

Genetic divergence studies for tospovirus resistance, yield and yield related components in tomato genotypes*

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Abstract : Using Mahalanobis D^2 statistics method, genetic diversity was studied. Seventy genotypes were grouped into seven different clusters. Cluster-I had 37 genotypes, cluster -II had 23 genotypes, cluster -III and IV had five and two genotypes respectively. While remaining cluster V, VI and VII were solitary clusters with single genotype. The D^2 value ranged from 189.935 between cluster V and VI to 1484.249 between cluster I and V, indicating the existence of wide genetic variability. It is desirable to select accessions from the cluster having higher inter cluster distance and fruit yield with tolerance for tospovirus as parents in the recombination breeding programme. The cluster means were calculated for each character and ranks were given based on scores obtained for all the eleven characters of the cluster. Cluster-I with 37 genotypes ranked first. Similarly other clusters VI, VII and III were next in order of ranking and can be utilized in further breeding programme.

Key word: Mahalanobis D^2 , genetic diversity, accessions, inter cluster distance, tospovirus

Introduction

The major biotic constraints in the cultivation and production of tomato are the occurrence of many insect and diseases. Tomato is susceptible to more than 200 diseases, important achievements in chemical, biological, cultural and genetic control methods have greatly reduced economic losses and sometimes have eliminated them. Viral diseases are a special case since they cannot be controlled by chemical treatments. Crop protection must then rely on genetic resistance or disease avoidance. Among the viral diseases, tomato spotted wilt virus is raising to an alarming proportions in India and becoming a limiting factor for tomato cultivation. In fact, early infection leads to loss up to 100 per cent thus tomato cultivation is almost precluded during summer season. Besides, disease intensity is increasing during the remaining period of the year. Presence of wide host range for the vector as well as virus ensures abundant inoculum in nature resulting in fast spread of the disease (Best, 1968). The balance of demand and supply could not be met throughout the year, especially during summer. Hence, Indian tomato industry is in a desperate need of tomato varieties tolerant to tomato spotted wilt virus to stabilize tomato production. Tomatoes infected by Tospovirus show a wide range of symptoms, their appearance and severity depend on the genotypes, the plant development stage, the time of infection, the various isolate and the environmental conditions. The symptoms observed on tomatoes in the field were tip necrosis, necrotic spots on leaves, petioles and stems of the infected plants, finally wilting of the plants, infected plant produced fruits often showing chlorotic concentric rings.

Many indirect approaches like checking the vector population by using trap crop and application of systemic insecticides may reduce infection to certain levels. Application of large amount of vector killing pesticides is not only uneconomical but also has environmental health hazards. Since the host range of both virus and vector are quite diversified and widely distributed, it is impracticable to adopt crop health measures such as eradication of collateral or alternate hosts. It is difficult to advocate roguing of infected plants. Added to this, there is no commercial tomato cultivar with inherent resistance against the disease together with acceptable marketing quality. Therefore, it is imperative to concentrate on the development of cultivar that are resistant to disease or disease escaping cultivar. Host plant resistance, the most important disease control strategy is environmentally sound with low running costs. As the virus solely banks upon the thrips for its spread, use of vector resistant cultivars will help to break virus vector host transmission cycle (Krishana Kumar, 1993) Therefore, breeding tomato cultivars possessing inbuilt resistance either for virus or vector or both is an appropriate approach for the management of tomato spotted wilt virus. For the development of a resistant variety, source of resistance should with a broad genetic base; donors of resistance are the pre-requisite and should be identified by well established technique of the screening of germplasm and further assessment of diversity of the genetic material

Material and methods

The material consisted of 70 genotypes maintained in the germplasm collection at the Division of Horticulture,

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University of Agricultural Sciences, Dharwad. The seeds of different genotypes were sown on the sterilized Seedbed during mid January (16th January) 2007. The seedlings were raised by following regular nursery practices except use of any insecticides. The seedlings of 34 days old were transplanted to the main field for disease screening of tomato spotted wilt virus under natural condition at a spacing of 60 cm x 60 cm H-4 (Vegetable) block of Main Agriculture Research Station of University of Agricultural Sciences, Dharwad. The experiment was carried out by using randomized block design (RBD). Entries planted in a single row of 25 seedlings per row in two replications. Observations recorded for 11 characters viz., plant height, fruit clusters per plant, fruits per cluster, fruits per plant, average fruit weight, yield per plant, locules per fruit, TSS, tomato spotted wilt virus (TSWV) symptoms severity and per cent fruit set. Recommended package of practices were followed to raise the crop without any plant protection measures so as to encourage enough population build up of thrips and transmission of TSWV disease. The observations on symptom development of TSWV were recorded 70 days after transplanting for calculating per cent and severity of disease through visual grading as per the scale suggested by Joi and Summanawar (1989). Genetic diversity was calculated by using Mahalanobis D² analysis.

Results and discussion

The data obtained from evaluation of 70 tomato genotypes were used for testing divergence among genotypes by employing Mahalanobis D² statistics (Mahalanobis, 1936). For

all the genotypes, the correlated unstandardized mean values (X) for 11 characters viz., plant height, fruit clusters per plant, fruits per cluster, fruits per plant, average fruit weight, yield per plant, locules per fruit, TSS, tomato spotted wilt virus (TSWV) symptoms severity and per cent fruit set under consideration were transformed to the correlated standardized value (Y). The D² value which being the sum of square of differences for each 'Y' value was calculated for all combinations. Based on the D² values, the genotypes were grouped into seven clusters (Table 1) using Tocher's method as given by Rao (1952). Of the seven clusters studied, the cluster I was the largest comprising of 37 genotypes followed by II with 23 genotypes. The cluster III and IV comprising of five and two genotypes respectively and remaining three clusters (V, VI, VII) comprised of single genotypes each. Out of 11 characters studied, average fruit weight (95.11%) contributed maximum to the diversity followed by per cent tomato spotted wilt virus (TSWV) symptom severity (2.19%), TSS (1.24%) and per cent fruit set (0.79%). Whereas other characters did not contribute to the diversity (Table 3). The cluster pattern in tomato genotypes is depicted by Dendrogram in Fig.1. The inter cluster D² values are given in Table 2 and nearest and farthest cluster from each cluster based on D² value is given in Table 4. The inter cluster D² values were maximum (1484.249) between the cluster I and cluster VI. The minimum distance (189.935) observed between cluster V and VI indicated close relationship among the genotypes included. The cluster VI was the most diverse; as many other clusters showed maximum inter cluster distance with it. The intra cluster D² values are given in

Table 1. Grouping of tomato genotypes based on D² values

Sl. No.	Cluster	No. of genotypes	Name of the genotypes
1.	I	37	S-07, L# 39, L#22, ARGK-03, L#38-1, AR-13, Round F ₄ GK-2, S-19, L# 10, AR-14, AR-09, AR-PR-01, P-05, PKM-11, BF-2-1, S-52, GK-14R, Arka Alok, AR-08, DMT-2, Pusa Ruby PR-1, S-21, Alcobas oval 43, Alcobas oval, L#35, Sankranthi, S-05, S-22, Nandhi, DMT-3, S-61, S-20, P-6, PKM-04, PKM-17, BFL, BFL-02, L#26.
2.	II	23	Pink-04, L#268, L#26, PKM19-1, PKM-18, Pink-02, AR-01, H-03, PKM-15, L#12, AR-30, Megha (L-15), BF red, H-02, H-05, P-11, PKM-33-1, GK-1R, L# 36, H-01, L# 29, L# 05 (O) H-07
3.	III	5	L#44, 36-1, P-07, L# 27, DMT-1
4.	IV	2	L#34, PKM-16
5.	V	1	S-42
6.	VI	1	Vaibhav
7.	VII	1	L#37

Table 2. Average intra and inter cluster D² values of tomato genotypes

Cluster	I	II	III	IV	V	VI	VII
I	4.492	793.80	1090.017	451.258	1297.359	1484.249	213.573
II		150.263	333.865	355.434	525.001	707.413	587.332
III			151.018	647.549	237.040	412.001	883.765
IV				31.389	853.305	1038.333	240.888
V					000.000	189.935	1091.293
VI						000.000	1276.827
VII							000.000

Table 3. Per cent contribution of 11 characters towards diversity in tomato genotypes

Sl. No.	Characters	% contribution	Order of contribution
1.	Plant height	0.00	
2.	Number of branches	0.00	
3.	Fruit clusters per plant	0.00	
4.	Fruits per cluster	0.00	
5.	Fruits per plant	0.66	V
6.	Average fruit weight	95.11	I
7.	Fruit yield per plant	0.00	
8.	Locules per fruit	0.00	
9.	TSS	1.24	III
10.	Per cent TSWV symptom severity	2.19	II
11.	Per cent fruit set	0.79	IV

Table 2. The intra cluster distance was observed in the clusters I, II, III and IV, whereas remaining clusters comprised only one genotype each. The intra cluster distance was higher in cluster IV (31.39)

All genotypes spread over seven clusters and mean were scored across the cluster of all the 11 characters. The lowest cluster mean was given the 1st rank and next cluster possessing next best means were given 2nd, 3rd and so on, upto 7th rank for all the traits accordingly. The cluster III with overall score of 25 for 11 characters selected first rank followed by cluster IV, V, VII, VI and so on indicating the presence of most promising genotypes in them and can be extensively used for further breeding programme to generate new material. The cluster means of 11 different characters were compared and indicated considerable differences between clusters for all the characters studied (Table 5). Genotypes in cluster IV showed the lowest plant height (52

Table 4. The nearest and farthest clusters from each clusters

Sl. No.	Cluster	Nearest cluster with D ² values	Farthest cluster with D ² values
1.	I	VII (213.573)	VI (1484.249)
2.	II	III (333.863)	I (793.080)
3.	III	V (237.040)	I (1090.170)
4.	IV	VII (240.888)	VI (1038.333)
5.	V	VI (189.935)	I (1297.359)
6.	VI	V (189.935)	I (1484.249)
7.	VII	VII (213.573)	VI (1276.827)

cm) and those in Cluster-I had the highest mean (76.56) plant height. Maximum (13.50) and minimum (5.165) number of branches were observed in Cluster-VI and Cluster-V respectively. Number of fruit clusters per plant was the highest in Cluster-II with a mean value of 14.84 and it was the least in genotypes belong to the Cluster-IV (7.0). Number of fruits per cluster was the highest in Cluster-VI (4.67) and it was the least in genotypes belong to the Cluster-IV (2.58). Highest number of fruits per plant was recorded by the Cluster-VI (40) while Cluster-V (15) showed the least number of fruits per plant. The maximum average fruit weight was observed in the Cluster-VII (69.50 gm) where as minimum was observed in the Cluster-V (39 g). The maximum fruit yield per plant (1886 g) was observed in the Cluster-VI. Whereas minimum was observed in Cluster-V (583 g). Highest number of locules per fruit was recorded by the genotypes making up Cluster-VI (4.25) while Cluster-IV showed the least number of locules (2.34). When observed for TSS content of fruit genotypes of Cluster-I (5.51), the genotypes of Cluster-IV recorded the highest and lowest TSS content of fruit (3.25), respectively. The highest per cent tomato spotted wilt virus (TSWV) symptom severity was observed in the Cluster-I (54.35) while Cluster-VI showed least per cent TSWV symptom severity

Table 5. Cluster mean for 11 characters in tomato genotypes

Source of variation		Plant height per plant	No. of branches per plant	Fruit cluster	Fruits per cluster	Fruits per plant	Average fruit weight	Yield per plant	Locules	Total soluble solids	%Tomato spotted wilt virus symptoms	% fruit set	Overall rank	Rank
I	Mean	76.56	9.86	11.49	4.08	25.34	66.83	1207.31	4.21	5.51	54.35	73.99	33	III
	Rank	(1)	(2)	(3)	(2)	(2)	(2)	(3)	(6)	(1)	(7)	(1)		
II	Mean	58.92	7.25	8.58	2.88	17.44	53.27	831.72	3.36	4.02	36.30	52.41	42	IV
	Rank	(4)	(4)	(4)	(5)	(5)	(3)	(4)	(3)	(5)	(2)	(5)		
III	Mean	58.20	5.90	8.33	3.20	18.90	43.72	826.56	3.43	3.70	43.00	53.16	50	V
	Rank	(5)	(5)	(5)	(3)	(3)	(5)	(5)	(4)	(6)	(5)	(4)		
IV	Mean	52.00	5.33	7.0	2.58	15.42	40.81	628.53	2.34	3.25	52.5	46.93	66	VII
	Rank	(7)	(6)	(7)	(7)	(6)	(6)	(6)	(1)	(7)	(6)	(7)		
V	Mean	52.50	5.165	7.50	3	15	39	583	4.00	4.75	42.50	50.00	63	VI
	Rank	(6)	(7)	(6)	(6)	(17)	(7)	(7)	(5)	(2)	(4)	(6)		
VI	Mean	75.50	13.50	12.84	4.67	40	47	1886	4.25	4.25	22.50	69.47	25	I
	Rank	(2)	(1)	(2)	(1)	(1)	(4)	(1)	(7)	(3)	(1)	(2)		
VII	Mean	66.00	9.50	14.84	3	18.17	69.50	1261.22	2.67	4.05	37.50	60.00	30	II
	Rank	(3)	(3)	(1)	(4)	(4)	(1)	(2)	(2)	(4)	(3)	(3)		

(22.50). Highest fruit setting per cent was observed in Cluster-I (73.99), while Cluster-III showed least per cent fruit set (46.93). Similar genetic divergence was reported for all the yield and yield related character by Mahesh *et al.*, (2006) and Sharma

et al. (2006). Based on the above results further, screening for tospovirus resistance under natural and laboratory condition should be done and then use desirable lines may be used for further breeding programme.

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