accessions in relation to SSR primers studied. Some of the accessions having the same geographic origin were distributed in different sub-clusters suggesting their genetic diversity.

The twenty four tomato genotypes showed dissimilarity coefficient values ranging from 0.257 to 0.718 suggesting different levels of genetic diversity (Table 6). The highest dissimilarity was observed between EC 914107 in Cluster II and Shopian Sel-1 in Cluster III and EC 164656 in Cluster III and EC 144681 in Cluster II with value of 0.718. This suggests that they have the least number of common attributes among all pairs of genotypes. The minimum dissimilarity 0.257 was observed between genotypes EC 249515 and EC 157568 both falling in Cluster II. It was followed by EC 162518 and KSP-5 both falling in Cluster III and KSP-5 and EC 914119 both falling in Cluster III with dissimilarity

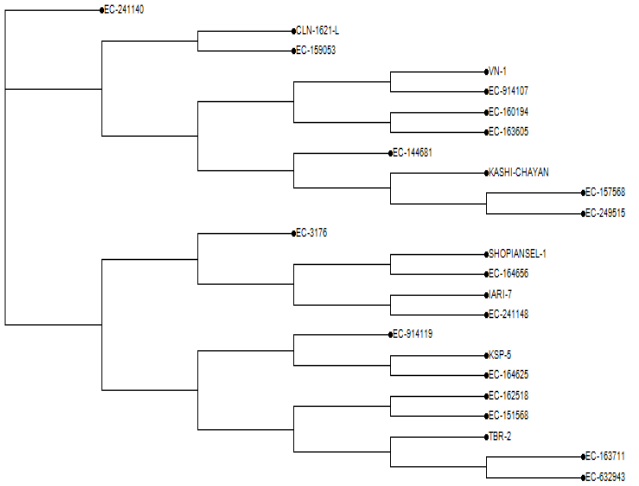


Fig. 1 : Distribution of tomato (*Solanum lycopersicum* L.) genotypes into different clusters as depicted by cluster dendrogram (Molecular analysis).

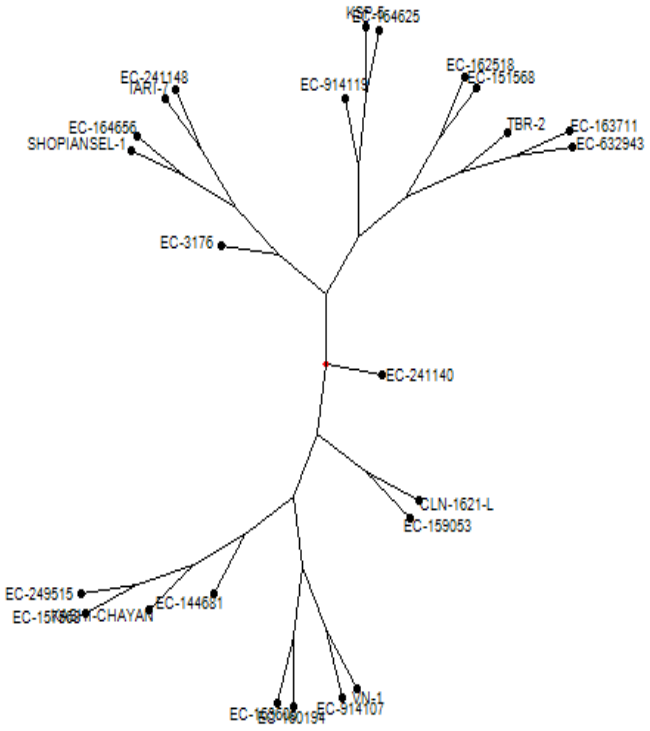


Fig. 2 : Clustering pattern depicted through tree diagram (Molecular analysis).

coefficient 0.324 each. This suggests that they have the most number of common attributes among all pairs of genotypes. The assessment of genetic distance using dissimilarity matrix was conducted by Maciel *et al.* (2018), Athinodorou *et al*. (2021); Ayenan *et al*. (2021).

SSR markers proved to be very informative in the assessment of genetic variation. The analysis with SSR markers disclosed wide variation within tomato genotypes. These were found suitable for use because of their ability to generate reproducible polymorphic bands. The present findings further strengthened previous reports that SSR markers can be used effectively to estimate genetic differences among genotypes and are in agreement with the results of He *et al.* (2003), Benor *et al*. (2008), Korir *et al.* (2014), Kaushal *et al.* (2017). Recent studies revealed the potential of SSRs in providing intra-specific diversity within genus.

The genotypes showing extreme behaviour with respect to the morphological traits under study were grouped into different clusters through molecular analysis as well i.e, these genotypes were found to be in different clusters under both cases indicating their genetic divergence. This can be attributed to different lineage of the genotypes or due to the large geographical separation that led to the accumulation of detectable genetic differences. There was no relationship between the spatial and genetic proximity of the germplasm apart from few genotypes which were from the same source. Genotypes collected from different agro-climatic zones showed diverse clustering which may be due to genetic variation.

However, the absence of significant geographical association suggests that movement of accessions from one region to another renders the historical derivations of gene bank accessions inaccurate. Molecular analysis with additional SSR markers and with greater genomic coverage could help to reveal genetic diversity accurately and also help to unambiguously differentiate those

Table 5 : Distribution of tomato (*Solanum lycopersicum* L.) genotypes into three clusters based on SSR marker analysis of 24 genotypes.

Cluster	Total number of genotypes	Genotypes
Cluster I	1	EC 241140 (15)
Cluster II	10	**IIA:** CLN-1621-L (12) and EC 159053(18) **IIB:** VN-1 (3), EC 914107 (6), EC 160194 (9), EC 163605 (21), EC 144681 (10), Kashi Chayan (16), EC 157568 (14) and EC 249515 (22),
Cluster III	13	**IIIA:** EC 3176 (11), SHOPIAN SEL-1 (5), EC 164656 (8), IARI-7 (2) and EC 241148 (20) **IIIB:** EC 914119 (7), KSP-5 (1), EC 164625 (17), EC 151568 (24), EC 162518 (23), TBR 2 (13), EC 163711 (4) and EC 632943 (19).

Table 6 : Dissimilarity matrix.

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
2	0.641																						
3	0.500	0.676																					
4	0.486	0.629	0.711																				
5	0.526	0.406	0.595	0.658																			
6	0.514	0.657	0.400	0.657	0.718																		
7	0.324	0.595	0.528	0.471	0.472	0.500																	
8	0.605	0.452	0.711	0.588	0.355	0.657	0.595																
9	0.595	0.531	0.452	0.618	0.611	0.606	0.583	0.694															
10	0.429	0.684	0.406	0.611	0.568	0.559	0.541	0.718	0.639														
11	0.514	0.529	0.658	0.529	0.486	0.600	0.500	0.438	0.639	0.667													
12	0.459	0.556	0.605	0.471	0.514	0.583	0.444	0.556	0.583	0.541	0.615												
13	0.400	0.543	0.514	0.500	0.457	0.611	0.472	0.500	0.485	0.486	0.528	0.625											
14	0.487	0.500	0.553	0.500	0.500	0.605	0.432	0.541	0.528	0.486	0.444	0.432	0.610										
15	0.472	0.529	0.583	0.485	0.528	0.600	0.457	0.611	0.559	0.556	0.556	0.541	0.528	0.564									
16	0.568	0.629	0.515	0.667	0.543	0.576	0.595	0.500	0.657	0.529	0.529	0.595	0.583	0.500	0.684								
17	0.333	0.611	0.406	0.684	0.486	0.515	0.457	0.611	0.600	0.424	0.595	0.500	0.441	0.526	0.700	0.571							
18	0.553	0.571	0.543	0.571	0.568	0.515	0.650	0.529	0.600	0.556	0.556	0.457	0.605	0.526	0.514	0.649	0.595						
19	0.441	0.629	0.639	0.452	0.500	0.657	0.514	0.545	0.657	0.611	0.485	0.595	0.406	0.541	0.571	0.629	0.529	0.611					
20	0.579	0.419	0.571	0.600	0.424	0.588	0.486	0.515	0.500	0.658	0.543	0.486	0.514	0.553	0.500	0.469	0.543	0.583	0.676				
21	0.394	0.629	0.469	0.703	0.583	0.531	0.514	0.703	0.484	0.485	0.649	0.556	0.543	0.541	0.611	0.629	0.485	0.571	0.703	0.639			
22	0.500	0.553	0.486	0.514	0.513	0.541	0.487	0.514	0.615	0.371	0.459	0.487	0.550	0.257	0.459	0.382	0.575	0.459	0.553	0.526	0.590		
23	0.324	0.514	0.528	0.471	0.429	0.658	0.486	0.471	0.583	0.500	0.500	0.400	0.382	0.513	0.541	0.471	0.412	0.541	0.471	0.441	0.556	0.487	
24	0.459	0.514	0.568	0.556	0.382	0.692	0.486	0.424	0.583	0.541	0.541	0.486	0.429	0.432	0.500	0.595	0.457	0.500	0.424	0.605	0.556	0.487	0.400

KSP-5 (1), IARI-7 (2), VN-1 (3), EC 163711 (4), Shopian Sel -1 (5), EC 914107 (6), EC 914119 (7), EC 164656 (8), EC 160194 (9), EC 144681 (10), EC 3176 (11), CLN-1621-L(12), TBR 2 (13), EC 157568 (14), EC 241140 (15), Kashi Chayan (16), EC 164625 (17), EC 159053(18), EC 632943 (19), EC 241148 (20), EC 163605 (21), EC 249515 (22), EC 162518 (23) and EC 151568 (24)

genotypes with identical allelic patterns as revealed by set of primers used in this study. Further, by maximizing the number of genotypes from different above agro ecological regions along with the use of a higher number of polymorphic SSR markers and improved estimation of genetic diversity could be worked out.

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