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ESTIMATION OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND THEIR ATTRIBUTES TRAITS IN TOMATO (*SOLANUM LYCOPERSICUM* L.)

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ABSTRACT

Twenty tomato genotypes were studied under the Lucknow condition of Uttar Pradesh. This was carried out at the Horticulture Research Farm of the Department of Horticulture, Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh, during the *Rabi* season of the year 2021-2022. After the experimentation for various characters, the data were compiled and analysed according to the design of the experiment (randomized block design). The data was recorded for nineteen different characters to study genetic variability, heritability, correlation coefficient, and path analysis in tomato (*Solanum lycopersicum* L.) among 20 tomato genotypes. Highly significant differences for all the characters indicated the presence of a substantial amount of genetic variability. The highest genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were observed for plant height, followed by fruit weight and the number of fruits per plant, indicating that these characteristics could be used as selection for crop improvement. The variance components were used to calculate the heritability (BS) for each of the features in order to estimate the relative magnitudes of genotypic and phenotypic variability provided by environmental variables.

Key words: Variability, tomato, GCV, PCV, heritability and genetic advance.

Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most important warm-season vegetable crops grown throughout the world. India holds the second-leading position as a leading producer of tomatoes in the world. Tomatoes are commercially popular for various reasons, such as their high yielding potential, dietary value, adaptation to wide climatic conditions, and adaptability for a variety of uses in both fresh and preserved form. It belongs to the family Solanaceae and has chromosome number 2n = 24. It produces chasmogamous flowers where predominately self-pollination is seen. Tomatoes are native to Peru in South America, but a large number of wild tomatoes are seen in Mexico, where they were domesticated. Now, it is cultivated in all tropical, subtropical, and temperate regions of the world (CM Rick, 1969). It was introduced in India in 1828 by the famous Royal Agri-Horticultural Society of India, based in Kolkata. It was introduced in India by the English traders of the East India Company in 1822. Tomato is also known as Love Apple, Apple of Peru, Amorous Apple, Golden Apple, and Wolf Peach. It is mostly known as "protective food" due to its nutritive value and antioxidant molecules such as carotenoids, particularly lycopene, ascorbic acid, vitamin E, and phenol compounds, mainly flavonoids. It also contains minerals like iron, phosphorus, and potassium (Stommel *et al.,* 2007).

Tomato is cultivated in almost every country in the

world and in many of the nations; it stands second to potato in terms of importance. Madhya Pradesh, Karnataka, Uttar Pradesh, Andhra Pradesh, Maharashtra, Telangana, and Gujarat are the major tomato-growing states in India. Tomatoes are a self-pollinated, day-neutral crop. For optimal production, the crop needs a temperature of 20-24°C. For a higher yield, the variation between day and night temperatures should be 6-8°C. Lycopene production necessitates a temperature range of 21-24 °C. The results of the present investigation have been discussed and interpreted in light of previous research work done in India and abroad. The experiment was conducted in a completely randomized block design with 20 treatments and three replications.

Materials and Methods

The present experiment, entitled Lucknow Condition of Uttar Pradesh, was carried out at the Horticulture Research Farm of the Department of Horticulture, Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh, during the *Rabi* season of the year 2021-2022. Twenty tomato germplasm accessions were collected from different sources (Table 1). Crops were successfully grown with a spacing of 60×60 cm, and all conventional practices and plant protection measures were implemented on time. For every entry, observations were recorded on five competitive plants that were chosen at random for each replication. These observations included nineteen quantitative and qualitative traits, including plant height at 30, 60, and 90 days after transplanting (cm), days to first flowering (days), days to 50% flowering, days to maturity (days), number of flowers/cluster, number of clusters/plant, number of locules/fruit, pericarp thickness (mm), number of fruits/truss, number of fruits/plant, average single fruit weight (g), yield/plant (kg), fruit length (cm), fruit diameter (cm), total soluble solids (°Brix), and acidity (%). The data regarding the above-mentioned characters were averaged and subjected to analysis of variance.

Statistical Analysis

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated following the standard procedure proposed by Burton and DeVane (1953). The categories for genotypic (GCV) and phenotypic coefficients of variation (PCV) given by Subramanian and Menon (1973) as low (0-10%), moderate (10-20%), and high (20% and above) were also adopted in the present investigation. Heritability in a broad sense was determined using Allard's (1960) formula. The estimates of broad sense heritability (h^2b) were also classified into three categories, as suggested

by Robinson *et al*., (1949) Genetic advance was calculated using the formula suggested by Lush. Genetic advance as a percent mean was also classified into 3 categories, *viz*., low (0-10%), moderate (10-20%), and high (20%) and above, as suggested by Johnson *et al*., (1955).

Results and Discussion

Genetic variability

The mean performance of 20 genotypes for nineteen characters exhibited a wide range of variations, and the mean performances were observed for all the traits (Table 1). An analysis of variance was carried out on various yield and yield-contributing traits for studying the variation. Variance due to genotypes was highly significant for all the characters studied, indicating that the genotypes selected for the present study were genetically different. The estimation of these variances showed that genotypic variations contributed the most to the phenotypic variations for all the traits studied. The analysis of variance revealed significant mean square estimates for all the characters, indicating sufficient genetic differences among the genotypes. The variation in the genotypes would be helpful in the development of superior varieties in further breeding programs.

The phenotypic variance ranged from 4.56 to 46.35, and the lowest variance was recorded for days to maturity (days) and the maximum was recorded for acidity (%),

Table 1: List of tomato genotypes used in the study and their source.

S. No.	Name of Variety	Sources
1	Kashi Amrit	IIVR, Varanasi
2	Kashi Amul	IIVR, Varanasi
3	Kashi Aman	IIVR, Varanasi
4	Kashi Adarsh	IIVR, Varanasi
5	Kashi Anupam	IIVR, Varanasi
6	Kashi Sarad	IIVR, Varanasi
7	Pusa Rubey	IARI, New Delhi
8	Pusa Gaurav	IARI, New Delhi
9	Pusa Upkar	IARI, New Delhi
10	Kashi Sarad	IIVR, Varanasi
11	Kashi Vishesh	IIVR, Varanasi
12	Pusa Rohini	IARI, New Delhi
13	Pusa Sheetal	IARI, New Delhi
14	Pusa Sadabahar	IARI, New Delhi
15	Punjab Chhuhara	PAU, Ludhiana
16	Many Makar	IIVR, Varanasi
17	Kashi Hemant	IIVR, Varanasi
18	Pusa Divya	IARI, New Delhi
19	EC-538407	IIVR, Varanasi
20	Himsona	Syngenta

Table 2: Estimates of mean, range, coefficients of variability, heritability and genetic advance.

Characters	Grand mean (x) ± SE	Range	Coefficients of variability		Heritability % in Broad Sense	Genetic advance	GA in % of mean
			PCV	GCV			
Plant height at 30 DAT (cm)	27.79±0.93	23.67-31.92	8.15	7.44	83	3.88	13.98
Plant height at 60 DAT (cm)	60.58±1.77	52.42-67.17	6.76	6.09	81	6.85	11.31
Plant height at 90 DAT (cm)	108.68±1.98	101-126.08	5.73	5.43	89	11.54	10.62
Number of primary branches	16.45±1.03	10.25-26.33	25.07	24.27	93	7.96	48.41
Days to first flowering (days)	45.97±1.37	41.33-52.17	7.25	6.6	83	5.7	12.4
Days to 50% flowering (days)	51.42±1.43	47.17-55.50	5.09	4.27	70	3.79	7.37
Number of flowers/clusters	10.71±0.96	6.00-16.83	29.34	24.92	90	5.86	54.75
Number of trusses per plant	16.92±0.65	9.50-24.17	28.54	28.28	98	9.77	57.74
Number of fruits per truss	6.35±0.45	3.67-9.25	27.18	26.23	93	3.31	52.16
Days to maturity (days)	103.09±1.11	101.5-105.5	4.56	2.25	50	0.12	0.12
Average single fruit weight (g)	51.35±1.70	29.67-80.75	29.25	29.07	98	30.55	59.5
Number of fruits per plant	84.69±8.77	29.67-159.1	45.81	44.63	94	75.85	89.56
Fruit length (cm)	5.48±0.22	3.42-7.03	20.79	20.4	96	2.25	41.23
Fruit diameter (cm)	4.47±0.07	3.63-6.23	16.56	16.48	99	1.51	33.81
Number of locules per fruit	4.83±0.16	2.50-8.00	33.36	33.19	99	3.28	68.03
Pericarp thickness (mm)	5.37±0.13	3.25-7.42	25.37	25.25	99	2.78	51.79
TSS(°Brix)	4.69±0.06	3.33-6.42	23.15	23.12	99	2.7	47.58
Acidity (%)	0.41±0.01	0.18-0.86	46.35	46.26	99	0.39	95.12
Yield / plant (kg)	4.29±0.51	1.25-8.01	45.93	44.35	93	3.78	88.21

followed by yield per plant (kg) and number of fruits per plant. The genotypic coefficient of variance (GCV) ranged from 2.25 to 46.26. High GCV was observed for acidity (%) followed by number of fruits per plant and yield per plant (kg), whereas the lowest GCV was recorded in days to maturity. The investigation revealed that the phenotypic variation was high as compared to the genotypic variation for all the traits studied, indicating the influence of environment, and it was found to be highest for fruit yield per plant, average fruit weight, and plant height. These results are in agreement with the observations of Maurya *et al.*, (2020) and Lekshmi (2017).

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were found to be higher for acidity (%), yield per plant (kg), and number of fruits per plant, which suggested a prevalence of greater phenotypic and genotypic variability among the accessions. The wide difference between GCV and PCV in terms of number of branches per plant and days to 50 percent flowering implied its susceptibility to environmental fluctuation. In the present study, the highest estimates of GCV and PCV were recorded for fruit yield per plant.

Heritability and genetic advance

Genetic variability may be due to additive, dominant, or epistatic gene action. In the present study, the broad sense heritability estimates were high for all the traits of interest, and they ranged from 50 to 99. High heritability was recorded for all the traits, and the maximum heritability was recorded in fruit diameter (cm), number of locules per fruit, pericarp thickness (mm), TSS (°Brix), acidity (%), number of trusses per plant, average single fruit weight (g), fruit length (cm), number of fruits per plant, number of fruits per truss, yield per plant (kg), number of primary branches, number of flowers/cluster, Plant height at 90 DAT (cm), plant height at 30 DAT (cm), plant height at 60 DAT (cm), days to 50% flowering (days), respectively, whereas lower heritability was recorded for days to maturity (Table 2). Such high values of heritability for plant height, number of branches per plant, average fruit weight, number of fruits per plant, and number of fruits per cluster imply that it may be due to environmental influence, and selection based on phenotypic performance would be reliable. In traits with high heritability, genotypic variance is greater than environmental variance, and these characters could be considered and exploited for selection in earlier generations. Whereas, in traits with low heritability, the influence of environmental factors is strong for their expression, and genotype selection based on these characters may be postponed to later generations.

A high genetic advance was observed for acidity (%), number of fruits per plant, yield per plant (kg), number of

locules per fruit, Average single fruit weight (g), number of trusses per plant, number of flowers per cluster, number of fruits per truss, Pericarp thickness (mm), number of primary branches, TSS (°Brix), fruit length (cm). These results are in close conformity with those of Mohamed *et al*., (2012) and Mishra *et al*., (2018). Naveen (2017) and Kumar (2019) also reported high heritability and genetic advance as per cent of mean (GAM) for plant height, number of branches per plant, average fruit weight, number of locules per fruit, number of fruits per plant, and fruit yield per plant, indicating the predominance of additive gene action for these characters. These traits may be controlled by additive gene action. High heritability with low genetic advance was reported for plant height, days to 50% flowering, number of branches per plant, and number of fruits per plant, which implies that it is controlled by non-additive gene action.

Conclusion

This study's findings can inform future tomato breeding efforts. Plant height, number of branches, average fruit weight, number of locules per fruit, number of fruits per plant, and fruit yield all show strong heritability (>75%) and genetic improvements. Traits with high heritability and genetic advancement are primarily influenced by additive gene action, allowing for further selection-based development.

Acknowledgments

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