

Genetic variability Studies in Advanced inbred Population of Tomato (*Solanum lycopersicum* L.)

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ABSTRACT: The current study was designed to assess variances between genotypes and within genotypes, estimate genetic parameters, and identify promising genotypes for future utilization from the pooled population of the cross 16P2 × Kashi Hemanth in tomato (*Solanum lycopersicum* L.). The evaluation was done in the farmers' field at Kanaykanahalli village, Belurtaluq, Hassan district during 2020-2022. Analysis was done for 29 ABLs along with five checks in RBD design. Traits such as plant height, number of branches, number of fruits per plant, average fruit weight, yield per plant, fruit length, fruit width, number of locules, pericarp thickness, TSS, firmness, and lycopene exhibited high heritability and genetic advance as per cent mean. These findings put forward the contribution of additive gene effects to the heritability of these parameters, suggesting significant potential for improvement through selection.

Keywords: Tomato, Genetic variability, GCV, PCV, Heritability, Genetic advance, ABLs.

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is an important remunerable vegetable of India and all over the world belongs to the family Solanaceae having diploid chromosome number of 24. The plant is cultivated primarily for its edible fruit, which can be enjoyed in multiple ways, including raw consumption, cooking, or utilization in various processed forms such as juice, ketchup, sauce, pickles, pastes, puree, and powder (Verma *et al.*, 2021). It is widely recognized as a nourishing food and highly valued for its abundance of minerals, organic acids, and essential vitamins, particularly vitamins A and C (Kalloo, 1991).

Understanding the expression of plant characteristics relies on the combined influence of genetic factors and the environment (Ambresh *et al.*, 2017). Therefore, before initiating a breeding program, it is crucial to examine the variation and heritable components of yield-related traits in the existing genotypes. It is important to separate the overall observed phenotypic variation into heritable and non-heritable components using genetic parameters such as coefficients of variation, estimates of heritability, and genetic advance. These biometric tools are valuable for devising suitable

breeding strategies and harnessing the inherent variability (Golani *et al.*, 2007).

The current investigation was carried out in F₆, F₇ and F₈ populations of tomato and data is pooled from all three seasons to gather information about the genetic potentiality of the population. Hence, selection with particular objectives is most effective and selfing of those selected genotypes helps the development of inbred lines. Hence, the present study was conducted to study the genetic variability, heritability and genetic advance for yield and its contributing characteristics in the late segregating population of tomato.

MATERIAL AND METHODS

Experimental studies was undertaken during the year 2020-2021 and 2021-22 at farmer's field, Kanaykanahalli, Belurtaluk, Hassan district. The material comprised of 29 selected lycopene rich and high yielding F₆ lines of the cross 16 P2 × Kashi Hemanth (Meghana, 2019) along with five checks *viz.*, Arka Rakshak, Arka Samrat, Arka Apeksha, Pusa Ruby and Pusa Rohini. The experiment was carried out during three seasons including early *rabi*, *kharif* and late *rabi* seasons. The experiment was carried out in a Randomized Complete Block Design with two

replications under study. The replication-wise mean data was used for statistical analysis.

RESULTS AND DISCUSSION

A. Variability

The analysis of variance showed significant variations among the genotypes for all the traits, highlighting the presence of ample variability in the selected material under study. This emphasizes the potential for choosing appropriate initial breeding material to enhance crop improvement efforts (Table 1). However, the absolute variability in different characters does not permit the identification of the characters showing the highest degree of variability. Hence, PCV and GCV values were computed. The coefficient of variation, whether genotypic or phenotypic, proves valuable in assessing the extent of variability in various traits, providing a measure of the range of variability (Fig. 1). Plant height, number of branches, number of fruits, average fruit weight, fruit length, yield/plant, pericarp thickness, TSS and firmness showed high levels of both GCV and PCV, a good deal of variability in those characters signifying the effectiveness of selection of desirable types for improvement. Fruit width, number of locules and lycopene showed moderate GCV and PCV values. Days to 50 % flowering, on the other hand, exhibited low GCV and PCV values, indicating a limited range of variation and the least opportunity for advancement by selection. The range shown in the given table also indicated sufficient variability in the given experimental material. These findings are consistent with previous

studies by Somraj *et al.* (2017); Ibaad (2018); Kaushal *et al.* (2019).

B. Heritability and Genetic Gain

Upon examining the outcomes regarding heritability and genetic advance as a percentage of mean (GAM), it became evident that the characters under study exhibited high heritability estimates. This observation implies that selection would be more effective due to the reduced impact of the environment, and there is potential for improvement in these characteristics in future breeding programs. All the traits under examination exhibited high heritability (Table 2). High heritability depicts that the environment has the least role to play in these traits and the selection of such traits is worthy. The moderate values show the role of non-additive gene action which includes dominance and epistasis and it also shows the influence of environments upon the traits. Hence selection of such traits might not be effective. Similar types of findings were reported by Golani *et al.* (2007). However, heritability coupled with genetic advance was more useful than heritability alone in predicting the resultant effect for selecting the best individual as explained by Kumar *et al.* (2013). These findings agree with the works of Dutta *et al.* (2018); Kaushal *et al.* (2019). All traits recorded high levels of GAM except days to fifty per cent flowering. Days to fifty per cent flowering (12.40) recorded moderate levels of GAM (Table 2). These findings agree with the reports of Rajolli *et al.* (2017); Ligade *et al.* (2017).

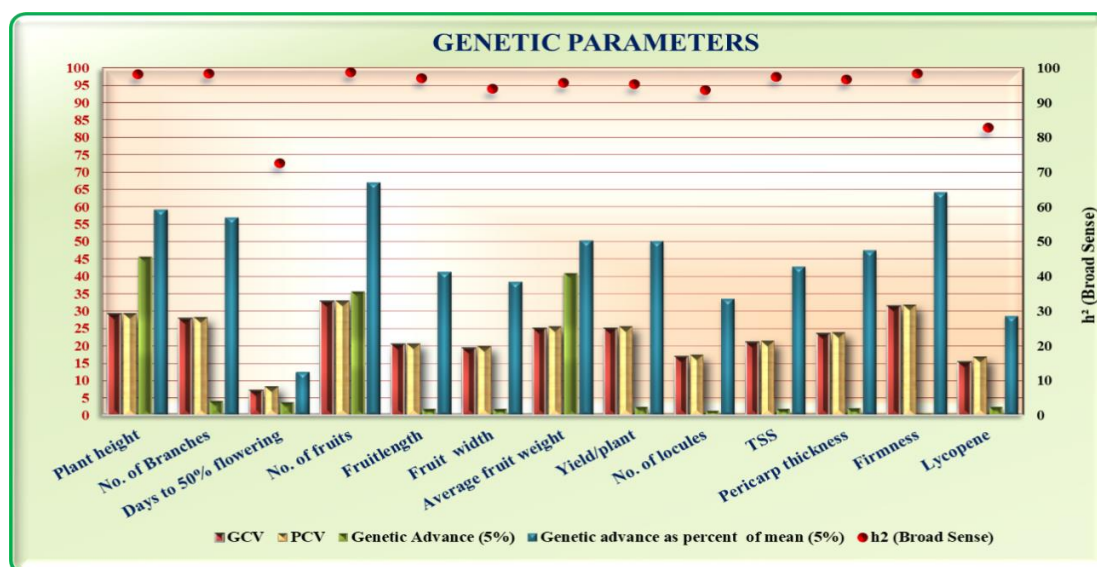


Fig. 1. Variability in the pooled population of tomato.

Table 1: ANOVA for RIL populations of the cross 16P2 × Kashi Hemanth in the pooled population

Source	Df	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃
Replication	1	12.33	0.03	0.07	0.50	0.06	0.03	1.12	0.06	0.03	0.11	0.00	0.00	1.23
Treatment	33	1011.31**	8.24**	10.94**	605.74**	1.60**	1.59**	842.62**	3.08**	0.96**	1.63**	1.92**	0.08**	3.56**
Error	33	8.86	0.07	1.73	3.78	0.02	0.05	17.80	0.07	0.03	0.02	0.03	0.00	0.33

Note: * significant at 0.05% probability, ** Significant at 0.01% probability

Df = Degrees of freedom; X₁ = plant height; X₂ = Number of branches; X₃ = Days to 50 % flowering; X₄ = Number of fruits; X₅ = Fruit length; X₆ = Fruit width; X₇ = Average fruit weight; X₈ = Yield per plant; X₉ = Number of locules; X₁₀ = TSS; X₁₁ = Pericarp thickness; X₁₂ = Firmness; X₁₃ = Lycopene

Table 2: Genetic parameters of variability for growth, yield and quality attributes based on pooled data over three seasons in tomato.

Characters	Mean	Range		GCV (%)	PCV (%)	h ² (%)	GAM (%)
		Minimum	Maximum				
Plant height (cm)	77.07	43.77	153.1	29.05	29.31	98.26	59.32
Number of branches	7.21	4.68	15.71	27.89	28.12	98.37	56.99
Days to 50 % flowering	30.41	26.80	34.09	7.06	8.27	72.74	12.40
No. of fruits	53.00	24.51	91.85	32.73	32.94	98.76	67.01
Average fruit weight (g)	82.17	53.02	122.76	25.01	25.59	95.86	50.35
Yield/plant (kg)	4.97	2.78	6.89	24.79	25.76	92.66	49.16
Fruit length (cm)	4.36	2.60	5.62	20.35	20.66	97.06	41.30
Fruit width (cm)	4.55	2.36	5.99	19.26	19.84	94.17	38.49
Number of locules	4.06	2.41	5.05	16.80	17.36	93.67	33.49
Pericarp thickness (mm)	4.14	2.74	5.76	23.44	23.82	96.77	47.49
TSS (° Brix)	4.25	2.20	5.48	21.05	21.33	97.42	42.80
Firmness (kg/cm ²)	0.64	0.35	1.27	31.47	31.71	98.44	64.32
Lycopene (mg/100g)	8.31	4.35	10.90	15.27	16.78	82.81	28.62

CONCLUSIONS

The ratio between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) exhibited minimal variations implying that environmental factors had limited influence on the expression of most traits. Traits such as plant height, number of branches, number of fruits per plant, average fruit weight, yield per plant, fruit length, fruit width, number of locules, pericarp thickness, TSS, firmness, and lycopene exhibited high heritability and genetic advance as per cent mean, suggesting significant potential for improvement through selection.

FUTURE SCOPE

It provides an opportunity for breeders to develop different varieties having high yields with good lycopene content and resistance to diseases. Diverse genotypes with desirable traits open a broad genetic base for hybrid seed production by using economically viable seed production techniques. Furthermore, this highlights potential challenges in utilizing tomato genotypes and provides insights into future directions for tomato breeding programs, drawing from the evolving insights gained through tomato breeding efforts (Verma *et al.*, 2021).

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