

RESEARCH ARTICLE :

Assessment of breeding potential of tomato (*Lycopersicon esculentum* mill.) germplasm for productivity and adaptability traits

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SUMMARY : Tomato (*Solanum lycopersicum* L.) yield in India is below world averages and to increase productivity under semi arid regions, it is necessary to develop superior varieties/hybrids with better root traits. The efficiency of selection depends upon the nature and magnitude of genetic variability and diversity of desired traits. Thirty exotic genotypes of tomato were assessed to determine the nature and magnitude of variability, their association and divergence. The analysis of variance (ANOVA) revealed highly significant differences among all genotypes for the traits studied. High genotypic coefficients of variability (GCV), and heritability coupled with high genetic gain, were observed for fruit yield per plant, fruits per plant, root dry weight, SCMR, shoot dry weight, root volume and specific leaf area, indicating that these traits are under additive gene effects and more reliable for effective selection. Correlation indicated that fruit yield was significantly and positively associated with root length, number of fruit per plant, plant height, root to shoot ratio and SCMR. Path analysis revealed that the average plant height (1.143) had the highest direct positive effect on fruit yield per plant followed by fruits per plant (0.419), root length (0.352) and branches per plant (0.302). Direct selection on the basis of number of fruit per plant, branches per plant, and SCMR is reliable for yield improvement in tomato. Thirty accessions were grouped into five divergent clusters and intercross among genotypes of cluster II and V, cluster II and IV and cluster III and V will create wide spectrum of variability to produce transgressive segregants with better fruit yield and root traits in tomato. Thus, the lines EC 676730, EC 686531, EC 677076, EC 677080, CLN 2070A and EC 686703 were identified as high fruit yielding and better adaptive traits.

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BACKGROUND AND OBJECTIVES

Tomato is one of the most popular and versatile vegetable crop grown widely all over the world. It is a day neutral, self-pollinated

crop belongs to the family solanaceae and consists of annual or short lived perennial herbaceous plant. It plays an important role in human nutrition as a source of lycopene, ascorbic acid, β-carotene and also rich in

medicinal value. It is grown in kitchen gardens, commercial fields and also in green house or controlled environmental conditions.

Low moisture stress is the major constraint for tomato production under semi-arid tropical countries like India. Many new cultivars have been developed to meet the diverse need and varied climatic condition. So far, breeders have made attempts to breed high yielding genotypes under rainfed conditions based on only morphological and yield attributing traits. It is also realized that breeding for yield *per se* is increasingly becoming difficult because of high Genotype x Environment interaction. Among the many traits that associated with drought tolerance, root traits and water use efficiency (WUE) are considered to be most relevant as the former is related to acquisition of water from soil and latter referring to efficient use of absorbed water. Improvement of these traits has been shown to improve the rate of productivity in several species by Sheshshayee *et al.* (2003).

A breeding program should aim to combine high-yield traits, high water use efficiency (WUE) and drought resistance traits in one variety and such water-saving crop breeding will be important for both limited irrigated land and dryland farming. The available variability in a population can be partitioned into genetic parameters such as co-efficients of variation, heritability and genetic advance to serve as basis for selection of desirable genotypes. High heritability indicates less influence of environment in the observed variation by Songsri *et al.* (2008), Eid, (2009), while high heritability along with high genetic advance is an indication of additive gene action for such traits, making it most amenable to selection (Tazeen *et al.* 2009). Correlation study determines the association between various traits and their relative magnitude is measured by path co-efficient analysis; enable the plant breeder to deduce the extent of environmental influence on yield. Genetic diversity is an important tool for a crop improvement programme, as it helps in the development of superior recombinants and also role in selection of parents having wider variability for different traits (Manonmani and Fazlullah Khan, 2003, Nayak *et al.* 2004). Among the various techniques identified/developed to study the genetic divergence, the Mahalanobis D_2 (Mahalanobis, 1936) is reliable and most frequently used. The grouping of genotypes into different clusters is done by following Tocher's method as

described by Rao (1952). Improvement in self-pollinated crops like tomato is generally achieved by selecting the genotypes with desirable trait combinations existing in nature or by hybridization (Meena *et al.*, 2013). Hence, the present investigations was carried out considering 30 germplasm with respect to root trait, WUE and important yield traits for feasibility of developing drought tolerant genotypes with high fruit yield in tomato.

RESOURCES AND METHODS

The experimental material included 30 tomato germplasm *viz.*, (1) EC-608438, (2) EC-608468, (3) EC-610643, (4) EC-685705, (5) EC-677041, (6) EC-676743, (7) EC 677204, (8) EC-676730, (9) EC-610654, (10) EC-521038, (11) EC-686531, (12) EC-68687, (13) EC-68698, (14) EC-686702, (15) EC-686703, (16) EC-588221, (17) EC-677065, (18) EC-677078, (19) EC-677034, (20) EC-677076, (21) EC-677080, (22) EC-676770, (23) EC-608271, (24) EC-608377, (25) EC-608394, (26) EC-608419, (27) EC-676816, (28) H-7996, (29) CLN-2070A collected from NBPGR, New Delhi, and AVRDC, Taiwan.

These thirty genotypes were transplanted in Randomized Block Design in the root structure of 20 m length, 1.5 m height and 2.4 m width on either side of central 30 cm permanent wall. Each genotype consists of six plants each per replication and was replicated twice. The spacing adopted was 60 x 30 cm and all the recommended cultural practices were followed during the growth and development period of the crop in order to raise a healthy crop. Plants were grown for 80 days and then root structures were dismantled partly and only three plants out of six, along with roots were separated using water for recording root and shoot traits *viz.*, shoot length, shoot dry weight, root length, root dry weight, root volume and root: shoot ratio. The remaining three plants were used to record observation on growth and yield traits *viz.*, days to fifty per cent flowering, number of branches per plant, WUE traits like SPAD chlorophyll meter reading (SCMR), Specific leaf area (SLA) and fruit yield per plant. SCMR was measured using SPAD chlorophyll meter-502 Minolta Corp., Ramsey, New Jersey, USA., SLA was computed by measuring leaf area and leaf dry weight [SLA =leaf area (cm²)/ leaf dry weight (g)]. Significantly positive association between SPAD readings and chlorophyll content per leaf area was reported by Xiong *et al.* (2015). Root volume was

measured by quantifying the amount of water displacement by roots. The experimental plot was located at crop physiology department experimental plot, UAS, GKVK, Bangalore which is located at an altitude of 930 m above mean sea level 12° 58' North and 77° 35' East latitude and longitude, respectively.

The analysis of variance was calculated using the methodology suggested by Gomez and Gomez (1983). Genetic variability was assessed using first-degree statistics mean, range and second degree statistics phenotypic co-efficient of variance (PCV) and genotypic co-efficient of variance (GCV) were computed (Burton and De vane, 1953). Genetic parameters such as broad-sense heritability (h^2) (Lush, 1945) and genetic advance, expected genetic advance as per cent mean (GAM) were also estimated (Johnson et al. 1955). Correlations and path analysis was carried out according to procedure given by Al-jibouri et al. (1958) and Goulden (1959), respectively. Data recorded on the above traits were subjected to Non-hierarchical Euclidean cluster analysis (Beal, 1969; Spark, 1973) and grouping of 30 genotypes into different clusters was done using Tocher's method.

OBSERVATIONS AND ANALYSIS

Analysis of variance for the means of all the measured traits showed significant differences ($P < 0.001$) among the accessions (Table 2), indicated the presence of exploitable variability for enhancing genetic potential of tomato (Table 1).

Genetic variability :

The results of the present study recorded moderate to high variability for all the quantitative traits under study. The magnitude of genetic variability for days to fifty per cent flowering among tomato accessions varied from 45 to 60.5 days with an average value of 49.08. The genotypes EC 588221, EC 677034, EC 677076 and EC 608271 were of early flowering hence provide mechanism of drought escape. The number of branches per plant varied from 4.5 to 9.5 and lines EC 677065, H 1996, EC 588221 and EC 677041 had more branches per plant. The genotypes EC 608419, EC 677076, EC 676743 and EC 677078 with higher mean values for fruits per plant and it range from 16.5 to 118. The fruit yield per plant is most important trait and genotypes EC 676743, EC

Table 1 : Analysis of variance for morphological, physiological and root traits among tomato germ plasm

Source of variation	Degrees of freedom	Morphological traits					Physiological traits				Root traits		
		Days to 50% flowering	No of branches plant ⁻¹	No of fruits plant ⁻¹	Fruit yield plant ⁻¹	Shoot length	Shoot dry weight	SCMR	SLA	Root length	Root: Shoot ratio	Root volume	Root dry weight
Treatment	29	19.52	2.63*	1170.57*	3.49*	223.35*	332.18*	154.88*	1839.87*	287.10*	0.05*	42.23*	11.46*
Replication	1	2.82	0.61	220.42	0.24	80.27*	72.38	0.02	14.14	14.11	0.01	6.06	1.21
Error	29	0.95	0.80	49.14	0.12	25.9	25.35	0.86	14.71	45.10	0.01	4.05	0.72
C.D. (P=0.05)		1.99	1.83	14.34	0.72	10.43	10.29	1.89	7.84	13.73	0.23	4.12	1.73
CV		1.99	13.92	11.84	11.47	7.55	11.11	3.52	2.59	10.50	11.74	10.97	14.45

Table 2 : Genetic variability for different Morpho-Physiological and root traits in tomato

Characters	Mean ± S.E	Range	GCV	PCV	h^2 (Broad Sense)	Genetic advancement	Gen. Adv as % of Mean
Days to 50% flowering	49.08 ± 0.69	45.00 - 60.50	6.21	6.52	80.68	7.66	15.60
No of branches per plant	6.43 ± 0.63	4.50 - 9.50	14.90	20.39	53.39	1.85	28.73
No of fruits per plant	59.22 ± 4.96	16.50 - 118.00	39.99	41.70	91.94	46.77	78.99
Plant height (cm)	67.50 ± 3.60	48.25 - 99.00	14.72	16.54	79.15	23.33	34.56
Shoot dry weight (g)	45.32 ± 3.60	20.50 - 79.00	27.33	29.50	85.82	23.64	52.15
Root dry weight (g)	5.86 ± 0.59	3.20 - 16.00	39.53	42.08	88.21	4.48	76.47
Root length (cm)	63.95 ± 4.75	42.15 - 98.80	17.19	20.15	72.85	19.34	30.24
Root: Shoot ratio	1.09 ± 0.09	0.76 - 1.55	15.31	20.02	58.44	0.26	24.11
Root volume (cm ³)	18.35 ± 1.42	10.50 - 32.50	23.80	26.21	82.48	8.17	44.53
SCMR	26.32 ± 0.66	15.97 - 49.08	33.34	33.52	68.89	17.98	68.29
SLA (cm ² g ⁻¹)	148.02 ± 2.71	94.92 - 209.17	20.41	20.57	78.41	61.73	41.71
Fruit yield (kg)	3.06 ± 0.25	0.58 - 4.58	42.32	43.85	73.15	2.57	84.14

677076, EC 610654 and EC 608419 were found to be superior with maximum fruit yield. Plant root system plays an important role in regulation of water uptake and extraction from deep soil layers. A positive linear relationship between root and shoot length was noticed among genotypes EC676743, EC677034 and these had higher mean value for shoot and root length. The range of values for shoot length and root length are 48.25 - 99.00 cm and 42.15 - 98.80 cm, respectively. Different germplasm lines recorded root volume ranging from 10.50 - 32.50 cm³ and average being 4.59 cm³. The genotypes EC 676743, EC 677065, EC 68698 and EC 608271 had higher mean value for root volume. Root dry weight varies from 3.2 - 16.0g and genotype EC 676743, EC 608438, EC 676730 and EC 610643 had higher mean values for this trait. Root length and dry weight showed significant positive correlation with grain yield under stress in rice. Alternate approaches for measuring WUE include measuring SLA, SCMR. SLA is used as alternate method for estimation of genetic variability for transpiration efficiency or water use efficiency (WUE) and Similarly SCMR can also provide a good estimate of leaf chlorophyll content. Variation for SCMR is from

14.57 - 41.60 and for SLA it ranged from 99.43- 209.72 cm²g⁻¹. The genotypes EC 608419, EC 676770, EC 677065 and EC 677034 with lower SLA found to have higher water use efficiency. While for SCMR the genotypes EC 677041, EC 610654, EC 521038 and EC 676770 had higher chlorophyll content. Thus, the lines EC 676730, EC686531, EC677076, EC677080, CLN2070A and EC686703 were identified as high fruit yielding and Water use efficient based on root and shoot traits. Highly significant differences among the accessions for growth and yield attributes in tomato was reported also by several workers (Sachan and Singh, 2003; Kumar *et al.*, 2003; Singh and Raj, 2004; Paul *et al.*, 2006; Chaitali and Bini, 2007; Hidayatullah *et al.*, 2008), which indicated the enough genetic variability hence the scope for improvement of this crop.

The genotypic co-efficient of variation (GCV) ranged from 6.21 in days to 50% flowering to 42.32 in fruit yield per plant. Similarly, PCV ranged from 6.52 (days to 50% flowering) to 43.85 (fruit per plant). The high GCV and PCV observed for fruit yield(42.32,43.85), root dry weight(39.53,42.08), fruits per plant (39.99, 41.70), SCMR(33.34, 33.52), shoot dry

Table 3 : Genotypic and phenotypic correlation co-efficient studies in tomato

Characters		X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
Days to 50% flowering (X1)	P	1.000	-0.162	-0.182	-0.349**	-0.474**	-0.132	-0.538**	0.295*	-0.416**	-0.218	-0.238	-0.409**
	G	1.000	-0.228	-0.217	-0.416**	-0.520**	-0.188	-0.638**	0.396**	-0.474**	-0.238	-0.234	-0.457**
Branches per plant (X2)	P		1.000	-0.024	-0.066	0.152	-0.055	0.135	-0.242	0.295*	0.159	-0.027	0.015
	G		1.000	-0.107	-0.263*	0.058	-0.200	0.101	-0.456**	0.304*	0.202	-0.034	-0.049
Fruits per plant (X3)	P			1.000	0.219	0.027	0.177	0.320*	-0.142	0.236	0.416**	0.099	0.583**
	G			1.000	0.216	-0.008	0.156	0.349**	-0.151	0.247	0.435**	0.101	0.579**
Plant height (X4)	P				1.000	0.705**	0.316*	0.503**	0.388**	0.464**	0.305*	0.115	0.360**
	G				1.000	0.807**	0.348**	0.578**	0.389**	0.546**	0.334**	0.129	0.404**
Shoot dry weight (X5)	P					1.000	0.296*	0.543**	0.074	0.545**	0.088	0.306*	0.272*
	G					1.000	0.319*	0.580**	0.180	0.527**	0.087	0.319*	0.252
Root dry weight (X6)	P						1.000	0.315*	0.006	0.443**	0.107	0.122	0.241
	G						1.000	0.325*	0.088	0.507**	0.113	0.135	0.226
Root length (X7)	P							1.000	-0.579**	0.578**	0.315*	0.397**	0.617**
	G							1.000	-0.525**	0.642**	0.362**	0.469**	0.706**
Root to shoot ratio (X8)	P								1.000	-0.154	-0.029	-0.315*	-0.329*
	G								1.000	-0.101	-0.038	-0.412**	-0.389**
Root volume (X9)	P									1.000	0.291*	0.148	0.292*
	G									1.000	0.323*	0.156	0.301*
SPAD chlorophyll meter reading (X10)	P										1.000	-0.111	0.279*
	G										1.000	-0.112	0.283*
Specific leaf area (X11)	P											1.000	0.162
	G											1.000	0.171

weight(27.33,29.50), root volume(23.80,26.21) and specific leaf area(20.41,20.57) indicated the existence of wide spectrum of variability for these yield and WUE traits and offer greater opportunities through phenotypic selection (Table 2). Moderate PCV and GCV values recorded for Root length (17.19, 20.15), Root: Shoot ratio (15.31, 20.02), branches per plant (14.90, 20.39) and plant height (14.72, 16.54) while, days to fifty per cent (6.21, 6.52) recorded lowest. The estimates of PCV were higher than GCV for all the traits. However, small difference for many traits except branches per plant, root to shoot ratio and root dry weight, indicated less influence of environment over expression of the traits (Manikya and Reddy, 2011). Hence, selection for improvement of tomato for these attributes is likely to be most effective.

Estimates of heritability in the broad sense were very high for fruits per plant (91.94%), root dry weight (88.21%), shoot dry weight (85.82%), root volume (82.48%) and days to fifty per cent flowering (80.68%), indicated the possibility of improvement through phenotypic selection. Plant height (79.15%), SLA (78.41%), fruit yield (73.15%), Root length (72.85%), SCMR (68.89%), root: Shoot ratio (58.44%) and branches per plant (53.39%) had moderate heritability (Table 2). Similar results have been reported by Tasisa *et al.* (2011) and Ulla *et al.* (2012). Fruit yield per plant (84.14), No of fruits per plant (78.99), Root dry weight (76.47), SCMR (68.29), Shoot dry weight (52.15), Root volume (44.53) and SLA (41.71) showed high Genetic Advance. However, Parnse (1957) reported that greater usefulness of considering estimate of GAM as an effective selection tool lies in its association with high heritability. The traits fruit yield per plant, fruits per plant, root dry weight, SCMR, shoot dry weight, root volume

and SLA showed high values for both GAM and heritability, which indicates simple inheritance system for these traits and prevalence of additive gene action. These results are accordance with Jayasudha and Sharma (2010), Nwosu *et al.*, 2014.

Correlation co-efficient :

The correlation studies provide information about association between any two traits. The degree of association between fruit yield per plant and its contribution can be estimated by correlation co-efficient at genotypic and phenotypic levels. All possible phenotypic and genotypic correlation co-efficient between fruit yield and its components was calculated and is given in Tables 1. For most of the traits genotypic correlation co-efficient was found higher than phenotypic correlation co-efficient indicating a strong inherent association among various traits. Similar findings were also observed by Mohanty (2003), Singh (2009) and Nagariya *et al* 2015.

Days to 50% flowering showed negative association with all traits studied except root to shoot ratio (0.29* and 0.39**) has positive correlation at phenotypic and genotypic level. Similarly number of branches per plant has significant positive correlation with root volume (0.29* and 0.30*). Number of fruits per plant exhibited significant positive association at phenotypic and genotypic level with root length (0.32* and 0.35**), SCMR (0.42**and 0.44**) and fruit yield per plant (0.58**and 0.58**). Plant height showed significant positive association with all traits studied except SLA, branches and fruits per plant. Plant height(0.70** and 0.81**), root length (0.54** and 0.58**), root dry weight(0.29*and 0.32*), root volume(0.54** and 0.53**), SLA(0.31*and 0.32*)

Table 4 : Direct (diagonal) and indirect effect of different traits on fruit yield per plant in tomato at phenotypic level

Characters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	R ²
Days to 50% flowering (X1)	0.063	-0.069	-0.091	-0.475	0.236	-0.046	-0.225	-0.229	0.246	0.077	0.056	-0.457
Branches per plant (X2)	-0.014	0.302	-0.045	-0.301	-0.026	-0.049	0.036	0.264	-0.157	-0.065	0.008	-0.049
Fruits per plant (X3)	-0.014	-0.032	0.419	0.247	0.004	0.039	0.123	0.087	-0.128	-0.141	-0.024	0.579
Plant height (X4)	-0.026	-0.079	0.091	1.143	-0.366	0.086	0.204	-0.225	-0.283	-0.108	-0.031	0.404
Shoot dry weight (X5)	-0.033	0.018	-0.003	0.923	-0.454	0.079	0.204	-0.104	-0.273	-0.028	-0.077	0.252
Root dry weight (X6)	-0.012	-0.060	0.065	0.398	-0.145	0.248	0.114	-0.051	-0.262	-0.037	-0.033	0.226
Root length (X7)	-0.040	0.031	0.146	0.661	-0.263	0.081	0.352	0.302	-0.332	-0.117	-0.113	0.706
Root to shoot ratio (X8)	0.025	-0.138	-0.063	0.445	-0.082	0.022	-0.184	-0.579	0.052	0.012	0.099	-0.389
Root volume (X9)	-0.030	0.092	0.104	0.624	-0.239	0.126	0.22	0.058	-0.518	-0.105	-0.037	0.301
SPAD chlorophyll meter reading (X10)	-0.015	0.061	0.182	0.381	-0.039	0.028	0.127	0.022	-0.167	-0.324	0.027	0.283
Specific leaf area (X11)	-0.015	-0.011	0.042	0.147	-0.14	0.033	0.165	0.238	-0.081	0.036	-0.241	0.171

recorded significant positive association with shoot dry weight at both level, but at phenotypic level with fruit yield per plant (0.27*). Root length, root volume, plant height and shoot dry weight showed positive association with root dry weight. The physiological trait such as SCMR exhibited significant positive association with fruit yield (0.27* and 0.28*), root length; root volume, plant height and fruits per plant. SLA was negatively associated with SCMR but non-significant. However it has significant positive correlation with shoot dry weight and root length. Fruit yield per plant is positively and significantly ($P < 0.01$) correlated to number of fruits per plant (0.58 and 0.57), plant height (0.36 and 0.40), root length (0.62 and 0.71), root volume (0.29 and 0.30) and SCMR (0.27 and 0.28). This may be explained by increased number of fruit bearing inflorescence (plant height), greater photosynthetic products available for

partitioning to fruit production (SCMR) and greater opportunity for intake of mineral nutrition (root length and volume). Therefore, a breeder interested in improvement for fruit yield in tomato may select plants with high SCMR, deep roots and fruits per plant.

Path-co-efficient analysis :

The simple correlation alone, however, is not a true reflection of the nature of association of the different traits with each other because of complex relationships and do not lead to any meaningful interpretations. Path-co-efficient analysis is a standardized partial regression co-efficient, which splits the correlation co-efficients into the measures of direct and indirect effects of a set of independent variables on the dependent variable (Dewey and Lu in 1959). In the present investigation, the phenotypic correlations of fruit yield per plant with

Table 5 : Cluster mean values of different traits in tomato

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
Cluster 1	48.29	6.55	55.06	67.21	47.41	5.66	63.09	1.09	18.36	24.62	137.72	3.05
Cluster 2	51.71	5.96	48.71	60.33	37.21	5.61	59.86	1.04	15.35	18.66	175.71	2.57
Cluster 3	47.75	7.42	90.63	77.44	55.00	7.38	79.73	1.01	23.96	42.39	169.54	4.19
Cluster 4	47.50	5.65	79.50	76.80	42.25	7.50	60.50	1.28	19.17	29.27	94.92	3.46
Cluster 5	51.00	4.50	57.50	73.75	31.00	3.50	47.75	1.55	16.00	41.67	96.30	1.86

Table 6 : Average intra and inter cluster distances (D2 values)

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	12.80	19.95	23.32	18.00	24.04
Cluster 2		13.44	30.30	32.19	37.31
Cluster 3			15.22	23.18	20.69
Cluster 4				00.00	12.18
Cluster 5					00.00

Table 7 : Per cent contribution of various traits for divergence in tomato

Source	% contribution
Days to 50% flowering	1.80 %
No. of branches per plant	10.04%
No. of fruits per plant	3.81 %
Shoot length (cm)	10.10 %
Shoot dry weight (g)	10.69 %
Root dry weight (g)	11.15 %
Root length (cm)	1.00 %
Root: Shoot ratio	0.90 %
Root volume (cm ³)	2.76 %
SCMR	8.54 %
SLA (cm ² g ⁻¹)	14.04 %
Fruit yield per plant (kg)	25.17 %

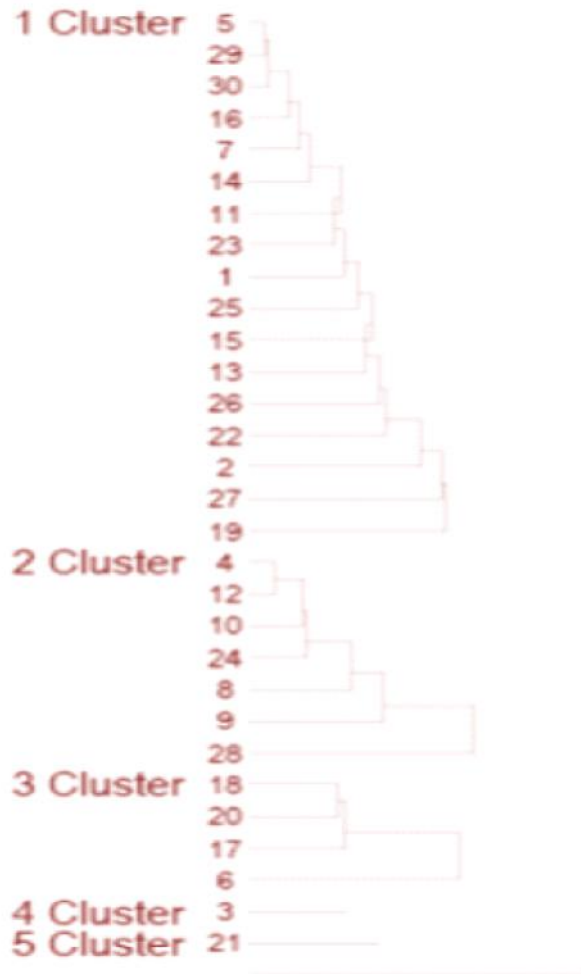


Fig. 1 : Clustering pattern of 30 tomato genotypes

selected seven yield traits and root traits were partitioned into their corresponding direct and indirect effects through path co-efficient analysis (Table 2).

In the present investigation (Tables 4) average plant height (1.143) had the highest direct positive effect on fruit yield per plant followed by fruits per plant (0.419), root length (0.352), branches per plant (0.302) and root weight (0.248). Average plant height showed positive indirect effect on fruit yield per plant through most of the traits except branches per plant and days to 50% flowering. Number of fruits per plant was having positive indirect effect through plant height, root length, root to shoot ratio and root weight. Shoot dry weight exhibited positive indirect effect through plant height, root length, root dry weight, and branches per plant. Fruits per plant, root length plant height, branches per plant were having positive indirect effect through SCMR, While root to

shoot ratio, root length and plant height through SLA. Direct and indirect effect of various traits on fruit yield per plant indicated that there is an agreement between direction and magnitude of direct effect of various traits and correlation with fruit yield per plant. Thus a significant improvement in fruit yield can be expected through simple selection in the component traits with high positive direct effects. Phenotypic path-co-efficient analysis indicated the importance of plant/shoot height, fruits per plant and root length in the improvement of fruit yield per plant owing to the information of direct positive effect and highly significant positive correlation with fruit yield. This observation of the present study are in accordance with the reports of Vikram and Kohli (1998), Mohanty (2002a, 2002b), Joshi *et al.* (2004), Asati *et al.* (2008), Ara *et al.* (2009), Ghosh *et al.* (2010), Al-Aysh *et al.* (2012) and Manna and Paul (2012).

D₂ analysis :

Information on the extent of genetic diversity among accessions is very important as the greater is parental diversity, greater is the chance of developing higher yielding improved lines (Singh *et al.*, 2012). Among the various methods developed, the Mahalanobis D₂ (Mahalanobis, 1936) is reliable and most frequently used. Further, the grouping of the accessions based on Tocher's method will be more useful in choosing suitable parents for heterosis breeding (Prashanth *et al.*, 2008).

On the basis of D₂ values, 30 exotic accessions were grouped into five divergent clusters (Table 2), indicating adequate genetic diversity for the traits studied. The cluster divergence was proved by the high inter-cluster and low intra cluster D₂ values. The cluster I had the highest number of genotypes (17) followed by cluster II (7) and cluster III (4). The cluster IV and V were monogenotypic. The clustering pattern graph clearly indicated no parallelism between geographical distribution of genotypes and genetic divergence. Therefore, geographical diversity could not be related to genetic diversity in the material investigated (Singh *et al.* (2006), Reddy *et al.* (2013) and Basavaraj *et al.* (2010). The selection of genotypes for hybridization to generate diverse new gene combinations should be based on genetic diversity rather than geographic diversity (Pawar *et al.*, 2013).

The intra-cluster distance indicates the divergence among the genotypes within the clusters and inter-cluster

indicates diversity between clusters. The maximum intra-cluster distance was recorded within cluster III (15.22) followed by cluster II (13.4) and cluster I (12.8). The maximum inter-cluster distance is observed between cluster II and V (37.31) followed by cluster II and IV (32.19), II and III (30.30). These results reveals that maximum divergence between genotypes of cluster II with genotypes of cluster V, indicating the genotypes when used in hybridization programme produce superior segregants. The information obtained from inter-cluster distances may be used to select genetically diverse and superior genotypes. The parents possessing maximum genetic divergence is expected to yield the heterotic F1 and desired segregants in segregating generations. Intercrossing of divergent groups may lead to greater opportunity for crossing over and recombination, which may release hidden variability (Kumar *et al.*, 2010). The minimum inter-cluster distance was observed between cluster IV and V (12.18) followed by cluster I and II (19.94) and cluster III and V (20.69). In general, lesser intra-cluster distance than inter cluster distance suggested homogenous and heterogeneous nature of the genotypes within and between the clusters, respectively Pawar *et al.*, (2013). These results are conformity with the findings by Veershetty (2004), Mehta and Asati (2008) and Kumar *et al.* (2010) and Sinha *et al.*, 2014.

The contribution of each trait towards total genetic diversity is presented in Table 6. The traits, fruit yield per plant (25.17), specific leaf area (14.04), root dry weight (11.15) and shoot dry weight (10.69) contributed high for divergence. Thus, these traits may be given high emphasis while selecting the accessions for hybridization programme to generate large variability and will provide immense scope for the improvement of fruit yield through selection. The other traits like root: shoot ratio (0.90%), root length (1.00%), days to 50% flowering (1.80%) and root volume (2.76%) contributed very little for divergence. The results were in accordance with Sinha *et al.*, 2014.

The Table 5 demonstrates the mean values for twelve traits in five clusters, which vary in their value differently from each other. The genotypes included in cluster III and IV recorded minimum days to 50% flowering (47). Numbers of branches per plant (7.42), plant height (77.44) and shoot dry weight (55.00) were highest for cluster III. Selection of parents is the most important aspect of crop improvement programme and highly diversified

parents were selected based on the yielding ability of the respective parents. The economically important traits such as fruits per plant (90.63), high fruit yield per plant (4.19) was supreme for the cluster III which indicates that the genotypes included in these clusters could effectively be used for the tomato improvement programme for increasing yield-contributing traits. The physiological traits SCMR and SLA, which directly correlates with yield per plant, was high for the cluster III (42.39) and cluster IV (94.92) respectively. In case of root traits, the cluster III for root length (79.73) and root volume (23.96), the cluster V for root to shoot ratio (1.55), the cluster IV for root dry weight (7.50) possess the highest values. It is suggested that hybridization among the genotypes of above said clusters would produce segregants for more than one economic trait. The choice should be based on genetic distance and depending upon the objective of the breeding programme. Many workers have observed that more diverse the parents within its overall limits of fitness, the greater are the chances of heterotic expression in F1's and a broad spectrum of variability in segregating generations (Arunachalam, 1981). In choosing parents for hybridisation programme the clustering pattern could be employed that would likely to render the maximum possible variability for various economic traits (Hazra *et al.* (2010) and Kumar *et al.* (2010). Moreover, it will be effective to intercross genotypes belonging to more diverse clusters like cluster II and V, cluster II and IV and cluster III and V to create wide spectrum of variability to produce transgressive segregates with better fruit yield and root traits in tomato.

Conclusion :

In conclusion, in the present study thirty exotic tomato genotypes were assessed to know the genetic variability, association and magnitude of genetic divergence for Physio-morphological traits, root traits and fruit yield. High genetic variability was observed for fruit yield per plant, fruits per plant, root dry weight, SCMR, shoot dry weight, root volume and specific leaf area. However, D2 analysis classify these genotypes into five clusters, of which genotypes of cluster-II and V and cluster-III and V are complementary for maximum traits and could be selected for hybridization to develop promising F1 hybrids or transgressive segregants for improvement in fruit yield and root traits.

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