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PATTERN OF GENETIC DIVERSITY AND VARIABILITY IN TOMATO*

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Fourty four genotypes of Tomato (*Lycoperscon esculentum* Mill.) which includes bacterial wilt resistant; tolerant and susceptable lines were evaluated for variability and magnitude of genetic divergence using Mahalanobis D^2 analysis. Genetic coefficient (GCV) variation of was substantial for weight of the fruits per plant and for number of fruits per plant. The GCV was moderate for number of secondary branches and low for other characters. The D^2 analysis grouped all accessions into 11 clusters. Source of the genotypes had no relation with genetic diversity. High yielders with resistance to bacterial wilt were grouped into close cluster. Average fruit weight per plant; number of fruits per plant; survival per cent; contributed much for clustering and genetic divergence. A number of genotypes with resistance to bacterial wilt have been identified for further improvement of the crop.

Key words : Tomato, genetic diversity, variability

Tomato (*Lycopersicon esculentum* Mill.) is grown over 2,90,279 hectares in India producing around 46,03,446 tonnes of fruits. It occupies significant position among vegetables because of its varied utility as raw and ripe fruits for **salads** and as vegetable for cooking. It is also used to make juices, puree, paste, cocktail, ketchup, soup, canned tomato and tomato concentrate. Considering the antiquity of cultivation, it is presumed that domestication of tomato took place in Mexico, however the Andean zone is likely to be the centre of origin of wild tomato. The productivity of tomato in India is 1,58,500 kg/ha against 2,39,130 kg in the Netherlands, 188571 kg/ha in U.K. and 1,50,000 in Belgium. However, this crop suffers from diseases like bacterial wilt, fusarium wilt, late and early blight, fruit rot etc. In the Andaman and Nicobar Islands which have congenial climatic conditions for the development and spread of diseases, bacterial wilt causes the maximum damage (Ramesh and Ansari 1993). Tomato production in these islands can be increased only

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if bacterial wilt resistant lines are used in breeding programme to select superior genotypes. An attempt has been made to study the variability and magnitude of genetic diversity in bacterial wilt resistant lines screened by Sharma *et al.* (1994) at the Central Agricultural Research Institute, Port Blair, India.

MATERIALS AND METHODS

The material for the present investigation comprised 44 accessions collected from various sources. The 44 accessions were planted in a randomized block design with three replications spaced of 50 × 50 cm apart between the rows and the plants. Each row was 3.5m long and 3 such rows were taken for each treatment. Recommended agronomic practices were followed in raising the crop. Observations on five randomly selected plants for 13 traits were recorded. Multivariate analysis (Mahalanobis, 1936; Rao, 1952) was done on mean values for computing the genetic divergence between accessions and the D^2 values thus obtained were used for clustering the accessions using Tocher's method. The Wilk's lambda test criterian was used for testing the significance of genotypes.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the accessions for 11 of the 13 characters studied. The range, mean and coefficient of variability are presented in Table 1. The highest GCV of 123.58 per cent was recorded for weight of fruits per plant followed by number of fruits per plant (78.23%). The GCV was moderate for number of secondary branches and variability was slow for other characters. This is in agreement with Kale *et al.* (1988) and Kumar *et al.* (1980). Based on D^2 values, the accessions were grouped into eleven clusters (Table 2). Cluster I has been formed with 19 accessions, cluster II comprised six accessions, cluster IV, IX and X had 2 accessions each, cluster V had three and other four cluster had one each. The accessions LE 79, 88BWR5, 83-211. Pusa Ruby, EC 165393, 88BWR 1, CI 9d-0-0-3-6 and 84 BWR 14 are the lines which had long distance from the rest. The cluster wise mean values for the thirteen characters are presented in table 3. In general, cultivars in cluster 1 were low yielders alongwith accession in cluster XI. Highest yielding accessions were in cluster VI, VII, VIII and IX (Table 3). Cluster IX and IV had large fruited accessions. Percentage of survival over 80 per cent was higher in the accessions in cluster X, VIII, V and in cluster VII. Accessions in cluster VI and IX had 70 per cent survival. Other accessions in the other clusters had moderate to law survival per cent because of bacterial wilt (Table 3). Number of primary and secondary branches were higher in the genotypes falling in cluster VIII.

Table 1. Genetic parameters of 12 metric characters of tomato

Character	Range		Mean	PCV	GCV
	Min.	Max.			
Days to flower	15.33	26.33	23.14	8.76	6.86
Plant height (cm)	22.77	61.00	43.25	29.00	20.73
Plant spread (cm)	25.67	68.93	47.92	27.00	16.83
No of primary branches	1.00	513.00	2.94	45.24	38.18
No of secondary branches	1.00	7.23	2.60	58.81	54.55
Wt of fruit/plant (gm)	5.50	782.34	225.36	138.23	123.58
No of fruits/plant	2.07	67.46	12.65	115.85	105.73
Av. fruit weight (gm)	1.73	78.19	18.34	88.86	78.23
Size of the fruit (cm)	1.27	4.57	2.88	30.23	23.56
No of locules/fruit	2.00	5.19	2.95	37.60	21.18
T.S.S (%)	3.23	7.93	4.96	24.52	19.60
Acidity	2.70	7.13	4.00	25.25	21.15

Table 2. Formation of clusters and accessions included in each cluster

Cluster Number	No. of Strains	Accession number/varieties of entries
I	19	LE 256, LE 259, LE 330, LE 337, LE 345, LE 915, LE 592, EL 12966, PKM 1, LE 522, 714-1-72, LE 528, EL 37234, 512, LE 721, LE 537, LE 514, Arka Shorab Punjab Shukara
II	6	LE 323, LE 427, LE 168704, LE 96, 84BWR3, KT-1
III	6	BT-1, LE 314, LE 354, EC 165395, LE 593, 13004/P
IV	2	84BWR-6, 88 BWR-1
V	3	84 BWR-1, c19d-0-03-6, EC 165393
VI	1	C19-0-0-3-6
VII	1	88 BWR-5
VIII	1	83-211
IX	2	84 BWR 14, LE 79
X	2	84 BWR-7, c15955-223-D_4-2-2-0
XI	1	Pusa Ruby

The genetic divergence (Table 4) was maximum between cluster VI and X (5564.45), I and VI (5443.99) followed by between cluster I and VII (4516.67) I and VIII (4500.21), I and IX (4327.05) and III and VI (4229.58) (Table 4). Selecting such divergent genotype for hybridization might result in better segregants and higher heterotic response. However, it is always better to cross

Table 3. Cluster means for 13 characters in tomato

Cluster	No. of genotypes	Days to flower	Plant height (cm.)	Plant spread (cm)	No. of primary branches	No. of Secondary branches	No. of fruits per plat	Wt. of fruits per plant (gm)	Average fruit weight (gm)	Size of the fruit (cm)	No. of locules per fruit	T.S.S%	Acidity	Percent survival
I	19	19.98	40.81	44.06	2.20	1.65	5.41	44.95	9.35	2.44	2.59	5.11	3.95	32.78
II	6	19.33	43.73	46.98	3.27	3.52	27.22	368.91	17.00	2.80	3-30	5-59	4.23	51.90
III	6	23.93	39.99	43.09	3.09	3.02	11.76	194.43	17.51	2.94	3.01	4.83	4.57	39.79
IV	2	24.50	43.39	47.10	4.08	3.30	5.37	296.08	51.72	2.36	4.47	4.37	3.67	54.29
V	3	23.77	36.35	56.89	3.43	2.90	32.78	369.97	17.17	2.89	2.59	4.99	4.93	80.95
VI	1	22.17	42.60	59.50	4.32	4.35	25.80	770.50	26.84	3.57	3.57	3.79	5.30	71.43
VII	1	23.17	56.44	57.90	3.52	3.95	21.34	632.58	29.87	3.57	3.33	4.50	4.57	80.71
VIII	1	21.00	61.37	68.90	5.00	4.30	29.38	479.45	16.33	3.30	2.60	4.53	4.33	85.71
IX	2	23.00	35.40	39.30	4.40	2.10	78.00	609.80	78.18	4.13	3.30	4.17	3.17	71.43
X	2	22.67	57.67	59.60	3.00	3.60	17.51	450.46	26.13	3.43	2.60	4.78	3.23	95.71
XI	1	23.33	50.43	51.60	3.17	3.20	1.00	22.08	28.05	2.03	2.53	4.67	4.43	52.86

Table 4. Intra and inter-cluster divergence D^2 values in 44 genotypes of tomato

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	130.19	517.11	215.19	1342.30	2047.86	5443.99	4516.67	4500.21	4327.05	250.12	3413.48
II		286.54	260.25	748.30	902.61	3562.19	2623.29	2141.72	2764.18	530.72	1808.58
III			103.40	744.75	1370.75	4229.58	3424.14	3005.71	3041.21	192.66	2779.20
IV				108.25	1309.41	2991.63	2139.91	1475.57	1057.46	866.41	1715.21
V					366.13	1381.37	997.60	562.62	2190.90	2118.24	589.78
VI						52.81	105.57	576.50	1562.53	5564.45	272.21
VII							1218.63	588.62	1363.03	2316.66	124.34
VIII								0000.00	1206.74	2059.85	1961.92
IX									0000.00	178.63	678.87
X										0000.00	1767.92
XI											0000.00

parents having high to moderate genetic divergence with high to medium survival per cent combined with high yields. EC 165395, 88 BWR1, 84 BWR14 CL5955-223-D_4-2-20, 84 BWR7, 88 BWR5, 84BWR6 and LE 79 considering high mean value alongwith high to moderate genetic distance were promising accessions. These may be crossed in several combinations or in a complete diallel fashion to achieve high yields combined with resistance to bacterial wilt. In tomato, D^2 analysis showed that genotypes possessing similar characteristics were grouped together even though, they were from different sources. Hence geographic diversity had no relation with genetic diversity. Perhaps selection to bacterial wilt resistance alongwith higher yields must have been the cause for the clustering. The genetic architecture of such population could be the result of prolonged selection by various natural and artificial forces. Successful use of D^2 analysis to assess the relative combination of different components of yield to the total divergence and to determine the nature of forces operating at intra and inter cluster levels have been emphasised by various workers in tomato (Patil and Bojappa, 1988; Kalloo, 1984; Skebe and Benne, 1989).

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