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Genetic variability, Skewness and Kurtosis based genetics for fruit yield and yield attributing characters in F_3 generation of tomato (*Solanum lycopersicum* L.) cross EC521069 × EC362941

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ABSTRACT

An experiment was carried out at College of Horticulture, Mudigere, to access the genetic variability in F_3 population of tomato cross EC521069 × EC362941. The genotypic coefficient of variation and phenotypic coefficient of variation were higher in plant height, number of fruit clusters per plant, number of fruits per plant, fruit yield per plant and average fruit weight. High broad sense heritability and genetic advance over percent of mean was observed for number of primary branches per plant, number of fruit clusters per plant, number of fruits per plant, fruit yield per plant, fruit length and fruit diameter, pericarp thickness and number of locules per fruit, indicating these traits are controlled by additive gene action. The frequency distribution showed positive skewness with positive platykurtic distribution for fruit yield per plant, fruit length, fruit diameter and average fruit weight which were negative for Number of fruit cluster per plant, number of fruits per plant, pericarp thickness and number of locules per fruit.

Key words: *PCV, GCV, Heritability, Skewness, Kurtosis*

Introduction

Tomato (*Solanum lycopersicum* L.) 2n=24, is an important self-pollinated, day neutral and widely grown solanaceous vegetable in India as well as in world.

In India, tomato ranks third among vegetables in its area and production after potato and onion, occupying an area of 0.86 million hectares with annual production of 20 million tonnes with productivity of 23.86 tonnes per hectare. Karnataka is the second leading tomato producing state after Madhya Pradesh in the country (Anon, 2022).

Indeterminate tomato varieties are highly suitable for protected cultivation. Hence, there is continuous need to strengthen the crop improvement programme in tomato and ultimately developing new varieties or hybrids suitable for protected cultivation to fulfill the demand in off-season and satisfying to the present day needs of farmers and consumers as well. Growing tomatoes in green house can further increase the yield and improve the quality.

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Considering the potentiality of this crop, there is a need for improvement and to develop varieties suited to specific agro-ecological conditions and also for specific end use. Assessing the genetic variation and degree of transmission for desirable characters under protected conditions is essential for initiating the crop improvement programme in this crop (Reddy *et al.*, 2023).

In this regard, present investigation was carried out to know the variability present in the F_3 population of tomato cross EC521069 × EC362941.

Materials and Methods

The present investigation was carried out at College of Horticulture, Mudigere under protected condition in *Summer* 2023. Two hundred indeterminate tomato plants of F_3 generation of cross EC521069 × EC362941 were planted with row to row distance of 60 cm and plant to plant distance of 45 cm. All the recommended cultural practices and plant protection measures were followed. Observations were recorded from each plant of for various quantitative characters and the data were subjected to statistical analyses. The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2_{bs}) and the expected genetic advance (GA) for different characters content were calculated as suggested by Burton and Devane (1953) and Johnson *et al.* (1955) respectively. Skewness (third-degree statistics) and Kurtosis (fourth-degree statistics) were estimated as per Snedecor and Cochran (1974) to understand the nature of the distribution of ten quantitative traits in the F_3 population of cross EC521069 × EC362941.

Results and Discussion

The results on the mean, range, variability, heritability, genetic advance as per cent of mean, skewness and kurtosis for various characters in F_3 population of tomato are presented in Table 1.

Genetic variability is the prerequisite for crop improvement which will provide wider scope for selection. In this investigation, the results revealed that there is low difference between genotypic variance and phenotypic variance indicating higher contribution of genotype in expression of phenotype. The traits *viz.*, plant height, number of fruit clusters per plant, number of fruits per plant, fruit yield per plant and average fruit weight showed high PCV

Table 1. Estimates of genetic parameters for yield and yield attributes in F_3 population of tomato cross EC521069 ×EC362941

Sl. No.	Characters	Mean	Range		GV	PV	GCV (%)	PCV (%)	h^2_{bs} (%)	GA	GAM (%)	Skewness	Kurtosis	Kurtosis Type
			Min.	Max.										
1.	Plant height (cm)	193.12	122.00	268.00	178.02	188.23	92.18	97.47	94.57	26.73	13.84	0.391	-0.245	Platykurtic
2.	Number of primary branches per plant	5.06	2.00	9.00	0.64	0.83	12.65	16.42	77.04	1.45	28.59	0.369	-0.370	Platykurtic
3.	Number of fruit clusters per plant	17.51	6.00	24.00	3.68	4.55	21.02	26.01	80.82	3.55	20.29	-0.069	-0.282	Platykurtic
4.	Number of fruits per plant	35.13	8.00	49.00	13.05	13.96	37.16	39.73	93.53	7.20	20.49	-0.097	-0.497	Platykurtic
5.	Fruit yield per plant (kg)	2.36	0.68	3.80	0.53	0.62	22.41	26.48	84.63	1.38	58.40	0.076	0.224	Platykurtic
6.	Fruit length (cm)	4.58	2.98	6.91	0.65	0.75	14.23	16.34	87.09	1.55	33.89	1.707	2.348	Platykurtic
7.	Fruit diameter (cm)	4.53	3.26	7.92	0.60	0.70	13.22	15.43	85.68	1.48	32.57	0.689	2.889	Platykurtic
8.	Average fruit weight (g)	67.21	35.00	125.00	24.48	27.05	36.42	40.25	90.48	9.69	14.42	0.276	0.068	Platykurtic
9.	Pericarp thickness (mm)	5.68	3.02	7.98	0.81	1.20	14.26	21.11	67.55	1.52	26.83	-0.104	-0.226	Platykurtic
10.	Number of locules per fruit	3.68	2.00	7.00	0.47	0.72	12.84	19.46	65.98	1.15	31.26	-0.008	-1.058	Platykurtic

and GCV indicating higher variation present in the population for these characters. The results were in accordance with the findings of Sinha *et al.* (2020), and Pooja *et al.* (2022).

Moderate PCV and GCV was recorded by number of primary branches per plant, fruit length, fruit diameter and number of locules per fruit; moderate GCV and high PCV was observed in pericarp thickness pointing out that there is a degree of variation in the trait's expression due to both genetic and non-genetic factors. This provides an opportunity for breeding and selection to improve the trait while acknowledging that environmental factors also influence its expression. The similar results were obtained by the researchers Nitish (2014) for number of locules per fruit.

Estimates of high heritability (>60 %) coupled with high genetic advance as per cent over mean (>20 %) recorded for number of primary branches per plant, number of fruit clusters per plant, number of fruits per plant, fruit yield per plant, fruit length and fruit diameter, pericarp thickness and number of locules per fruit. This supports the notion that selection could actually improve certain features by highlighting the significance of additive gene effects. These results are in agreement with Adhi *et al*. (2013) for fruit length, Patel *et al*. (2013), Anyaoha *et al.* (2023) and Srivatsava *et al.* (2023) for fruit yield per plant, Ullah *et al*. (2015) for fruits per plant and Pooja *et al*. (2022) for fruit diameter.

High heritability coupled with moderate genetic advance over mean was observed in plant height and average fruit weight. The high heritability is due to the positive impact of environment rather than genotype and selection for such trait keen observation in upcoming generation and then selecting it will be helpful.

The study of distribution using skewness (third-degree statistics) and kurtosis (fourth degree statistics) provides insight about nature of gene action and number of genes controlling the traits, respectively. Positively skewed and positive platykurtic distribution indicated complimentary gene action and higher number of genes responsible, respectively for fruit yield per plant, fruit length, fruit diameter and average fruit weight. The trait which has positively skewed distribution needs an intense selection from the available variability to uplift the genetic gain (Reddy *et al.*, 2023).

Plant height and number of primary branches per plant recorded positively skewed with negative platykurtic distribution. Number of fruit cluster per plant, number of fruits per plant, pericarp thickness and number of locules per fruit had negatively skewed distribution with negative platykurtic distribution suggesting duplicate dominant gene action and higher number of genes having decreasing effects. This type of distribution will help to protect the individual plant from deleterious alleles arising from existing variability. The results are in line with the results of Yogendra (2011).

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Conflict of interest

The authors have declared that no conflict of interest exists.

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