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Genetic Diversity and Variability for Yield and Yield Traits in Tomato (*Solanum lycopersicon* L.)

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Abstract A study was conducted to assess the genetic diversity and variability among 32 tomato genotypes. A wide range of variation was observed among the genotypes for all the characters understudied. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters. High heritability coupled with high genetic advance as percent mean observed for days to 50% flowering, plant height, number of primary and secondary branches, chlorophyll content, number of fruits per cluster, fruit weight, fruit diameter, total soluble solids, number of locules, pericarp thickness,lycopene content and ascorbic acid. High heritability coupled with high genetic advance indicates additive gene action plays a significant role in governing and simple selection can improve these traits. Mahalanobis D^2 statistics stated the extensive genetic diversity among the accessions which grouped into six clusters by Tocher's method based on D^2 values. Cluster V was the biggest with 15 genotypes followed by cluster III with 9 genotypes, cluster I with 5 genotypes and clusters II, IV and VI were solitary. The maximum intra-cluster distance recorded in cluster V (4106.23) followed by cluster III (2320.24) and cluster-I (1710.90). The cluster II, IV and VI showed zero intra-cluster distance. Selection of divergent parents based on these cluster distance would be useful in selecting the accessions for hybridization and formulating a comprehensive strategy to develop superior hybrids or superior segregants in tomato.

Keywords Genetic variability, Heritability, Genetic divergence, Mahalanobis D^2, Clusters.

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Introduction

Tomato (*Solanum lycopersicon* L.) is one of the most excellent vegetable crops of India as well as around the world belong to the family Solanaceae with 2n=24 (Kumar et al. 2010, Kumar and Dudi 2011) and native to West Coast of South America (Mexico and Peru). It is the most important vegetable crop next only to potato because of its more extensive adaptability, high yielding potential and multipurpose uses (Reddy et al. 2013), grown as annual or short-lived perennial herbaceous plants. India, tomato occupies an area of 0.87 million ha with an annual production of 17.50 million tonnes and productivity of 20.11 tonnes per hectare. The plant is determinate, semi-determinate and in determinate and plays a significant role in every kitchen as food and nutritional security, also occupies the important position in the post-harvest industry (Kumar et al. 2010).

The ultimate goal of any crop improvement program is to improve the plant traits for agronomic and economic superiority, which depends on the magnitude of genetic diversity and extent of variability to which the desirable trait is heritable. Extensive screening of germplasm accessions for desirable characteristics can help in identifying genotypes suitable for a specific breeding program. Thorough knowledge of the amount of genetic variability existing in the crop for various characters is essential for taking up crop improvement program. Hence, the generation of information on nature and magnitude of variability present in the existing plant material is requisite for further improvement in the yield.

Mahalanobis D^2 analysis is a useful tool in quantifying the degree of divergence between natural population at the genotypic level and to assess the relative contribution of different components to the total divergence both at inter and intra-cluster level. The progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants. Therefore, genetically distinct genotypes should be used in a hybridization program to get preferred recombinants. Therefore, the study was undertaken to assess and evaluate the genetic diversity and variability in tomato accessions collected from diverse origin.

Materials and Methods

The experiment conducted at College of Horticulture, Mudigere, Karnataka during 2015-16. Thirty two genotypes were evaluated in RBD with 2 replications. Each genotype planted in a single row of 4 meter length at the spacing of 60 cm between row 45 cm between plants. The observations recorded on 5 randomly selected plants in each accession on 17 different characters i.e., days to 50% flowering, plant height (cm), number of primary branches, number of secondary branches, chlorophyll content (mg/g), number of fruit clusters per plant, number of fruits per cluster, number of fruits per plant, fruit weight (g), fruit yield per plant (g), fruit diameter (cm), total soluble solids (TSS), number of locules, pericarp thickness (mm), pH of fruit juice, lycopene (mg/g), and ascorbic acid (mg/100g). The mean data were subjected to estimate genetic components and divergence utilising Mahalanobis D^2 statistic as suggested by Mahalanobis (1936) using statistical software *WINDOSTAT* 9.1 developed by *INDOSAT* services Ltd, Hyderabad, India. Accessions grouped into various clusters following the Tocher's method as suggested by Rao (1952).

Results and Discussion

Analysis of variance (Table 1) revealed highly significant differences among the genotypes for all characters studied indicating the existence of vast genetic divergence among the genotypes.

Estimates of genetic parameters like mean, range, the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability, genetic advance as percent means presented (Table 2). The phenotypic coefficient of variation (PCV) was though higher than the genotypic coeffi-

Table 1. Analysis of variance for different yield and yield parameters of tomato germplasm. **Significant at 1% probability level. Where, 1= Days to 50% flowering, 2=Plant height (cm), 3=Number of primary branches, 4=Number of secondary branches, 5=Chlorophyll content (mg/g), 6=Number of fruit clusters per plant, 7=Number of fruits per cluster, 8=November of fruits per plant, 9=Fruit weight (g), 10=Fruit yield per plant (g), 11= Fruit diameter (cm), 12=Total soluble solids (TSS), 13=Number of locules, 14=Pericarp thickness (mm), 15=pH of fruit juice, 16= Lycopene (mg/g), 17=Ascorbic acid (mg/100g).

Sources of variation	DF	1	2	3	4	5	6	7	8
Replication	1	18.06	1201.66	3.84	162.05	0.012	290.10	1.77	11995.18
Genotypes	31	53.36**	5371.92**	12.90**	718.17**	0.014**	22.07**	9.27**	2143.33*
Error		1.03	16.71	0.14	5.16	0.0003	13.01	0.34	1044.65
SEm±		0.70	2.84	0.26	1.58	0.012	2.51	0.40	22.49
CV (%)		3.45	2.99	9.38	4.72	2.92	17.28	10.24	19.49
CD (p=0.05)		2.07	8.33	0.76	4.63	0.036	-	1.19	65.91
CD(p=0.01)		2.79	11.22	1.02	6.23	0.048	-	1.60	88.69

Table 1. Continued.

Sources of variation	DF	9	10	11	12	13	14	15	16	17
Replication	1	31.68	4710050	2.77	0.42	0.14	0.13	0.28	0.04	16.31
Genotypes	31	859.27**	690759.18**	2.07**	2.94**	5.30**	2.73**	0.24**	64.20**	135.73**
Error		1.12	338495.61	0.08	0.03	0.17	0.06	0.01	0.10	0.73
SEm±		0.73	404.91	0.20	0.12	0.28	0.16	0.07	0.22	0.59
CV (%)		3.15	23.19	8.36	3.56	12.49	15.09	2.86	3.43	3.26
CD (p=0.05)		2.16	1186.59	0.59	0.35	0.84	0.49	0.23	0.65	1.74
CD (p=0.01)		2.91	1596.48	0.80	0.48	1.14	0.65	0.30	0.88	2.35

cient of variation (GCV) for all the characters under study, but the narrow range of difference indicated that most of the characters least influenced by the environmental factors. High values of PCV and GCV obtained for plant height, number of primary and secondary branches, number of fruit clusters per plant, number of fruits per cluster, number of fruits per plant, fruit weight, fruit yield per plant, fruit diameter, total soluble solids, number of locules, pericarp thickness, pH of fruit juice, lycopene and ascorbic acid content indicating variation of these characters contributed markedly to the total variability. Further, narrow range of differences between PCV and GCV reported that any selection pressure operated on these characters might help to realise the improvement in early generations. Similar results were also obtained by Kumar et al. (2014), Kaushik et al. (2011), Ghosh et al. (2010) and Sahanur et al. (2012).

High heritability observed for days to 50% flowering, plant height, number of primary and secondary branches, chlorophyll content, number of fruits per cluster, fruit weight, fruit diameter, total soluble solids, number of locules, pericarp thickness, pH of fruit juice, lycopene content and ascorbic acid content. Whereas, number of fruit clusters per plant, number of fruits per plant and fruit yield per plant had low heritability. These findings are agreeable to Saji

Table 2. Estimates of mean, range, components of variance, heritability and genetic advance for yield and yield components in tomato. GV - Genotypic variance, PV - Phenotypic variance, GCV-Genotypic coefficient of variation, PCV - Phenotypic coefficient of variation, h^2 (bs) - Heritability (broad sense), GAM - Genetic advance as percent of mean.

Characters	Mean	Range Min	Range Max	PV	GV	GCV (%)	PCV (%)	h^2 % (broad) sense)	GAM
Days to 50% flowering	29.51	19.5	39.50	27.20	26.16	17.32	17.66	96.18	35.01
Plant height (cm)	136.55	51	215	2694.32	2677.60	37.89	38.01	99.38	77.81
Number of primary branches	3.99	1.16	10.50	6.52	6.38	63.28	63.97	97.85	128.95
Number of secondary branches	48.06	18.41	90.16	361.67	356.50	39.28	39.56	98.57	80.34
Chlorophyll content (mg/g)	0.60	0.44	0.79	0.007	0.007	13.87	14.18	95.75	27.97
Number of fruit clusters per plant	4.79	0.33	17.33	17.54	4.52	75.54	76.78	25.80	46.44
Number of fruits per cluster	5.72	1.83	11.16	4.81	4.46	36.90	38.30	92.85	73.25
Number of fruits per plant	29.51	7	183.47	1593.9	549.34	132.8	135.2	34.46	96.02
Fruit weight (g)	33.57	1.78	80.14	430.19	429.07	61.68	61.76	98.74	97.14
Fruit yield per plant (g)	699.34	84.80	2366.00	514627.4	176131.7	60.01	62.86	34.23	72.32
Fruit diameter (cm)	3.51	1.10	5.35	1.08	0.99	28.40	29.61	92.02	56.13
Total soluble solids (TSS)	4.92	2.90	7.9	1.48	1.45	24.47	24.73	97.92	49.89
Number of locules per fruit	3.32	2	8	2.74	2.56	48.15	49.74	93.69	96.02
Pericarp thickness (mm)	1.59	0.06	4.98	1.39	1.33	72.65	74.20	93.86	98.74
pH of fruit juice	3.93	3.15	4.89	0.12	0.11	8.62	9.08	90.07	16.86
Lycopene content (mg/g)	9.36	0.32	21.75	32.15	32.05	60.44	60.53	99.68	124.31
Ascorbic acid (mg/100g)	26.27	4.67	39.56	68.23	67.49	31.27	31.44	98.92	64.07

Table 3. Grouping of thirty two tomato genotypes based on D^2 analysis.

Sl. No.	Clusters	Number of genotypes	Name of genotypes
1	I	5	AB-205, AR-17, AR-5, AR-50, PKM-1
2	II	1	AR-7
3	III	9	AR-47, AR-56, Cherry tomato L-03686, AR-90, AR-4, AR-34, AR-20, Cherry tomato P2L-0091, AR-4
4	IV	I	Black prince
5	V	15	Poland pink, AR-19, AR-29, AR-28, AR-23, P-4, AR-30, Cherry tomato L-01696, TLB-133, Bony best, AR-18, Cherry tomato L-04784, Cherry tomato L-02846, TLB-205, PATRIOT
6	VI	1	TLB-130

(2012) and Kumar et al. (2014). High heritability of these traits indicated that variation generated mainly due to genetic factors and role of environment. Hence, the improvement can be obtained by simple selection.

The high heritability coupled with high genetic advance as percent mean observed for days to 50% flowering, plant height, number of primary and secondary branches, chlorophyll content, number of fruits per cluster, fruit weight, fruit diameter, total soluble solids, number of locules, pericarp thickness, lycopene content and ascorbic acid. This suggests the importance of additive genetic component for the inheritance of these traits that can be improved by visual selection. These results are following the report of Reddy et al. (2013), Nowsu et al. (2014) and Patel et al. (2013).

Based on the relative magnitude of D^2 values, all the genotypes grouped into six clusters (Table 3). The cluster divergence proved by high inter-cluster and low intra-cluster D^2 values. Among the six clusters, cluster V was the largest having 15 genotypes, followed by cluster III with nine genotypes, cluster I consisting of five genotypes and clusters II, IV and VI were solitary. The clustering pattern in the present study showed that accessions of different geographical areas clubbed in one group indicating that there was no prallelism between genetic diversity and geographic origin. These results conform with the findings of Shirasawa and Hirakawa (2013), Sharma et al. (2006).

Table 5. Percent contribution of different characters towards total diversity in tomato.

Sl. No.	Characters	% Contribution
1	Lycopene content (mg/g)	43.35
2	Fruit weight (g)	26.61
3	Ascorbic acid (mg/100g)	16.33
4	Plant height (cm)	5.24
5	Total soluble solids	3.63
6	pH of fruit juice	2.02
7	Pericarp thickness (mm)	1.01
8	Secondary branches	0.6
9	Primary branches	0.2
10	Days to 50% flowering	0.2

Another feature that came to light was that genotypes that originated in one region had been distributed into different clusters, indicating that accessions with same geographic origin could have changed for various characters under selection. This could be due to selection or genetic drift, which helps in creating more diversity rather than genetic distance. Therefore, selection of accessions for hybridization to generate different new gene combinations based on

Table 4. Average intra and inter-cluster D^2 values of different clusters in tomato.

Clusters	I	II	III	IV	V	VI
I	**1710.90**	3745.70	3983.61	3039.88	3553.43	7586.94
II		**0.00**	3802.73	6399.77	3612.49	3637.65
III			**2320.24**	3776.44	4202.67	3006.89
IV				**0.00**	7186.36	7926.81
V					**4106.23**	8450.15
VI						**0.00**

genetic diversity rather than geographic diversity. The divergence within the cluster (intra-cluster distance) indicates the divergence among the accessions falling in the same cluster.

The intra and inter-cluster D^2 values among 32 accessions presented in Table 4. The intra-cluster distance varied from 0.00 (cluster II, IV and VI) to the maximum distance of 4106.23 in cluster V. This reveals the presence of different genotypes within different clusters. The inter-cluster D^2 values ranged widely with the minimum value of 1710.90 in cluster I and the maximum value of 8450.15 between cluster V and VI. These observations are by the views of Meena and Bahadur (2015), Iqbal et al. (2014) and Nalla et al. (2014). It is desirable to select genotypes from clusters showing high inter-cluster distance (cluster V and VI) also with high fruit yield as parents in recombination breeding programs for obtaining desirable segregants.

The percent contribution of 17 characters for genetic divergence (Table 5) showed that among 17 characters studied, most important character contributing to the divergence was lycopene content followed by fruit weight and other component traits including ascorbic acid, plant height, total soluble solids, pH of fruit juice, pericarp thickness, number of primary and secondary branches per plant. Analysis of cluster means indicates diversity demonstrated by different clusters for a character. Based on the means, it is possible to know the character influencing divergence. The variation observed in the cluster also mean points to the degree of variability. In the present study, it found that considerable amount of genetic diversity among the genotypes with respect fruit yield, fruit weight and lycopene content. These results are in line with of findings of Meena and Bahadur (2015). The superior cluster concerning fruit yield was cluster IV, concerning fruit weight, cluster IV and cluster II, to lycopene content. Depending upon the breeding objective, the potential lines to be selected from different clusters as parents in a hybridization program may depend on genetic distance.

References

Ghosh KP, Islam AK, Mian MA, Hussain MM (2010) Variability and character association in F_2 segregating populationof different commercial hybrids of tomato (*Solanum lycopersicum* L.). J Appl Sci Environ Managen14 (2) : 91—95.

Iqbal Q, Saleem MY, Ameed A, Asghar M (2014) The Assessment of genetic divergence in tomato through agglomerative hierarchical clustering and principal component analysis. Pak J Bot 46 (5) : 1865—1870.

Kaushik SK, Tomar DS, Dixit AK (2011) Genetics of fruit yield and its contributing characters in tomato. J Agric Biotech and Sustain Develop 3 (10) : 209—213.

Kumar M, Dudi BS (2011) Study of correlation between yield and quality characters in tomato (*Lycopersicon esculentum* Mill.). Elect J Pl Breed 2 (3) : 453—460.

Kumar R, Ram CN, Chandra D, Vimal SC, Bhartiya HD (2014) Appraisal studies on variability, heritability and genetic advance in tomato (*Solanum lycopersicon* L.). Pl Arch 14 (1) : 367—371.

Kumar S, Rattan P, Sharm AJP, Gupta RK (2010) D^2 analysis for fruit yield and quality components in tomato (*Lycopersicon esculentum* Mill.). Ind J Pl Genet Resour 23 (3) : 318—320.

Mahalanobis PC (1936) On the generalized distance in statistics. The proc Nat Inst Sci Ind 1 (2) : 49—55.

Meena OP, Bahadur V (2015) Breeding potential of indeterminate tomato (*Solanum lycopersicum* L.) accessions using D^2 analysis. SABRAO J Breed and Genet 47 (1) : 49—59.

Nalla MK, Rana MK, Singh SJ, Sinha AK, Reddy KP, Priyadarshani PM (2014) Assessment of genetic diversity through D^2 analysis in tomato (*Solanum lycopersicon* (Mill.) Wetted.).Int J Innov and Appl Studies 6 (3) : 431—438.

Nowsu DJ, Onakoya OA, Okere AU, Babatunde AO, Popoola AF (2014) Genetic variability and correlations in rainfed tomato (*Solanum* spp.) accessions in Ibadan, Nigeria. J Agric Sci 4 (5) : 211—219.

Patel SA, Kshirsagar ADB, Attar V, Bhalekar MN (2013) Study on genetic variability, heritability and genetic advance in tomato. Int J Pl Sci 8 (1) ;:45—47.

Rao CR (1952) Advanced Statistical Methods in Biometrical Research. J Wiley and Sons, Inc, New York.

Reddy BR, Reddy MP, Reddy DS, Begum H (2013) Correlation and path analysis studies for yield and quality traits in tomato (*Solanum lycopersicum* L.). IOSR J Agric and Vet Sci 4 (4) : 56—59.

Sahanur RSS, Lakshman, Maitra NJ (2012) Genetic variability and heritability studies in tomato. Ind J Pl Sci 7 (1) : 58—62.

Saji S (2012) Heritability studies of fruit related traits in (*Solanum lycopersicum* L.) germplasm. J Biol life Sci 4 (2) : 2157—2160.

Sharma HR, Sharma D, Thakur AK (2006) Study on analysis of genetic divergence in tomato (*Lycopersicon esculentum* Mill.). J Hort Sci 1 (1) : 52—54.

Shirasawa K, Hirakawa H (2013) DNA marker applications to molecular genetics and genomics in tomato. J Pl Breeding 63 : 21—30.