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Prediction of heterosis based on genetic divergence in tomato

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ABSTRACT

Tomato germplasm collected from different sources and lines developed through pedigree method of breeding were assessed and based on Mahalanobis D^2 analysis totally 67 genotypes were grouped in to 7 clusters where, maximum of 44 genotypes entered in cluster I, followed by 11 genotypes in cluster II, 7 genotypes in cluster IV, two genotypes in cluster III and the clusters V, VI and VII had solitary genotype each. Totally 14 lines and 2 testers representing three clusters were selected and crossed to get 28 hybrids. After evaluating the hybrids and parents, D^2 values of respective crosses (d^2 values between parents of the cross) were correlated with heterosis values for various traits. Heterosis over better parent was positively and significantly associated with D^2 values for only β-carotene (r_p = 0.4404) and ascorbic acid (r_p = -0.438) content of fruit. Heterosis over the best parent was significantly correlated with D^2 values (Table 2) for number of primary branches at 30 DAT (r_p = 0.4548), days to first (r_p = -0.4293) and days to fifty per cent flowering (r_p = -0.4652), days to first fruit maturity (r_p = -0.3878), polar (r_p = -0.4794) and equatorial (r_p = -0.5990) diameter of the fruit, number of fruits per plant (r_p = -0.5156) and average fruit weight (r_p = -0.5690) indicating the possibility of prediction of heterosis based on D^2 values and D^2 values can be useful in at least rejection of inferior combinations in tomato.

Key words: D^2 values, genetic divergence, heterosis, tomato.

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the most popular and widely grown vegetables in the world. The species *lycopersicum* possesses a wealth of genetic diversity and cultivated tomato is one of the nine species belonging to this genus. Apart from the cultivated species, the wild species do have a great potential value because of diversity of their germplasm (Rick, 6). The success of a breeding programme depends upon the extent and magnitude of variability existing in the germplasm. Commercial F_1 hybrids are very common in tomato and selection of newer parents for higher magnitude of heterosis is a continuous process. Generally, diverse plants are expected to give high hybrid vigour and the information on genetic divergence of various traits particularly of those that contribute to yield and quality would be most useful in planning the breeding programme. Mahalanobis's (3) generalised distance is a very sensitive and potent biometrical tool in quantifying the degree of divergence between biological populations and also to assess the relative contribution of different components to the total divergence both at inter- and intra-cluster levels (Singh and Singh, 9; Singh *et al.*, 8). However, selection of parents based on genetic distance to get high heterosis is valid only when a relation between genetic distance and magnitude of heterosis exists. If the genetic distance is a true indicator of heterosis for a given trait then efficiency of breeding programme can be enhanced greatly. Therefore, an investigation was carried out to study the relation between genetic divergence and heterosis in tomato.

MATERIALS AND METHODS

Study was carried out with 69 tomato genotypes comprising of seven open-pollinated varieties developed by public sector organisations and nine entries collected from different institutes and 51 entries developed at Kittur Rani Channamma College of Horticulture, Arabhavi through pedigree method of breeding. Mahalanobis's (3) D^2 statistics was used for assessing the genetic divergence between 67 genotypes. The original correlated unstandardised character mean values were transformed into standardised uncorrelated values to simplify the computational procedure. The D^2 values were obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated (Ys) values of any two genotypes. Using all D^2 values, the genotypes were grouped into clusters using Tocher's method as described by Rao (4). The intra- and inter-cluster distances were calculated by the formula given by Singh and Chaudhary (9). From the set of these 67 genotypes, 14 lines possessing good fruit quality attributes were selected representing different clusters. The lines TP1, TP11 and TP14 belonging to Cluster II and TP19 belonging to cluster IV and TP2, TP3, TP4,

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TP5, TP6 TP7, TP8, TP10, TP12 and TP13 belonging to Cluster IV were selected. Two bacterial wilt resistant varieties, *viz*., Arka Alok (AAlok belongs to cluster II) and Arka Abha (AAbha belongs to cluster I) developed at IIHR, Bangalore were selected as testers. Each of these 14 lines was crossed with each of two testers to develop 28 F_1 hybrids. These hybrids were evaluated along with parents for various growth, earliness, yield and quality parameters. Heterosis over better parent and the best parent were worked out for each cross. Inter-or-Intra (both parents belonging to same cluster) cluster distances, *i.e.*, D^2 values of respective crosses (d^2 values between parents of the cross) were correlated with heterosis values for various traits. Simple correlation coefficients (product movement correlation coefficient) were worked out (n = 28).

RESULTS AND DISCUSSION

Existence of genetic variability among the genotypes for the character to be improved is the most basic requirement for successful selection. In the present investigation, variance due to genotypes was highly significant for all the characters studied. Grouping of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding. The material for present study includes 67 genotypes. Nevertheless, considerable diversity was implied by the magnitude of all the possible D^2 values, which ranged from 86.717 to 243.70 (Table 1).Such genetic diversity has also been reported previously in tomato (Sharma *et al.*, *7*; Singh and Singh, 10). Sixty-seven genotypes were grouped into 7 clusters, which had considerably high intra- and inter-cluster D^2 values. A maximum of 44 genotypes entered in cluster I, followed by 11 genotypes in cluster II, 7 genotypes in cluster IV, two genotypes in cluster III and the clusters V, VI and VII had solitary genotype in each. The cluster IV showed maximum intra-cluster distance (D^2 = 68.998) followed by cluster I (D^2 = 61.060), cluster II (D^2 = 57.351) and cluster IV (D^2 = 23.327). The clusters V, VI and VII had no intra-cluster distance (D^2 = 0.000) as they possessed single genotype in each and the genotypes belonging to these clusters were not selected for heterosis studies. From this set of genotypes 14 lines and 2 testers were selected, which represented three different clusters (I, II, IV) which possessed maximum intra-cluster distances and good horticultural traits. Selection was planned to get mating of genotypes of within and between clusters. Heterosis over better parent and the best parents for 30 traits were correlated with D^2 values. Results indicated that heterosis over better parent was positively and significantly associated with D^2 values (Table 2) for only β-carotene content (r_p = 0.4404) and it was negatively and significantly associated with D^2 values for ascorbic acid content of fruit (r_p = -0.4383). For β-carotene content, eight hybrids exhibited significant and positive heterosis over better parent (Table 3). If genetic distance between parents is higher, the magnitude of heterosis can be expected to be higher for β-carotene content of fruit in tomato. For ascorbic acid content of fruit also eight hybrids exhibited significant positive heterosis over better parent (Table 3). As the D^2 values negatively correlated with heterosis values (over better parent), narrow genetic distance between parents (with in the specified range) can result in higher heterosis for ascorbic acid content of fruit in tomato.

Heterosis over the bes t parent was significantly correlated with D^2 values (Table 2) for number of primary branches at 30 DAT (r_p = 0.4548), days to first flowering (r_p = -0.4293), days to fifty per cent flowering (r_p = -0.4652) and days to first fruit maturity (r_p = -0.3878). For number of primary branches two hybrids (TP5 × AAlok and TP14 × AAbha) showed positively significant heterosis over the best parent where as for days to first flowering five hybrids and for days to first fruit set one hybrid (TP3 × AAbha) exhibited significant heterosis in desirable direction (Table 4) and number of hybrids exhibiting significant heterosis was related

Table 1. Average intra- and inter-cluster D^2 values for 21 characters in tomato genotypes.

Cluster	I	II	III	IV	V	VI	VII
I	61.060	100.910	152.372	100.683	148.365	146.309	192.943
II		57.351	86.717	117.993	169.519	137.105	116.576
III			23.327	132.551	239.740	145.533	111.742
IV				68.998	222.521	106.005	211.820
V					0.000	243.700	207.860
VI						0.000	209.086
VII							0.000

Note: Diagonal values indicate intra-cluster distances.

Table 2. Correlation coefficients of D^2 values with corresponding heterosis values for growth, earliness, yield and quality parameters in tomato.

Sl. No.	Parameter	Better parent heterosis	Best parent heterosis
1.	Plant height (cm) at 30 DAT	0.0578	0.1527
2.	Plant height (cm) at 60 DAT	0.2662	0.3126
3.	Plant height (cm) at 90 DAT	0.2370	0.2958
4.	Plant spread (cm) at 60 DAT	-0.0076	0.0088
5.	Plant spread (cm) at 90 DAT	0.0819	0.1396
6.	No. of primary branches at 30 DAT	0.1542	0.4548*
7.	No. of primary branches at 60 DAT	-0.1310	0.1083
8.	No. of primary branches at 90 DAT	-0.1343	0.1042
9.	Stem girth (cm) at 30 DAT	-0.2929	-0.2202
10.	Stem girth (cm) at 60 DAT	-0.1552	-0.0607
11.	Stem girth (cm) at 90 DAT	-0.1341	-0.0481
12.	Days to first flowering	-0.0289	-0.4293*
13.	Days to 50 per cent flowering	-0.0485	-0.4652*
14.	Days to first fruit set	0.0110	-0.3931*
15.	Days to first fruit maturity	0.1844	-0.3878*
16.	Per cent fruit set	-0.2319	0.3338
17.	Polar diameter of fruit	-0.1909	-0.4794**
18.	Equatorial dia. of fruit	0.1391	-0.5990**
19.	No. of fruits per cluster	0.2648	0.3235
20.	No. of fruits per plant	0.1768	0.5156**
21.	Average fruit weight (g)	-0.1510	-0.5690**
22.	Early yield/ plant (kg)	0.1156	-0.2366
23.	Total yield/ plant (kg)	0.0743	-0.2554
24.	Pericarp thickness (mm)	0.3196	-0.0538
25.	No. of locules/ fruit	-0.3498	-0.2810
26.	TSS (°Brix)	0.1852	0.0559
27.	Titrable acidity (%)	0.1098	0.1832
28.	Ascorbic acid (mg/ 100 g)	-0.4383*	-0.1357
29.	Lycopene content (mg/ 100 g)	-0.1532	-0.3734
30.	β-carotene (µg/ 100 g)	0.4404*	0.0902

*, ** significance at 5 and 1% levels, respectively.

to the magnitude of correlation coefficient and hence, heterosis can be fairly predicted based on D^2 values for these traits.

Although heterosis for yield in tomato was reported very oftenly (Singh and Singh, 11; Baishya *et al*., 1; Tiwari and Lal, 12; Sharma *et al*., 7), number of lines and hybrids need to be developed and screened is very high which engulfs lot of resources and time. Therefore, methods to enhance the efficiency of heterosis breeding are very important. Easy way of screening lines can be based on genetic distance provided there is relation between genetic distance and heterosis (Hazra *et al*., 2; Rathi *et al*., *5*). Among yield parameters, polar (r_p = -0.4794) and equatorial (r_p = -0.5990) diameter of the fruit, number of fruits per plant (r_p = -0.5156) and average fruit weight (r_p = -0.5690), the D^2 values had highly significant association with heterosis values over the best parent (Table 2).

Table 3. Heterosis (%) for polar and equatorial diameter of fruit, number of fruits, average fruit weight, ascorbic acid and β-carotene content in tomato.

Cross	Fruit polar dia.	Equatorial fruit dia.	No. of fruits/ plant	Average fruit weight	Ascorbic acid	β-carotene	D^2 value
	BTP	BTP	BTP	BTP	BP	BP	
TP1 × AAlok	-32.54**	-6.09**	-39.07**	-20.48**	0.23	-5.09	57.351
TP1 × AAbha	-28.58**	-7.16**	-38.86**	-26.36**	-11.63**	-37.30**	100.91
TP2 × AAlok	-32.54**	-0.45**	-40.08**	-12.97**	7.76**	99.72**	100.91
TP2 × AAbha	-33.20**	-12.65**	-36.30**	-29.30**	5.85**	-11.22	61.06
TP3 × AAlok	-27.14**	-17.22**	-29.84**	-27.89**	-23.72**	-5.34	100.91
TP3 × AAbha	-32.80**	-13.87**	-30.06**	-36.69**	4.14**	-54.24**	61.06
TP4 × AAlok	-6.45**	-12.65**	-34.30**	-16.68**	-36.56**	65.02**	100.91
TP4 × AAbha	-25.42**	-15.54**	-36.40**	-31.23**	-33.18**	8.87	61.06
TP5 × AAlok	-30.30**	-10.51**	-23.83**	-30.35**	-50.27**	-39.88**	100.91
TP5 × AAbha	-15.28**	-12.19**	-22.71**	-22.01**	16.25**	-10.71	61.06
TP6 × AAlok	-24.24**	-10.21**	-34.18**	-21.73**	-40.49**	44.44**	100.91
TP6 × AAbha	-33.33**	-5.18**	-27.05**	-12.32**	-17.89**	-4.54	61.06
TP7 × AAlok	-20.02**	-7.31**	-36.85**	-34.56**	-43.91**	95.53**	100.91
TP7 × AAbha	-8.56**	-11.27**	-38.41**	-18.16**	-7.24**	-63.40**	61.06
TP8 × AAlok	-2.37**	4.26**	-35.40**	24.14**	17.76**	-6.96	100.91
TP8 × AAbha	-22.39**	-18.44**	-27.18**	-21.92**	0.88	17.44**	61.06
TP9 × AAlok	-43.34**	-22.10**	10.68**	-52.31**	-11.89**	15.21*	117.993
TP9 × AAbha	-31.88**	-16.61**	-4.57**	-36.18**	-20.21**	-44.52**	100.683
TP10 × AAlok	-30.03**	-13.87**	-23.27**	-30.62**	-40.92**	11.07	100.91
TP10 × AAbha	-26.48**	-19.20**	-21.04**	-40.12**	-14.76**	-14.57*	61.06
TP11 × AAlok	-47.03**	-20.57**	8.01**	-46.42**	49.21**	-11.69	57.351
TP11 × AAbha	-38.73**	-20.42**	-20.27**	-45.59**	-20.62**	33.93**	100.91
TP12 × AAlok	-37.15**	-9.60**	-42.65**	-31.60**	-7.29**	66.35**	100.91
TP12 × AAbha	-23.45**	-7.62**	-29.29**	-5.69	10.49**	-28.99**	61.06
TP13 × AAlok	-38.99**	-14.78**	-27.83**	-36.60**	-9.80**	3.21	100.91
TP13 × AAbha	-29.51**	-13.71**	-21.27**	-30.76**	12.87**	-20.34**	61.06
TP14 × AAlok	-31.35**	-7.46**	-29.39**	-16.77**	30.42**	-16.63**	57.351
TP14 × AAbha	-28.98**	-17.68**	-28.50**	-39.38**	37.60**	-1.64	100.91
CD at 5%	0.202	0.201	2.088	6.997	1.644	11.8	

*, ** indicate significance at 5 and 1% levels, respectively.
BP – Heterosis over better parent, BTP = Heterosis over the best parent

Majority of the hybrids exhibited significantly negative heterosis over the best parent for polar and equatorial diameter of the fruit and average fruit weight (Table 3) and correlation between genetic distance (D^2 values) and heterosis (over the parent) was negative for these traits. As the correlation coefficient values are higher for these yield parameters, the D^2 values can be strong indicators of heterosis where, narrow distance (within specified range) can result with higher heterosis. For number of fruits per plant, heterosis values positively correlated with D^2 values where, more the distance between parents, higher heterosis can be expected (Hazra *et al.* 2, Rathi *et al.*, 5). For yield per plant, D^2 values did not correlate with heterosis and it is

Table 4. Heterosis (%) over the best parent for number of primary branches per plant and earliness parameters in tomato.

Cross	No. of primary branches per plant at 30 DAT	Days to first flowering	Days to fifty per cent flowering	Days to first fruit set	Days to first fruit maturity	D^2 value
TP1 × AAlok	-26.51**	49.96**	30.31**	29.32**	8.99**	57.351
TP1 × AAbha	-18.21**	33.94**	14.86**	20.00**	7.41**	100.91
TP2 × AAlok	-12.39**	-8.03**	13.63**	12.00**	5.82**	100.91
TP2 × AAbha	0.00	9.95**	9.09**	0	6.34**	61.06
TP3 × AAlok	-7.43**	-32.02**	25.77**	13.32**	14.80**	100.91
TP3 × AAbha	-33.95**	-8.03**	6.04**	-10.68**	0.52	61.06
TP4 × AAlok	-19.82**	-5.99**	22.72**	9.32**	7.93**	100.91
TP4 × AAbha	-12.39**	9.95**	12.13**	4.00**	8.45**	61.06
TP5 × AAlok	7.43**	17.99**	25.77**	16.00**	15.34**	100.91
TP5 × AAbha	-30.60**	33.94**	22.72**	17.32**	5.82**	61.06
TP6 × AAlok	-10.78**	-35.98**	24.22**	12.00**	14.28**	100.91
TP6 × AAbha	-19.82**	29.99**	25.77**	14.68**	9.52**	61.06
TP7 × AAlok	-2.47**	-38.02**	33.31**	25.32**	17.98**	100.91
TP7 × AAbha	-36.42**	47.98**	31.81**	25.32**	14.28**	61.06
TP8 × AAlok	-24.78**	1.97*	30.31**	12.00**	7.93**	100.91
TP8 × AAbha	-14.86**	37.96**	25.77**	22.68**	2.11	61.06
TP9 × AAlok	-0.86	9.95**	7.59**	2.68*	1.58	117.993
TP9 × AAbha	-9.91**	29.99**	27.27**	13.32**	11.10**	100.683
TP10 × AAlok	-0.86	13.97**	15.13**	12.00**	4.76**	100.91
TP10 × AAbha	-19.08**	23.99**	18.18**	10.68**	2.11	61.06
TP11 × AAlok	-0.86	25.97**	12.13**	2.68*	1.06	57.351
TP11 × AAbha	0.74	27.95**	19.67**	14.68**	4.76**	100.91
TP12 × AAlok	-4.21**	21.95**	18.18**	12.00**	12.69**	100.91
TP12 × AAbha	-23.17**	29.99**	19.67**	13.32**	4.23**	61.06
TP13 × AAlok	-22.30**	25.97**	25.77**	18.68**	14.28**	100.91
TP13 × AAbha	0.00	31.95**	16.68**	10.68**	6.87**	61.06
TP14 × AAlok	-28.12**	9.95**	24.22**	12.00*	4.76**	57.351
TP14 × AAbha	3.22**	21.95**	19.67**	10.68**	0.52	100.91
CD at 5%	1.666	3.381	2.533	2.518	2.179	

*, ** significance at 5 and 1% levels, respectively.

attributed to mutual cancellation of heterosis observed for yield parameters in opposite direction. Therefore, D^2 values cannot be directly used to select the top hybrids for yield, rather they can be used to reject (negative selection) the bottom combinations (crosses) based on yield parameters which are strongly associated with total yield in tomato. Further there is need for assessing the relation between genetic distance and heterosis at different ranges of d^2 values with large sample size to establish the phenomenon of prediction of heterosis based on genetic distance.

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