



Genetic Variability Studies for Growth, Yield and Quality Traits in Tomato (*Solanum lycopersicum* L.) Germplasm under North Eastern Dry Zone of Karnataka, India

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

An experiment was carried out at College of Agriculture, University of Agricultural Sciences, Raichur under north eastern dry zone of Karnataka, India during *late-kharif* season of 2022-23 by using twenty-five tomato genotypes to study the variability, heritability and genetic advance for

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growth, yield and quality traits. Analysis of variance revealed that significant variability was observed among the genotypes of tomato for all character's studied. Genetic variability revealed that a lot of variation was observed among the genotypes studied. In general, the lowest difference in phenotypic and genotypic coefficients of variation indicated lowest environmental influence in controlling the expression of the traits. Based on genetic variability studies, high PCV and GCV and high heritability coupled with high genetic advance as per cent of mean were recorded for plant height, number of nodes per plant, number of branches per plant, number of locules per fruit and titrable acidity, average fruit weight, fruit yield per plant and fruit yield per hectare indicating the existence of wider genetic variability for these traits in the germplasm under study.

Keywords: Genetic variability; tomato; germplasm; heritability; genetic advance.

1. INTRODUCTION

“Tomato is considered as the 2nd greatest significant vegetable crop in the world after potato. Tomato is a member of the family Solanaceae. The botanical name of tomato is *Solanum lycopersicum* L. and having a chromosome number of $2n = 2x = 24$ and all the species of tomato are native of western South America. Tomato is one of the most important “protective foods” because of its special nutritive value” [1]. “Tomato is one of the most important vegetable crops in the world and ranks second after potato and ranks third in priority in India after potato and onion. As we all know food and nutritional security related concerns can only be solved with an increase in the yield of the vegetables” [2]. “Genetic variability is a very important component of plant breeding which is a major tool being used to cope with the ever-increasing pressure of an expanding world population on food production. “Information on genetic variability of different characters of a crop and about the useful genes in each accession which is properly evaluated to identify the potential accessions is necessary prior to breeding programme for improvement in any crop. Since most of the plant characters of economic importance are polygenic in nature and are highly influenced by environment, it is necessary to work out whether the observed variability is heritable or due to environment. This suggests the imperative need to work out the phenotypic variation into heritable and non-heritable components. Genotypic and phenotypic coefficients of variability helps to assess the divergence of the characters. Selection would be more meaningful for the characters which exhibit high genetic variability, heritability along with high genetic gain. Realizing the economic potential of the crop, there is an urgent need to isolate such breeding lines which have desirable horticultural traits, better quality coupled with high yield potential” [3]. The genetic parameters such as

genotypic coefficient of variation, heritability and genetic advance enable selection on a sound genetic basis, which helps in improving the yield and its attributing characters in tomato.

The findings of this research can guide farmers in selecting appropriate cultivars for specific agro-climatic regions, enhance breeding programs by identifying valuable genetic resources, and can benefit both small-scale and large-scale farmers by increasing their yields and incomes. Furthermore, this evaluation process not only aids in the selection of suitable varieties for cultivation but also provides valuable insights into future breeding programs. In the subsequent sections of this paper, we will delve into the methodology, results, discussion, and conclusions derived from the systematic evaluation of tomato genotypes.

2. MATERIALS AND METHODS

The experiment was conducted using twenty-four genotypes along with one check variety Arka Saurabh which was collected from different sources viz., NBPGR, New Delhi, Indian Institute of Horticultural Research (IIHR), Bengaluru, College of Horticulture (CoH), Bengaluru, College of Horticulture (CoH), Bagalkot and Kerala Agriculture University (KAU), Kerala and are enlisted in Table 1. The tomato genotypes were laid out in Randomized Complete Block Design (RCBD) with three replications for yield and yield attributing traits at Herbal Garden, College of Agriculture, UAS, Raichur during *late kharif* season, 2022-23.

Each genotype was raised in portrays and each genotype in each replication was transplanted in two rows each accommodating 12 plants at a spacing of 60 cm between the rows and 45 cm between the plants. Five plants from each replication and each plot were randomly tagged and selected for evaluating different quantitative

characters and the replicated mean values of various characters were subjected to statistical analysis. Genotypic and phenotypic coefficients of variation were estimated according to Burton et al. [4] and heritability estimates as per [5] and genetic advance estimates according to Johnson et al. [6].

3. RESULTS AND DISCUSSION

“The components of genetic parameters of variation for yield and its attributes exhibited a wide range of variability for the parameters studied. The values of phenotypic coefficient of variation (PCV) were of higher in magnitude than that of genotypic coefficient of variation (GCV) for all the characters indicating that the environment played an important role in influencing the expression of the traits. The relative values of genotypic and phenotypic coefficient of variation gives an idea about the magnitude of variability present in a population. The results obtained from the statistical analysis revealed high, medium and low estimates of genotypic and phenotypic coefficient of variation among the genotypes for different characters studied” [7].

Plant height at 90 days after transplanting showed high Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) of 25.44 per cent and 28.03 per cent, respectively. A very high heritability of 82.37 per cent along with a very high genetic advance over mean of 47.56 per cent were recorded among the genotypes. Moderate GCV (17.99 %) and PCV (22.53 %), high heritability of 63.73 per cent along with a high genetic advance over mean 29.58 per cent was reported by Internodal length at 90 DAT. Number of nodes per plant recorded high GCV and PCV of 20.51 % and 22.06 %, respectively with high heritability (86.39 %) and high GAM (39.26 %) at 90 DAT. High GCV (26.47 %) and PCV (27.52 %) were recorded along with very high heritability of 92.48 per cent coupled with high GAM of 52.43 per cent for number of branches per plant.

The days to first flowering recorded low GCV and PCV (8.39% and 9.69%, respectively) with high heritability of 75.05 per cent and moderate genetic advance over mean of 14.98 per cent. Days to 50 per cent flowering showed low GCV (7.82%) and PCV (8.17%) along with high

Table 1. Details of tomato genotypes used in the experiment and their source of collection

Sl. No.	Original Code	Source of collection
1	Anagha	KAU, Thrissur
2	Akshaya	KAU, Thrissur
3	S – 22	Local collection
4	14	COH, Bengaluru
5	15	COH, Bengaluru
6	16	COH, Bengaluru
7	IC-249514	NBPGR, New Delhi
8	EC-631409	NBPGR, New Delhi
9	EC-631361	NBPGR, New Delhi
10	EC-157568	NBPGR, New Delhi
11	EC-636877	NBPGR, New Delhi
12	EC-631368	NBPGR, New Delhi
13	EC-620427	NBPGR, New Delhi
14	EC-249508	NBPGR, New Delhi
15	EC-164677	NBPGR, New Delhi
16	EC-315489	NBPGR, New Delhi
17	EC-620361	NBPGR, New Delhi
18	EC-620366	NBPGR, New Delhi
19	Arka Meghali	IIHR, Bengaluru, Karnataka
20	EC-698849	NBPGR, New Delhi
21	EC-688516	NBPGR, New Delhi
22	Baari	COH, Bagalkot
23	RFT-S-1	COH, Bagalkot
24	Shalmala	COH, Bagalkot
25	Arka Saurabh	IIHR, Bengaluru, Karnataka

heritability of 91.71 per cent and moderate genetic advance over mean of 15.43 per cent. Moderate GCV (13.11 %) and PCV (14.61 %), high heritability of 80.53 per cent coupled with a high genetic advance over mean of 24.23 per cent were recorded for number of flowers per cluster. Moderate GCV (14.18 %) and PCV (15.42 %) were reported for number of clusters per plant which was coupled with high GAM along with high heritability (26.86 % and 84.54 %, respectively).

Moderate GCV (17.63 %) and PCV (18.50 %) were reported and coupled with high heritability of 90.90 per cent and high genetic advance over mean of 34.63 per cent for fruit length. Fruit girth showed low GCV and PCV (6.87 % and 10.33 %, respectively) along with low GAM and moderate heritability (9.41 % and 44.21 %, respectively). Average fruit weight recorded high GCV (28.84 %) and PCV (30.11 %) and estimates of GAM (56.88 %) and heritability (91.70 %) were very high for the character. Number of fruits per cluster showed moderate GCV (14.15 %) and PCV (15.82 %) with high GAM and high heritability (26.07 % and 80.00 %, respectively). Low genotypic coefficient of variation (8.07 %) and phenotypic coefficient of variation (10.17 %) and Moderate GAM (13.19 %) along with high heritability (62.98 %) were observed for number of fruits per plant. High GCV and PCV values of 20.89 per cent and 22.46 per cent and coupled with very high heritability of 86.54 per cent and high GAM of 40.04 per cent were observed for fruit yield per plant. Fruit yield per hectare recorded High GCV and PCV values of 21.20 per cent and 21.86 per cent with very high heritability of 94.04 per cent coupled with a high GAM of 42.35 per cent.

Pericarp thickness recorded moderate GCV (16.09 %) and PCV (17.99 %) with high estimates of genetic advance over mean (29.66 %) and high heritability (80.05 %). High GCV (30.45 %) and PCV (31.22 %) which was coupled with very high heritability of 95.10 per cent and very high GAM of 61.17 per cent were reported for number of locules per fruit. Total soluble solids showed moderate values of GCV and PCV (10.52 % and 12.78 %, respectively) with moderate GAM and high heritability (17.84 % and 67.77 %, respectively). Titrable acidity recorded high GCV and PCV values of 32.98 per cent and 33.62 per cent, respectively with estimates of very high heritability of 96.24 per cent and high GAM of 66.65 per cent [8].

“High GCV and PCV was reported for the traits viz., fruit yield per plant, average fruit weight, plant height, number of nodes per plant, number of branches per plant, number of locules per fruit and titrable acidity. The traits viz., internodal length, number of flowers per cluster, number of clusters per plant, fruit length, number of fruits per cluster, pericarp thickness, total soluble solids, shelf life recorded moderate GCV and PCV values. The difference between PCV and GCV values were minimum, indicating that the traits under study were less influenced by environment and these characters could be improved by following phenotypic selection. These results obtained from the studies carried out in tomato are in accordance with” Basavaraj et al. [9-12].

“Low PCV and GCV for the traits viz., days to first flowering, days to 50 per cent flowering, fruit girth, number of fruits per plant. The low estimates of coefficient of variation indicated that the genotypes included in the present study possessed less genetic variability for these characters, while characters having high estimates of coefficient of variation indicated greater genetic variability among the genotypes for these attributes for making effective selection” [7]. Similar results were found by Anuradha et al. [13,14] in tomato crop.

High heritability accompanied by high genetic advance over mean indicates operation of additive gene action which was observed in characters viz., plant height, internodal length, number of nodes per plant, number of branches per plant, number of flowers per cluster, number of clusters per plant, fruit length, average fruit weight, number of fruits per cluster, fruit yield per plant, pericarp thickness, number of locules per fruit and titrable acidity. These results are in agreement with the findings of Sushma et al. [15,16] in tomato.

Moderate genetic advance as per cent of mean with high or moderate heritability suggests the action of both additive and non-additive genes thereby favourable influence of environment in the expression. The same was reported in case of days to first flowering, days to 50 per cent flowering, fruit girth, number of fruits per plant and total soluble solids. Similar observations were recorded by Amarjeet et al. [17-20] in tomato.

Table 2. Estimates of genotypic and phenotypic coefficient of variation, heritability and genetic advances as per cent of mean for different parameters in tomato genotypes

SI. No.	Characters	Range		GrandMean	GCV(%)	PCV(%)	H ² (%)	GA(%)	GAM(%)
		Lowest	Highest						
1	Plant height (cm)	71.71	166.48	110.84	25.44	28.03	82.37	52.71	47.56
2	Internodal length (cm)	3.52	8.85	6.24	17.99	22.53	63.73	1.85	29.58
3	Number of nodes per plant	14.66	28.78	19.98	20.51	22.06	86.39	7.84	39.26
4	Number of branches per plant	8.63	18.68	11.97	26.47	27.52	92.48	6.28	52.43
5	Days to first flowering	18.33	24.67	22.65	8.39	9.69	75.05	3.39	14.98
6	Days to 50 per centflowering	20.33	28.33	24.89	7.82	8.17	91.71	3.84	15.43
7	Number of flowers per cluster	4.50	7.85	5.85	13.11	14.61	80.53	1.43	24.23
8	Number of clusters per plant	10.22	17.79	13.68	14.18	15.42	84.54	3.67	26.86
9	Fruit length (mm)	31.07	58.37	43.39	17.63	18.50	90.90	15.03	34.63
10	Fruit girth (mm)	39.71	58.57	49.47	6.87	10.33	44.21	4.65	9.41
11	Average fruit weight (g)	34.85	136.43	68.76	28.84	30.11	91.70	39.11	56.88
12	Number of fruits per cluster	3.40	5.41	4.44	14.15	15.82	80.00	1.16	26.07
13	Number of fruits per plant	22.11	30.76	24.94	8.07	10.17	62.98	3.29	13.19
14	Fruit yield per plant (kg)	1.19	2.49	1.59	20.89	22.46	86.54	0.64	40.04
15	Fruit yield per hectare (t ha ⁻¹)	42.37	88.51	56.54	21.20	21.86	94.04	23.95	42.35
16	Pericarp thickness (mm)	3.74	6.58	5.14	16.09	17.99	80.05	1.53	29.66
17	Total soluble solids (°Brix)	4.49	6.73	5.53	10.52	12.78	67.77	0.99	17.84
18	Titration acidity (%)	0.15	0.73	0.41	32.98	33.62	96.24	0.27	66.65
19	Number of locules per fruit	2.00	7.00	4.20	30.45	31.22	95.10	2.57	61.17
20	Shelf life (days)	9.00	15.00	12.24	11.55	12.46	85.91	2.70	22.05

GCV (%): Genotypic Coefficient of Variation; PCV (%): Phenotypic Coefficient of Variation; H²: Heritability; GA: Genetic Advance; GAM %: Genetic Advance Mean

4. CONCLUSION

On basis of current investigation, it is possible to conclude that simultaneous selection based on multiple characters viz., plant height, number of nodes per plant, number of branches per plant, number of locules per fruit and titrable acidity, average fruit weight, fruit yield per plant and yield per hectare having high estimates of genetic coefficient of variation and phenotypic coefficient of variation, heritability and genetic advance could be exercised for improvement through simple direct selection. Therefore, the aforesaid characters could be more promising to yield better hybrids in a further breeding programme and considered for selecting parental lines in a hybridization programme.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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