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Original scientific article

PERFORMANCE PREDICTION OF F_1 CROSSES IN EGGPLANT (*Solanum melongena* L.) BASED ON MORPHOLOGICAL AND MOLECULAR DIVERGENCE

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Identifying potential F_1 hybrid combinations based on the parental diversity can increase the breeding efficiency and saves the opportunity cost of time. In this work, the genetic diversity between eggplant genotypes was measured by Mahalanobis D^2 statistics and Sequence Related Amplified Polymorphism (SRAP) molecular markers. The genetic distances (GD) were correlated with heterosis and trait wise mean performance of F_1 crosses generated in a line × tester mating design for prediction of F_1 performance for agronomically important traits. The cluster analysis performed based on the Mahalanobis D^2 distance grouped all the eleven genotypes into two clusters and three clusters were formed based on the SRAP marker data. The polymorphic information content value generated by the 30 SRAP marker combinations ranged from 0.09 to 0.77 with a mean value of 0.38. For yield, the F_1 combinations exhibited the mid parent heterosis ranged from 3.99% to 83.34% and the heterobeltiosis from -35.67% to 57.19%. GD based on both phenotypic values and molecular marker data successfully predicted the heterotic patterns in the number of fruits per plant and other fruit morphological traits such as fruit

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length and fruit breadth which is a significant outcome of the study. A multiple linear regression model that included GD, GCA and SCA was more significantly correlated with heterosis for fruit yield than any genetic parameter alone.

Keywords: D^2 statistics, Genetic divergence, Heterosis, Multiple linear regression, SRAP markers

INTRODUCTION

Solanum melongena L. popularly known as eggplant, brinjal or aubergine is a solanaceous vegetable crop cultivated extensively in tropical and sub tropical parts of the world. Its culinary uses and therapeutic properties are well documented in the medieval Arabic, European and Asian literature. The brinjal crop once again revived in the 21st century, recognizing its phenolic and alkaloid contents and the health benefits associated with its consumption. The eggplant is characterized by significant extent of diversity with respect to colour, shape, size, etc (KOUNDINYA *et al.,* 2019). In recent years, cultivars with white coloured fruits gained unique attention, due to their affects on carbohydrate metabolism in the diabetic patients (KWON *et al.,* 2008). To develop the new cultivars in brinjal with specific traits, breeders often emphasize on heterosis breeding (CHADHA and SIDHU, 1982). Heterosis is a biological phenomenon which significantly increased the yield potential of several vegetable crops including eggplant. Since heterotic effects in F_1 combinations are associated with the parental diversity, selection of diverse parents is a pre requisite for successful hybrid breeding programme. Further, information on genetic diversity among the parents, their combining ability and heterotic patterns are necessary to maximize the genetic gain through heterosis (TROYER, 2004). The line × tester genetic analysis proposed by KEMPTHORNE (1957) has got more significance in determining the general combining ability (GCA) and specific combining ability (SCA) effects, as well as to study the nature of gene action. Moreover, the breeding efficacy in eggplant can be increased greatly by predicting the promising F_1 combinations ahead of extensive field trails. Such prediction is possible, if the relationship between hybrid performance and morphological and/or molecular traits is clearly understood.

In recent times, several attempts were made to predict the hybrid performance in F_1 combinations based on the morphological characters of the inbred lines, pedigree data (HAZRA *et al.,* 2010; BOYACI *et al.,* 2020) and most recently with the molecular markers (RODROAGUEZ-BURRUEZO *et al.,* 2008; KAUSHIK *et al.,* 2018; 2019). With the advancement of molecular biology, DNA based markers from genic regions have now been increasingly integrated in analysis of genetic structure of the genotypes in crop breeding programmes. Among the series of molecular markers, SRAP markers are of recent origin that basically target to analyze polymorphism in exonic region of the genome. Unlike other classes of molecular markers, SRAP markers have high reproducibility with reasonable throughput rate. These markers preferentially target the open reading frame regions of the genome and allow exploring the genetic variations in the genome more precisely (LI and QUIROS, 2001). Use of SRAP markers has the potential to understand the relationship between DNA polymorphisms and morphological traits responsible for phenotype expression (FERRIOL *et al.,* 2003). In eggplant, SRAP markers were successfully used by LI *et al.* (2010) for the first time to reveal the genetic diversity and also used by MUTLU *et al.* (2008) for screening the genes responsible for *Fusarium* wilt resistance and ZOHURA and HOQUE, 2019 for bacterial wilt resistance genes. Since genomic information is not required for

analysis, SRAP primers are widely used in genetic diversity studies of several vegetable crops (MANE *et al.*, 2013; KUMAR and AGARWAL, 2019). The correlation between heterosis, combining abilities and genetic distances measured based on the molecular data were studied by several workers with various degrees of success. Some studies have established a positive correlation (RODRÕÂGUEZ-BURRUEZO *et al.*, 2008; KAUSHIK *et al.*, 2018) and some other found less useful correlation for predicting the F_1 performance (KAUSHIK *et al.*, 2019). However, no studies have reported on prediction of F_1 performance in eggplant based on the interrelationships between genetic parameters, morphological traits and SRAP based marker data in eggplant. It was perceived that, the prediction accuracy of F_1 performance can be further improved by integrating the diversity analysis data with appropriate genetic parameters and accordingly conducted this study.

MATERIALS AND METHODS

The plant material used in this study comprised of 11 eggplant genotypes selected based on their white coloured fruiting character (Fig 1).

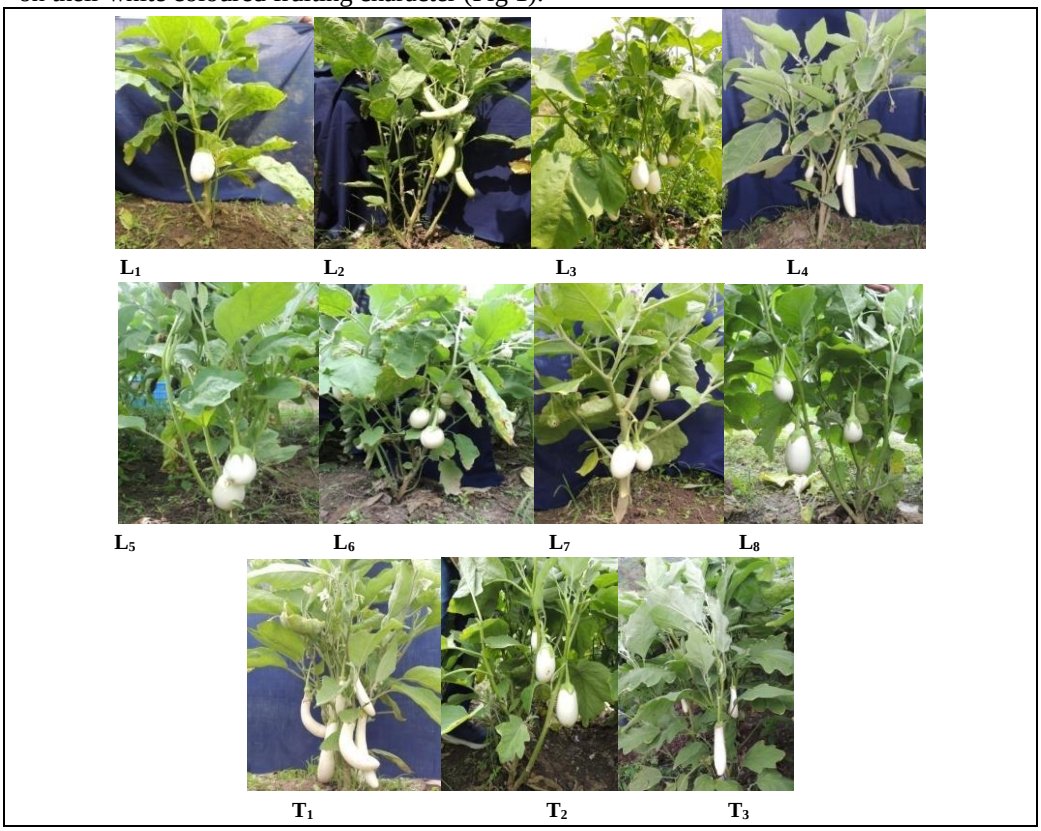

Fig 1. Plant and fruit architecture of the white eggplant genotypes [C-184 (L_1); CH-1045 (L_2); EC-169089 (L_3); IC-090696 (L_4); IC-112901 (L_5); KKM-1 (L_6); Kovvuru Local (L_7); Nadia Local (L_8); Indira Safed Bangan (T_1); Kashi Himani (T_2) and Shweta (T_3)]

The list includes C-184 (L_1); CH-1045 (L_2); EC-169089 (L_3); IC-090696 (L_4); IC-112901 (L_5); KKM-1 (L_6); Kovvuru Local (L_7); Nadia Local (L_8); Indira Safed Bangan (T_1); Kashi Himani (T_2) and Shweta (T_3) collected from different geographical regions of India. The genotypes with broad genetic base Indira Safed Bangan (T_1); Kashi Himani (T_2) and Shweta (T_3) were used as testers in the breeding programme. 24 hybrid combinations were developed by crossing the genotypes in a line × tester mating design (8 lines × 3 testers) as proposed by KEMPTHORNE (1957) and numbered in a series from H_1 ($L_1 \times T_1$) to H_{24} ($L_8 \times T_3$). The field evaluation was conducted during the monsoon season of 2020 at Vegetable Research Farm, Dr Yashwant Singh Parmar University of Horticulture & Forestry, Nauni (Solan) Himachal Pradesh, India (30º 52" N and 77º 11" E at an elevation of 1275 m above sea level) in a randomized complete block design (RCBD) with three replications. Observations were recorded on days to 50% flowering (DFF), days to maturity (DTM), plant height (PH) (cm), stem girth (SG) (cm), number of fruits per plant (FPP), fruit length (FL) (cm), fruit breadth (FB) (cm), fruit weight (FW) (cm) and fruit yield (FY) (q ha^{-1}). Genetic diversity between the genotypes were measured based on the mean value of the nine traits using D^2 statistics given by MAHALANOBIS (1936). A dendrogram was constructed based on the inter cluster distances using the scale given by RAO (1952). The mid parent (MP) and better parent (BP) heterosis were computed as per the procedure outlined by FONSECA and PATTERSON (1968). GCA and SCA effects were estimated following GRIFFING's (1956).

Genomic DNA was extracted from young leaf tissue using the Cetyl Trimethyl Ammonium Bromide (CTAB) extraction protocol developed by MAROOF *et al.* (1994) with minor modifications. The DNA dissolved in 100 µl of TE and then stored at -20°C for further use. The quality and concentration of DNA was assessed using Optizen NanoQ® spectrophotometer (Mecasys®). SRAP analysis was done as per the protocol developed by LI and QUIROS (2001) with minor modifications. A total number of 30 SRAP primer pairs with consistent amplifications were selected to amplify the parental genotypes (Table 1). The PCR amplifications were performed in a 20 µl reaction mixture (total volume) containing 1 mM Tris-HCl (pH 8.3), 0.2 mM each of dNTPs, SRAP primer pair, 50 ng/µl template genomic DNA and 1 U Taq DNA polymerase. The amplifications were performed in a Thermocycler (Eppendorf®) using the PCR programme of initial denaturation 94°C for 4 min followed by eight cycles of three steps: one min denaturation at 94°C, one minute annealing at 35°C and one and half minute extension at 72°C. In the following 35 cycles denaturation at 94°C for 45 sec and the annealing temperature was adjusted from 43-49°C for 1 min (depending on the annealing temperature of the primer pair) with a final elongation step at 72°C for seven minutes**.** The amplified PCR products were electrophoresed in a 1.5% agarose gel in 0.5×TAE buffer (100 mM Tris HCl, pH 8.0, 83 mM glacial acetic acid, 0.5 M EDTA) containing 0.5mg/ml ethidium bromide at a constant voltage of 80 V for 3 h using a horizontal gel electrophoresis system (Bio-Rad). The amplified fragments were visualized and photographed under Alpha image® UV light (Alpha Innotech) using a gel documentation system.

SRAP marker analysis was done by scoring the polymorphic bands manually and the data was assembled in binary data matrix *i.e* '1' for presence of fragment and '0' for absence. For each SRAP marker, Polymorphic Information Content (PIC) was determined as described by SENIOR *et al.* (1998). SRAP marker data were subjected to analysis using Jaccard similarity

coefficient (JACCARD, 1908). The results were subjected to hierarchical cluster analysis using the Unweighted Paired Group Method using Arithmetic averages (UPGMA) algorithms with an aid of NTSYS-PC program. The genetic distance (GD) was calculated using these similarity coefficients, as (GD between parental pair of hybrid = 1 - coefficient of GS of that parental pair). The linear correlation between GD of parental pair of each F_1 combination, SCA and heterosis for different traits was worked out. The linear regression line was drawn, and coefficient of determination (R^2) was calculated (SNEDECOR and COCHRAN, 1989) to test the significance levels between pair of parameters. A multiple linear regression model was developed including heterosis for yield as dependent variable and GD(phenol), GD(srap), GCA(a) and SCA as dependent variables using *R* Studio open source software (version 1.0.136).

Table 1. SRAP primers used in the study

Oligo Code	Primer seq 5'- 3'	% GC	Tm
Me1	TGAGTCCAAACCGGATA	53%	46.8
Me2	TGAGTCCAAACCGGAGC	53%	43.3
Me3	TGAGTCCAAACCGGAAT	47%	44.3
Me4	TGAGTCCAAACCGGACC	44%	45.4
Me5	TGAGTCCAAACCGGAAG	56%	52.2
Em1	GACTGCGTACGAATTAAT	44%	43.3
Em2	GACTGCGTACGAATTTGC	56%	49.2
Em3	GACTGCGTACGAATTGAC	47%	44.3
Em4	GACTGCGTACGAATTTGA	47%	49.2
Em5	GACTGCGTACGAATTAAC	53%	53.3
Em6	GACTGCGTACGAATTGCA	47%	42.9

RESULTS AND DISCUSSION

Genetic divergence based on phenotypic values (GDpheno)

The analysis of variance indicated wide variations among the parental genotypes for all the characters studied. The cluster analysis performed based on the Mahalanobis distance grouped all the eleven genotypes into two clusters (Fig 2a), the first comprising of five genotypes L_3, L_5, L_7, L_8, T_2 and the second cluster comprised of L_1, L_2, L_4, L_6, T_1 and T_3. The inter cluster distance between the two clusters was measured to be 55.104. Cluster 1 recorded the highest mean values for plant height (97.54cm), stem girth (9.44cm), fruit breadth (15.85cm) and fruit weight (87.16g) whereas cluster 2 recorded the highest mean value for number of fruits per plant (15.37), fruit length (12.94 cm) and yield/ha (334.22 q). In the present study, the pattern of distribution of genotypes into two clusters is observed to be based on fruit traits. Though the genotypes taken for the present study are less in number, the diversity present in the exclusive white colored genotypes is of high significance to develop the colour specific hybrids. The phenotypic characters could be efficient in revealing the genetic diversity among the eggplant cultivars (HAZRA *et al.* (2010); BEGUM *et al.* (2013); KAUR *et al.* 2021).

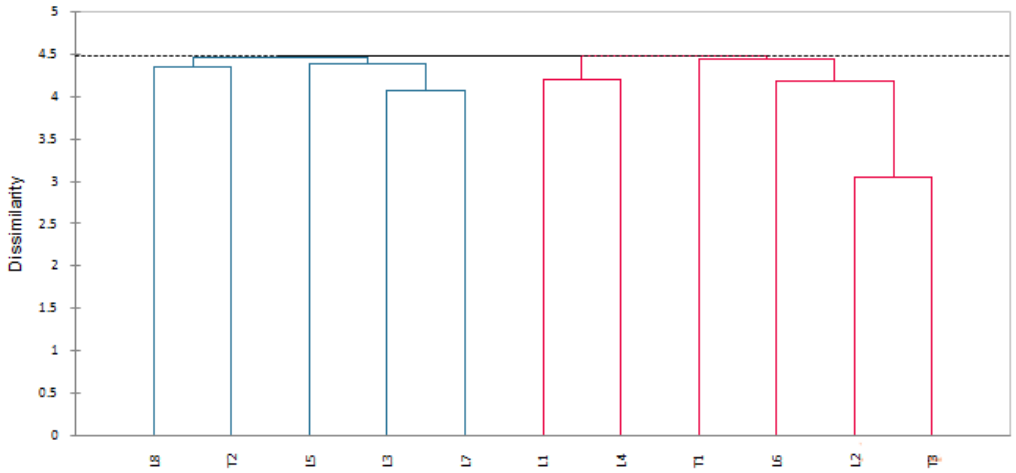

Fig 2a. Dendrogram of eggplant genotypes constructed based on the Mahalanobis D^2 distance

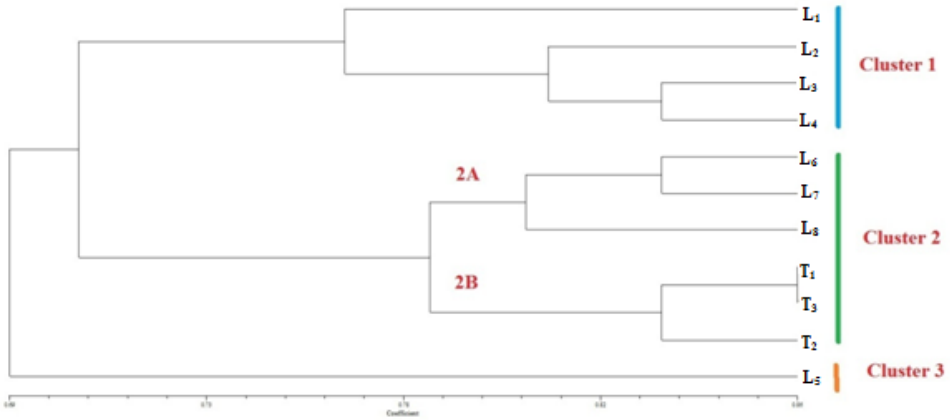

Fig. 2b Dendrogram of eleven parental genotypes based on the SRAP marker data

Genetic divergence based on SRAP marker data (GDsrap)

Among the 30 SRAP primer combinations, 25 primer combinations were found to be polymorphic thus, appeared to be useful to elucidate the molecular diversity in the eggplant genotypes. The number of band positions generated by these thirty primer pairs for the eleven genotypes was 101, which gave an average of 3.36 alleles per primer pair. Amplified alleles varied in size from 100 bp to1700 bp, represented by well resolved peaks (Fig 3). Nine rare alleles were identified during the present investigation, in which the genotype C-184 has four rare alleles at 1600 bp (Me1Em5), at 1100 bp (Me4Em3), at 1200 bp (Me3Em3) and fourth allele at 1500 bp (Me5Em5). Further, three rare alleles at 650 bp, at 700 bp and at 1500 bp (Me2Em6) were identified in the genotype IC-090696. In IC-112901, two rare alleles were identified, one allele at 1500 bp (Me3Em6) and one of 450 bp (Me5Em6). These rare alleles can be used for identification and characterization of the respective genotypes. The primer combinations Me1Em6, Me3Em2, Me4Em2, Me4Em4 and Me5Em1 were found to be monomorphic and thus not used in further studies. The PIC values of polymorphic SRAP markers ranged from 0.09 (Me2Em2) to 0.77 (Me3Em4) with the mean value of 0.38 (Table 2). A total number of 18 primer pairs *viz.*, Me1Em2, Me1Em4, Me1Em5, Me2Em3, Me2Em4, Me2Em5, Me2Em6, Me3Em1, Me3Em3, Me3Em4, Me3Em5, Me3Em6, Me4Em3, Me4Em5, Me4Em6, Me5Em2, Me5Em5 and Me5Em6 had PIC values more than the average. This indicated that SRAP markers could be efficiently applied to detect polymorphism even with a relatively low number of alleles.

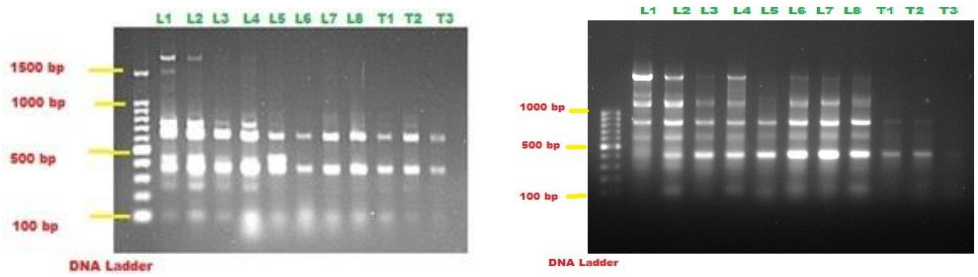

Fig. 3 SRAP profile of eggplant genotypes generated by the primer combination Me5Em5 and Me3Em3

SRAP markers are ORF region markers and diversity accounted by these markers is due to analysis of exonic parts. The Jaccard's similarity coefficient estimates showed a narrow window that varied from 0.60 (between L_1 and L_5) to 0.86 (between T_1 and T_3). Among the eleven genotypes, the pairs with lowest genetic similarity value *i.e.*, maximum diverse pairs were L_1 and L_5 (60% genetic similarity), L_1 and L_6; L_8 and L_5 (64% genetic similarity), L_4 and T_1; L_5 and T_2 (65% genetic similarity). The SRAP based GD used in the present study successfully predicted the potential high yielding hybrid combinations. All of the three cultivated genotypes of white fruited brinjal *viz.*, Indira Safed Bangan, Kashi Himani and Shweta fell in the same cluster determining the similarity among these genotypes. The UPGMA (un-weighted pair group

method with arithmetic mean) dendrogram was constructed using Jaccard's similarity coefficient of SRAP marker data generated on eleven genotypes employing the programme NTSYS-pc (Fig 2b). The dendrogram constructed from SRAP marker data grouped eleven eggplant genotypes into three clusters: Cluster I, II and III. To categorize the genotypes into different clusters, mean genetic similarity coefficient (0.73) was considered arbitrarily as a guideline, and genotypes classified into different clusters based on inter cluster similarity coefficient of 0.73 or less. Cluster I was formed at 0.765 Jaccard's coefficient of similarity. It consisted of four genotypes *viz.*, L_1, L_2, L_3 and L_4 in which L_3 and L_4 were closely related with each other by similarity coefficient of 0.92. Cluster I related with Cluster II and Cluster III at 0.844 Jaccard's coefficient of similarity. Cluster II consisted of two sub-clusters: sub cluster 2A and 2b. Sub cluster 2A consisted of three genotypes *viz.*, L_6, L_7 and L_8 whereas sub cluster 2B consisted of all the three testers *viz.*, T_1, T_2 and T_3. Cluster III consisted of only one genotype *i.e.*, L_5 which formed as a completely out group.

Table 2. Polymorphic Information content (PIC) values obtained with SRAP primers

Primer combination	Total number of bands	No of polymorphic bands	PIC Value	Primer combination	Total number of bands	No of polymorphic bands	PIC Value
Me1 Em1	2	1	0.35	Me3 Em4	6	6	0.77
Me1 Em2	4	4	0.76	Me3 Em5	2	1	0.48
Me1 Em3	2	1	0.30	Me3 Em6	3	2	0.53
Me1 Em4	3	1	0.40	Me4 Em1	3	1	0.09
Me1 Em5	4	3	0.71	Me4 Em2	1	0	0.00
Me1 Em6	1	0	0.00	Me4 Em3	3	3	0.55
Me2 Em1	5	1	0.20	Me4 Em4	1	0	0.00
Me2 Em2	2	1	0.09	Me4 Em5	6	5	0.55
Me2 Em3	7	5	0.44	Me4 Em6	5	4	0.44
Me2 Em4	3	2	0.64	Me5 Em1	1	0	0.00
Me2 Em5	6	4	0.41	Me5 Em2	2	1	0.46
Me2 Em6	4	3	0.74	Me5 Em3	3	2	0.29
Me3 Em1	2	1	0.50	Me5 Em4	2	0	0.09
Me3 Em2	1	0	0.00	Me5 Em5	7	5	0.65
Me3 Em3	6	4	0.47	Me5 Em6	4	3	0.51

The extent and distribution of genetic variability is a factor to achieve success in crop breeding programme. Though eggplant is a widely studied vegetable crop, the information on exclusive white coloured genotypes is scanty. Estimation of genetic diversity in eggplant using SRAP molecular system is relatively new and very few reports are available so far (CHEN *et al.*, 2013; ALTAYE, 2015; UYSAL *et al.*, 2019). In the present study, parental molecular diversity was assessed by thirty SRAP markers, among them 25 primer combinations showed polymorphism and produced 62 polymorphic alleles (61.38% polymorphism) with an average of 3.37 alleles per

marker. SRAP primers used in the present study had produced sufficient number of average alleles (3.36) similar to 4.4 per locus from 23 STMS primers (BEHRA *et al.,* 2006), 3.8 average alleles per locus from 22 SSRs (NAEGELE *et al.,* 2014) and 3.6 average alleles per locus from 22 Random Amplified Polymorphic DNA (RAPD) primers (KARIHALOO *et al.,* 1995). The applicability of genetic markers to analyze a trait depends on the extent of polymorphism detectable with the given markers. It is thus necessary to establish the PIC, which expresses the ability of a locus to discriminate between genotypes. Among the 30 primer pairs used, 18 combinations have PIC values more than the average and thus treated as highly informative for genetic diversity analysis. The SRAP marker data obtained was further used to determine the genetic relatedness among the studied genotypes. The dendrogram constructed shows that all the cultivated genotypes form a distinct cluster (cluster 2B) suggesting relatively high level of genetic similarity within these genotypes.

The SRAP diversity observed in the present study is comparable to the findings of UYSAL *et al.* (2019) who employed the SRAP molecular marker system to understand the genetic variability/similarity among the 32 eggplant genotypes using 10 SRAP primer combinations and had reported 73% polymorphism. The UPGMA dendrogram indicated the genetic similarity to an extent of 0.68-0.99 and all the genotypes were clustered into two groups. The results successfully exhibited the practical utility of SRAP marker system in studying the genetic diversity in eggplant. ALTAYE (2015) analyzed the genetic diversity using 132 primer combinations of SRAP markers among the 79 eggplant accessions representing 28 countries. A higher percentage of polymorphism of SRAP primers were observed in out groups. CHEN *et al.* (2013) employed SSRs and the SRAP markers to assess the genetic diversity among the 222 accessions of brinjal collected from 35 countries. In total 25 SRAP and 5 SSR primer combinations were used in the study. A high level of polymorphism was observed to the level of 75% for SRAP primers and 65% for SSR primers.

Per se performance, SCA and heterosis

A wide variation was observed among the parental genotypes and the resultant F_1 combinations for the characters studied (Table 3). Among the parental lines L_2 was found to be best performing line for DFF and FL; L_5 exhibited the maximum values for SG, FB and FW; FPP and yield was found to be highest in L_6. The tester genotype T_1 exhibited the better values for all the characters studied except for FB which was found highest in T_2. Among the crosses, the top four cross combinations with significantly ($p<0.05$) high fruit yield per hectare are H_{14} (397.40 q/ha), H_{18} (392.41 q/ha), H_4 (389.23 q/ha) and H_{20} (354.52 q/ha). The mean performance of hybrid combinations for the characters DFF, DTM were found to be less than the mean of line and tester values which is positive phenomenon for crop improvement for earliness. For the traits, PH, FPP, FL, FB, FW and FY the mean hybrid values are found to be highest than the average mean of lines and testers. Overall the hybrid combinations exhibited a 40% increase over the mean value of the parents for the trait FY which indicates that the yield can be increased through heterosis breeding significantly in eggplant.

Among the 24 F_1 combinations, six crosses were identified with significant positive SCA effects for fruit yield *viz.,* H_4 (232.00), H_7 (128.49), H_{13} (132.78), H_{14} (112.40), H_{16} (186.69) and H_{20} (114.01). Two cross combinations H_6 (-135.19) and H_{12} (-346.00) were found

to have significant negative SCA effects. Remaining crosses were identified as average specific combiners with non significant SCA effects ranged from -98.21 (H_8) to 95.23 (H_{18}). Considerable variation was observed for the fruit yield both in the parental genotypes and the F_1 hybrid combinations. The experimental results revealed that, 22 F_1 combinations exhibited significant positive heterosis over the mid parent while, 13 out of 24 hybrid combinations exhibited significant positive heterosis over the better parent for yield per plant. The mid parent heterosis for fruit yield ranged from 3.99% to 83.34%. The mid parent heterosis was found to be highest in the cross combination of H_{13} ($L_5 \times T_2$) (83.34%) followed by H_{16} ($L_8 \times T_2$) (79.27%). The heterobeltiosis for fruit yield ranged from -35.67% to 57.19% (Fig 4). The promising crosses with significantly higher positive heterobeltiosis for fruit yield are H_{14} ($L_6 \times T_2$) (57.19%), H_{16} ($L_8 \times T_2$) (57.13%), H_{20} ($L_4 \times T_3$) (46.35%) followed by H_{13} ($L_5 \times T_2$) (36.94%).

Table 3. Mean performance of the line, testers and hybrids for various economically important traits

Character	Lines			Tester			Hybrids		
	Range	Mean	Highest	Range	Mean	Highest	Range	Mean	Highest
DFF	39.00-54.22	45.64	L2	39.78-44.67	42.03	T1	39.78-53.56	44.43	H2
DTM	58.00-79.55	67.13	L6	57.11-61.33	59.44	T1	55.33-70.78	62.84	H6
PH (cm)	77.02-110.80	91.34	L7	97.62-112.34	105.35	T1	93.98-111.57	100.32	H8
SG (cm)	7.90-10.35	9.13	L5	9.26-9.79	9.44	T1	8.58-10.07	9.22	H5
FPP	3.00-21.44	12.41	L6	13.78-22.33	18.51	T1	7.33-23.22	15.96	H4
FL (cm)	6.48-17.34	10.22	L2	10.59-18.25	14.65	T1	8.61-19.91	12.75	H20
FB (cm)	2.75-6.19	4.77	L5	3.44-4.50	3.92	T2	3.16-6.18	4.56	H1
FW (g)	69.41-112.27	85.20	L5	79.12-93.94	88.80	T1	73.60-104.48	90.06	H5
FY (q/ha)	70.50-252.82	174.72	L6	242.24-297.03	262.99	T1	174.79-389.23	307.59	H4

The heterotic performance of cross combinations by and large depends on the combining ability of the parents used in the hybridization process. The earliest reports on combining ability studies in eggplant date back to the late 1940s (SAMBANDAM, 1962). In the present study the estimates of variance due to SCA (σ^2 SCA) was higher than the corresponding variance due to average GCA (σ^2 GCA) for fruit yield indicating the preponderance of non-additive genetic control (*i.e.*, dominant, additive × dominant and dominant × dominant effects) in determining the fruit yield (BAKER, 1978). Earlier some studies have also reported both additive and non-additive genetic control in yield and yield attributing traits in eggplant (MISTRY *et al.*, 2016; AKPAN *et al.*, 2016; KAUSHIK *et al.*, 2019). However, the experimental findings of the

present study support that, heterosis as the most preferable breeding approach for enhancing the yield potential of eggplant.

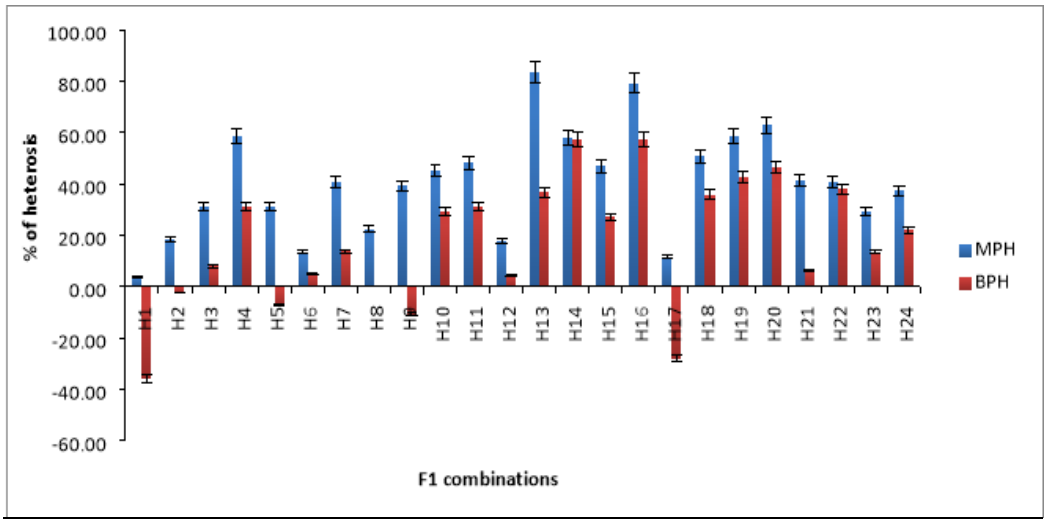

Fig 4. The mid parent and better parent heterosis for fruit yield in 24 F1 combinations

Correlation between GD and heterosis to predict the F_1 performance

The genetic distances between the pair of parental genotypes were successfully detected based on the phenotypic values (GDpheno) and SRAP molecular markers (GDsrap). The Spearman's rank correlation coefficients were computed among GDpheno and GDsrap with mean performance of F_1 combinations along with SCA, GCA, MPH and BPH (Table 4). Significantly positive correlations were found between GDpheno with GCA(m) and GCA(a) for FB; GDpheno with MPH and BPH for FPP and GDpheno with BPH for FL. Further, significantly positive correlations were found between GDsrap with SCA, MPH, BPH for FPP; GDsrap with mean for PH; GDsrap with BPH for FL. Significantly negative correlations were found between GDpheno with SCA for FW and FY; GDpheno with GCA(m) and GCA(a) for FL, GDpheno with MPH for FY and with BPH for FB. Whereas significantly negative correlations were between GDsrap with SCA for FL, GDsrap with GCA(m) for PH and BPH for DFF. In the present study, GD based on both phenotypic values and molecular marker data successfully predicted the heterotic patterns in the number of fruits per plant and other fruit morphological traits such as fruit length and fruit breadth which is a significant outcome of the study. However, the GD detected in the present study cannot effectively predict the MPH and BPH for yield in brinjal.

The linear regression of GDsrap on MPH and BPH were non-significant with R^2 values of 0.032 and 0.005, respectively. Further, GDsrap had positive correlation with SCA (r = 0.263) with a non significant R^2 value of 0.123. From the experimental findings it can be inferred that the variation attributed to SCA and MPH of hybrid combinations could be partially explained due to SRAP based GD of the parental genotypes. The Spearman's rank correlation studies

clearly indicated that, the fruit yield of F_1s is significantly and positively correlated with MPH (r = 0.751), BPH (r = 0.909) and the SCA (r = 0.560). In all relations, higher correlation of fruit yield of F_1s was observed with BPH (r = 0.909). The SCA was found significantly and positively associated with the MPH (r = 0.706). Since, performance of F_1 crosses is largely depends on the parental diversity, GCA and SCA effects, we tried to establish the relationship between these genetic parameters using a multiple linear regression model. The model included heterosis for yield as regressed variable and GD(pheno), GD(srap), GCA(a) and SCA as dependent variables. The correlations between mid parent heterosis and better parent heterosis for yield with GCA and SCA were found to be highly significant with an adjusted R value of 0.653 and 0.796, respectively. The correlations observed were found to be greater than those between hybrid yield, GD, GCA and SCA than any genetic parameter alone.

Table 4. Correlation between GD among parental genotypes, SCA, heterosis and hybrid trait value

Character	GD based on morphological data						
	Mean	SCA	GCA (m)	GCA (f)	GCA (a)	MPH	BPH
DFF	0.18	0.11	0.26	0.10	0.28	-0.24	0.48**
DTM	0.13	-0.05	0.15	0.09	0.18	0.10	-0.04
PH	-0.13	0.18	-0.09	0.20	0.04	-0.28	-0.46
SG	0.01	0.10	0.08	0.07	0.10	-0.23	-0.05
FPP	-0.20	-0.13	0.11	0.26	0.23	0.30*	0.47**
FL	-0.17	-0.30	-0.50**	-0.18	-0.51**	-0.25	0.44*
FB	0.16	0.23	0.32*	0.21	0.36*	-0.28	-0.84**
FW	-0.02	-0.42**	0.11	-0.18	0.02	0.25	0.19
FY	-0.22	-0.52**	0.00	0.21	0.05	-0.34*	0.08

GD based on SRAP marker data						
Mean	SCA	GCA (m)	GCA (f)	GCA (a)	MPH	BPH
0.32*	0.10	0.31	0.03	0.30	0.45*	-0.50**
0.07	-0.10	0.13	-0.11	0.03	0.25	0.18
0.44*	0.01	-0.46**	-0.11	-0.04	0.11	-0.42*
-0.15	-0.30	-0.16	-0.09	-0.18	0.25	0.02
-0.16	0.46**	-0.24	-0.09	-0.25	0.56**	0.39*
0.19	-0.59**	0.25	0.01	0.21	0.07	0.56*
-0.06	-0.21	-0.11	-0.03	-0.11	0.10	0.03
0.09	0.11	0.08	0.01	0.07	-0.29	0.14
-0.13	0.34	-0.34	-0.03	-0.34	-0.41*	-0.33

With increasing the number of parents, the number of hybrid combinations grows exponentially and identifying the potential F_1 combinations in field evaluation trails became tedious and extremely labour intensive. Thus, tools that allow predicting hybrid performance facilitate the pre-selection of parents more precisely (SHATTUCK *et al.*, 1993). The degree of heterosis in F_1 populations is correlated with the GD of parental genotypes, as the heterotic effect is considered to be higher when the parents are divergent (KUMAR *et al.*, 2020). It is generally conceived that, when the parents are diverse the heterotic effect increases (MOLL *et al.*, 1965).

However, this may not be generalized for the entire range of diversity available within a given crop species. Selection of diverse parents in a hybridization programme is necessary but the same may not guarantee the higher heterotic effect. Hence, selection of parental lines either based on GD or based on *per se* performance alone is not sufficient to make effective hybrid development programme (VUYLSTEKE, 2000). On reviewing the available literature, we found that this is the first attempt to study the interrelationships in eggplant genetic parameters based on the SRAP molecular marker system. Earlier SNPs based GD of parents and its correlation with the heterosis and SCA was studied by KAUSHIK *et al.* (2019) in eggplant and no significant correlations were reported between GD and SCA of eggplant cultivars. The *r* values between GD and hybrid trait values were found to be low in this study. In contrast to the results obtained in the present study, KAUSHIK *et al.* (2019) reported the significant negative correlations between GD of parental pair with the mean yield of F_1 combinations. RODROAGUEZ-BURRUEZO *et al.* (2008) also studied the interrelationships between GD of parents based on Amplified Fragment Length Polymorphism (AFLP) markers, hybrid performance for fruit weight in Spanish Local varieties and found relatively high correlations ($r>0.6$) between GD and the fruit yield of F_1 combinations.

CONCLUSION

The present study successfully demonstrated that, the SRAP molecular marker technique is a powerful tool to detect the polymorphism among the white fruited eggplant genotypes even with a relatively low number of alleles. SRAP markers offer a non specific genome side coverage which could well complement the constrains associated with the classical molecular marker techniques such as low polymorphism rate for RAPD, complexities for Restriction Fragment Length Polymorphism (RFLP) and availability of less number of Simple-sequence repeats (SSRs) and Single-nucleotide polymorphism (SNPs) markers. The study clearly established that, genetic distances based on phenotypic and molecular markers can be combined together to improve the predictability of the heterosis for various economically important traits. It will be interesting to study the genetic diversity in eggplant by including more number of genotypes to establish the sound interrelationship among the various genetic parameters.

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PREDVIĐANJE PERFORMANSI F1 UKŠTANJA U PATLIDŽANU (*Solanum melongena* L.) NA BAZI MORFOLOŠKE I MOLEKULARNE DIVERGENCIJE

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Izvod

Identifikovanje potencijalnih F1 hibridnih kombinacija na osnovu diverziteta roditelja može povećati efikasnost oplemenjivanja i uštedeti vreme. U ovom radu, genetski diverzitet između genotipova patlidžana je meren statistikom Mahalanobis D2 i SRAP molekularnim markerima (*Sequence Related Amplified Polymorphism*). Genetičke udaljenosti (GD) su bile u korelaciji sa heterozisom i srednjim performansama F1 ukrštanja generisanih u dizajnu linija × tester za predviđanje F1 performansi za agronomski važne osobine. Klaster analiza izvedena na osnovu Mahalanobis D2 udaljenosti grupisala je svih jedanaest genotipova u dva klastera, a tri klastera su formirana na osnovu podataka SRAP markera. Vrednosti PIC dobijene sa 30 kombinacija SRAP markera bile su u rasponu od 0,09 do 0,77 sa srednjom vrednošću od 0,38. Što se tiče prinosa, F1 kombinacije su pokazale srednju roditeljsku heterozu u rasponu od 3,99% do 83,34% i heterobeltiozu od -35,67% do 57,19%. GD na osnovu fenotipskih vrednosti i podataka o molekularnim markerima uspešno je predvideo heterotične obrasce u broju plodova po biljci i druge morfološke osobine ploda kao što su dužina i širina ploda, što je značajan rezultat studije. Model višestruke linearne regresije koji je uključivao GD, GCA i SCA bio je u značajnijoj korelaciji sa heterozom za prinos ploda nego sa bilo kojim genetskim parametrom sam.

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