



Genetic Variability, Heritability and Genetic Advance Studies in Diverse Genotypes of Tomato (*Solanum lycopersicum* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. Author PD conceptualized and prepared the manuscript. Authors UT, PK and MG critically supplemented the manuscript. Authors SD and SY assisted in preparing the manuscript. All authors read the final version of the manuscript, provided necessary suggestions and approved it for publication. All authors read and approved the final manuscript.

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ABSTRACT

The present experiment was conducted utilizing sixteen diverse genotypes of tomato in the autumn-winter season of 2022-23 for assessing the genetic variability, heritability and genetic advance for different growth, reproductive and yield attributes. Analysis of variance revealed significant differences among all the genotypes for all the characters. High degree of genetic

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variability was observed for all the traits that showed the traits were suitable for selection for further breeding purposes. GCV was higher than PCV for all the characters under study. High PCV accompanied by high GCV was recorded for fruit yield per plant (kg) and fruit yield per plot (kg), number of clusters per plant, plant height (cm), number of primary branches per plant, number of fruits per plant, locule number, average fruit weight (g), number of flower per cluster, however the difference between the PCV and GCV was paltry, which indicating the high contribution of genetic component in phenotypic expression of these characters that provide higher selection efficiency. High heritability along with low genetic advance was observed for, days to first flowering, days to first fruit setting, days to 50% flowering, fruit equatorial diameter (mm), polar diameter (mm), locule number, number of fruits/plant and fruit yield / plant (kg), whereas low heritability with low genetic advance was revealed for pericarp thickness (mm) and no of primary branches/plant which suggests that these traits are highly influenced by the environmental effects and governed by the non-additive gene action, hence selection would not be effects for these particular traits. High heritability coupled with high genetic advance (GA) was recorded for average fruit weight (g) and plant height (cm) which indicates the presence of additive gene action; hence selection could be employed for these traits and provide the opportunity for higher selection response.

Keywords: Tomato; variability; heritability; GCV; PCV.

1. INTRODUCTION

“The tomato scientifically known as *Solanum lycopersicum* L. holds significant importance as a vegetable crop globally due to its versatility, high yield potential, and adaptability. It is cultivated worldwide and finds application in both fresh consumption and various processed food industries. In India, it is commonly referred to as the 'poor man's orange' while in England, it is known as the 'love of apple.' Cultivated tomatoes are said to have originated in Mexico while wild tomatoes are believed to possess originated in the Peru-Ecuador region” [1]. “As a source of minerals, vitamins, and phytochemicals, tomatoes play a significant role in the human diet. Tomato is a rich source of vitamins (A and C), minerals (Ca, P and Fe) and a strong antioxidant against cancer and heart diseases” (Dhaliwal et al., 2003; Anonymous, [2]. “It is considered ‘Protective food’ as it has some special nutritive value and antioxidant properties due to the presence of lycopene and flavonoids” [3]. “It is a good supplier of lycopene and ascorbic acid, antioxidants, and chemoprotective chemicals; therefore, it may be called functional food” [4]. “The country's like India tomato agricultural area is around 0.841 million hectares . The total yield amounts to 20.34 million metric tonnes, with an average national productivity of 24.36 metric tonnes per hectare” [2]. India ranks second in area (11,280 thousand hectares) and production (204613 MT) next to China, while its productivity (25.6 tons/ha) is quite lower many of the major producing countries. Tomato is widely cultivated in Madhya Pradesh (M.P) and is a popular vegetable crop in

the region. The tomato cultivation area spans 47.45 thousand hectares, resulting in a total production of 1121 metric tonnes. The average productivity of tomatoes in M.P is 24.90 tonnes per hectare. (Anonymous, [2] Any breeding effort must have genetic variability as a pre-requisite. Elite genotype selection is favored by high variability in yield, yield-attributing characteristics, and qualitative metrics. High heritability and high genetic gain as a percentage of mean, on the other hand, provide a clearer picture of the selection process since they highlight the role additive genes play in the manifestation of any characteristic.

2. MATERIALS AND METHODS

2.1 Genotypes Materials

Sixteen tomato genotypes were transplanted in the autumn-winter season 2022-23 at the CRC-1 Farm, ITM University, Gwalior, (MP) in Randomized block design (RBD) with three replications. The details of the plant materials used are given in Table 1. Sixteen yield and yield attributing traits parameters were recorded.

2.2 Measured Parameters

“The yield-attributing traits included plant height, number of primary branches/plant, days to first flowering, days to 50% flowering, days to first fruit setting, days to first fruit harvest, number of cluster/plant, number of flowers per cluster, number of fruit per plant, average fruit weight, polar diameter, equatorial diameter, pericarp thickness” [5].

Table 1. List of tomato genotypes used with their sources

S.No.	Genotypes	Source
01	Kashi Aman	IIVR,Varanasi
02	Kashi Adarsh	IIVR,Varanasi
03	Kashi Amul	IIVR,Varanasi
04	Kashi Amrit	IIVR,Varanasi
05	Kashi Anupam	IIVR,Varanasi
06	Kashi Vishesh	IIVR,Varanasi
07	Kashi Hemant	IIVR,Varanasi
08	Kashi Sharad	IIVR,Varanasi
09	Pusa Uphar	IIVR,Varanasi
10	Pusa Sadabhar	IIVR,Varanasi
11	Pusa Rohini	IIVR,Varanasi
12	Pusa Sheetal	IIVR,Varanasi
13	Pusa Gaurav	IIVR,Varanasi
14	Pusa Ruby	IIVR,Varanasi
15	Punjab Chuhara	IIVR,Varanasi
16	H-24	IIVR,Varanasi

2.3 Analysis of Variance

The analysis of variance for the design for the experiment (RBD) was carried out according to the procedure outlined by Panes and Sukhatme (1967). The genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV), we reestimated according to Burton and de Vane (1953) and on the other hand, the estimation of heritability was done according to Johnson et al. (1955) and predicted genetic advance as per the method suggested by Allard (1960).

3. RESULTS AND DISCUSSION

The data recorded on all quantitative characters were subjected to analysis of variance to test whether there was significant variation among the genotypes. Analysis of variance has been presented in Table-2 show that the mean squares due to genotypes were highly significant for all characters suggesting significant variability among the traits under study and hence ample scope for selection was present. The coefficient of genotypic and phenotypic variability is a valuable measure in assessing the level of variability in a specific trait. It is also a useful metric for comparing the degree of variability across different quantitative characteristics. The estimated coefficient of variability indicates that the magnitude of phenotypic coefficient of variation was greater than that of genotypic coefficient of variation for all traits. The genetic variability estimates for different traits are genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic

advance and genetic advance as percent of mean which have been depicted in Table-2. The estimates high genotypic and phenotypic variance were recorded for number of fruit yield (kg/plot), fruit yield (kg/plant), average fruit weight, plant height, locule number and number of cluster per plant, day to first flowering, number of primary branches per plant while moderate genotypic and phenotypic variance were recorded days to first fruit setting, number of fruit per plant and day to 50% flowering, number of flower per cluster, fruit equatorial diameter (mm), polar diameter (mm), day to first fruit harvest, pericarp thickness (mm). "The magnitude of the phenotypic coefficient of variation (PCV) for all characteristics was larger than the magnitude of the genotypic coefficient of variation (GCV)" [5,6] Kumar et al. (2016), Pandey et al. [7] and Maurya et al. [5] also reported "higher values of PCV compared to GCV". "The higher PCV values in comparison to the GCV values suggested that there was some influence of environment on all the traits under study as reported" previously by Darand Sharma (2011). In the selection process, heritability and genetic advance are considered important parameters. Evaluating genetic variation and estimating heritability provides valuable insights into the effectiveness of selection. When genotypic coefficients of variation indicate variation among genotypes for a particular trait, estimating heritability becomes crucial. Heritability represents the proportion of a trait's variability that can be attributed to genetic factors and passed on to offspring. According to Johnson et al. [8] heritability estimates are classified as low (less than 20%), moderate (20-30%), or high (greater than 50%). In this study

heritability was found to be high for all the traits examined, suggesting a significant contribution of additive gene action to the expression of these traits. The heritability were high for all traits viz. plant height (99.61%), number of primary branches/plant (72.28%), days to first flowering (95.25%), days to 50% flowering (98.30%), days to first fruit setting (98.35%), days to first fruit harvest (84.15%), number of flower cluster/plant (97.78%), number of flowers per cluster (83.78%), number of cluster per plant (97.78%), number of fruit per plant (88.69%), average fruit weight (98.64%), polar diameter (89.90%), equatorial diameter (95.10%), locule number (81.75%), pericarp thickness (74.38%), and fruit yield kg/plant (95.93%). The highest estimate of genetic advance was recorded for maximum genetic gain (%) plant height (52.93%) followed by average fruit weight (g) (51.64%), day to first fruit harvest (28.59%), fruit yield(kg/plot) (26.75%), moderate genetic advance was number of cluster per plant (23.35%), low genetic advance was fruit equatorial diameter (mm) (16.30%), polar diameter (mm) (15.53%), day to 50% flowering (14.47%), days to first fruit setting (14.15%), day to first flowering(13.51%), number of fruit per plant(8.93), number of flower per cluster (1.97), number of primary branches/plant (1.91), locule number(1.66%), fruit yield (kg/ plant) (1.63%), pericarp thickness (1.08%). High estimates of genetic advance in per cent of mean was estimated for number of fruit yield (kg/ plot) (81.14%), fruit yield (kg/ plant) (80.60%), average fruit weight (g) (65.74%), plant height (cm)

(62.97%), locule number (49.14%), number of cluster per plant (47.52%) and day to first flowering (40.96%). Moderate genetic advance was estimated for days to first fruit setting (37.35%), fruit equatorial diameter (mm) (31.53%), day to 50% flowering (35.31%), number of primary branches per plant (35.16%), number of fruit per plant (35.09%) number of flower per cluster and (32.12%) whereas polar diameter (mm) (28.81), day to first fruit harvest (27.21%), pericarp thickness (mm) (21.41%) showed low genetic advance in per cent of mean. Similar findings have been reported earlier by Kumar et al. (2008), Ara et al. [9] Agarwal et al. [10] and Bhandari et al. [11] "When the estimate of genetic advance accompanies heritability, then the prediction of genetic gain under selection is more accurate" by Johnson et al. [8]. The classification of genetic advance as per cent of mean has been given by Johnson et al. [8] as low, when less than 10%, moderate when 10-20% and high when greater than 20%. "When high heritability is accompanied with high genetic advance, it suggests preponderance of additive gene action and in such case selection would be effective. On the other hand, high heritability along with low genetic advance is resultant of non-additive gene action and the selection would be ineffective. Low heritability coupled with high genetic advance suggests additive gene effect in governance of the trait, but high interference of environment in expression of the trait and therefore selection in early generation would be

Table 2. Analysis of variance (mean squares) for sixteen characters in sixteen tomato genotypes

Source of Variation	Replication	Treatment	Error	Total
Degree of freedom	2	15	30	47
Days to first flowering (DAT)	0.90	137.71**	2.25	45.43
Days to first fruit setting (DAT)	0.56	144.66**	0.81	46.71
Days to 50% flowering (DAT)	1.27	151.49**	0.87	48.96
Days to first fruit harvest (DAT)	42.33	730.07**	43.13	262.33
Average fruit weight (g)	23.80	1919.65**	8.78	619.27
Fruit equatorial diameter (mm)	3.15	200.92**	3.39	66.42
Polar diameter (mm)	3.56	196.70**	7.10	67.46
Locule number	0.51	2.57**	0.18	0.95
Pericarp thickness (mm)	0.36	1.23**	0.13	0.49
Number of flower per cluster	1.38	3.48**	0.21	1.30
Number of cluster per plant	0.79	397.11**	2.98	128.67
Number of fruits per plant	12.29	66.31**	2.70	23.41
Number of primary branches/plant	0.81	4.03**	0.46	1.61
Plant height (cm)	14.69	1990.69**	2.57	637.59
Fruit yield (Kg/plant)	0.15	2.00**	0.03	0.66
Fruit yield (Kg/plot)	9.26	528.36**	5.77	172.70

Table 3. Estimates of range, grand mean, phenotypic, genotypic, environmental, coefficients of variation, heritability in broad sense (h^2_{bs}) and genetic advance in per cent of mean (\overline{GA}) for sixteen characters in tomato genotypes

Genotypes	Var(g)	Var(p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to first flowering (DAT)	45.15	47.40	95.25	13.51	40.96	20.38	20.88
Days to first fruit setting	47.95	48.76	98.35	14.15	37.35	18.28	18.44
Days to 50% flowering	50.21	51.08	98.30	14.47	35.31	17.29	17.44
Days to first fruit harvest	228.98	272.11	84.15	28.59	27.21	14.40	15.70
Average fruit weight (g)	636.96	645.74	98.64	51.64	65.74	32.13	32.35
Fruit equatorial diameter (mm)	65.84	69.24	95.10	16.30	31.53	15.70	16.09
Polar diameter (mm)	63.20	70.30	89.90	15.53	28.81	14.75	15.56
Locule number	0.80	0.97	81.75	1.66	49.14	26.38	29.18
Pericarp thickness (mm)	0.37	0.49	74.38	1.08	21.41	12.05	13.97
Number of flower per cluster	1.09	1.30	83.78	1.97	32.12	17.04	18.61
Number of cluster per plant	131.38	134.36	97.78	23.35	47.52	23.33	23.59
Number of fruits per plant	21.20	23.90	88.69	8.93	35.09	18.09	19.21
Number of primary branches/plant	1.19	1.65	72.28	1.91	35.16	20.08	23.61
Plant height (cm)	662.70	665.28	99.61	52.93	62.97	30.63	30.69
Fruit yield (Kg/plant)	0.66	0.68	95.93	1.63	80.60	39.95	40.79
Fruit yield (Kg/plot)	174.20	179.96	96.79	26.75	81.14	40.04	40.69

ineffective. However, selection in the later generations might be effective in such cases. If low heritability is observed along with low genetic advance, then the character is predisposed to environmental effects leading to ineffective selection". [5] Burton and DeVane [12] proposed that "genetic coefficients of variability, together with heritability estimates, may be used to predict the degree of improvement predicted by selection. High heritability accompanied with high genetic advance as percent of mean was recorded for fruit yield/plant and fruit yield (kg/plot)" (Table 2). In these traits Singh et al. (2018) also observed "high PCV and GCV with high heritability and genetic gain for number of fruits/plant, locule number and average fruit weight". "High heritability for fruit weight, number of locules/fruit and yield of fruit was previously observed" by Golani et al. [13] Rai et al. [14] noticed "high heritability with high genetic gain for number of fruits per plant, average fruit weight and fruit yield per plant" [15,16,17].

4. CONCLUSION

The present investigations revealed the existence of good variability among genotypes with respect to different traits considered. Furthermore, moderate to high GCV, high heritability, and moderate to high genetic advance as a percentage of mean were reported

for all the features under study. This implies that there is a strong preference for additive gene activity and plenty of possibility for selection-based enhancement of the pertinent traits.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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