VARIABILITY STUDIES IN DIVERSE GENOTYPE OF TOMATO (*Solanum lycopersicum* L.) UNDER VARANASI CONDITIONS

ABSTRACT

The Current Study Assessed About 14 Tomato Genotypes For 15 Yield-Contributing Features At The Vegetable Farm Of The Department Of Horticulture, Institute Of Agricultural Sciences, BHU, Varanasi, During The Rabi Season Of 2019–2020. With Three Replications, The Experiment Was Set Up Using A Randomized Block Design. The Variance Analysis Of The Tomato Genotypes Revealed That There Were Substantial Differences Among All The Genotypes Considered. All Characteristics Had Very High Heritability Values, According To The Heritability Research. High Genetic Gain Was Also Seen For Traits Including Plant Height, Average Fruit Weight, Fruit Production Per Plant, And Fruit Output Per Hectare. All The Traits Evaluated Showed High Genetic Increase, Apart From Days To 50% Blooming. Apart From Few Characteristics, Such As Days To 50% Blooming And Quantity Of Fruits Per Plant, Which Had Low And Medium Values, Most Of The Characters Showed High PCV And GCV.

Keywords: [Tomato, yield, production, genetic variability, heritability, genetic gain]

1. INTRODUCTION

The *Solanum lycopersicum* L., commonly known as tomato, is a significant member of the Solanaceae family, also known as the Nightshade family. It is an important vegetable crop on consumption and production basis and holds a position second to potato in its importance. Tomatoes are a rich source of various health-promoting compounds and can be conveniently incorporated into a well-balanced diet [1]. Tomatoes are a widely consumed fruit that are not only consumed fresh, but also utilized in various processed products such as soups, juices, and sauces [2,3]. In recent years, there has been a growing recognition among consumers regarding the potential health benefits of various foods, and their ability to prevent the onset of chronic diseases and dysfunctions [4]. This trend has been observed over the past decade and has led to an increased interest in the role of food as a means of promoting overall health and well-being. The nutritional significance of tomatoes can be attributed to their diverse range of health-promoting compounds, such as vitamins, carotenoids, and phenolic compounds. This has been extensively documented in various studies [3, 5, 6]. Bioactive compounds exhibit a diverse array of physiological properties such as anti-inflammatory, anti-allergenic, antimicrobial, vasodilatory, antithrombotic, cardio-protective, and antioxidant effects [5]. The consumption of tomatoes is known to provide a significant number of carotenoids, particularly lycopene, to the human diet [7]. Tomatoes are a significant source of carotenoids and polyphenolic compounds, which are known to enhance their nutritional value and functional properties, as well as sensory attributes such as taste, aroma, and texture. The presence of antioxidants in tomatoes, specifically Vitamins C and E, has been reported in previous studies [8, 9]. Additionally, tomatoes contain significant quantities of various metabolites, including sucrose, hexoses, citrate, malate, and ascorbic acid [3].

The development of superior varieties/hybrids for various ago-ecological conditions with specific end use is imperative. The success and pace of conventional breeding is largely dependent on the presence of the desired genetic variability for the target traits [10]. The utilization of genetic resources is crucial in the development of new plant gene combinations and the selection of crop varieties that are better suited to the varying requirements of agricultural systems [11]. The significance of genetic variability was initially recognized by Russian scientist, who argued that a broad spectrum of variability offers greater potential for identifying a desirable genotype [12]. The efficacy of selection is contingent upon several factors, including the type and magnitude of genetic variation present, the degree to which desirable traits are heritable, and the anticipated genetic advancement for a given trait within a given population [13]. The assessment of variability and heritability in the gene pool of a crop species is a crucial step for a plant breeder to initiate an effective plant breeding program. This insight provides valuable information regarding the magnitude and extent of desirable traits present in the gene pool. Therefore, it is imperative for a plant breeder to conduct a thorough analysis of these factors before commencing a plant breeding program. The present study aimed to investigate the genetic variability, heritability, and genetic gain of various horticultural traits among different genotypes of tomato in Varanasi region.

2. MATERIAL AND METHODS

The experiment was conducted at Vegetable Research Farm of the Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during the Rabi season of 2019-2020. The latitude and longitude of the experimental site is 25°18’ N and 83°03’ E and is located at 129.23 m above mean sea level (MSL). The experimental site lies in the fertile Indo-Gangetic plain and is endowed with characteristic alluvial soil. This soil is well-drained and has low nitrogen coupled with medium levels of potassium and phosphorus and is therefore considered to be moderately fertile. The pH of the soil is neutral (7.2) to slightly alkaline (8.4) in nature. Randomized block design (RBD) was used as an experimental design with 14 treatments and three replications. The genotypes evaluated in this study were CTS-04-01, KS-229, VR-20, VTG-88, ATL-02-03, KS-227, DVRT-2, CO-3, Pant-T-7, Pant-T-8, VRFTS-5, DT-2, VRFTS-2, and CTS-05-03. The spacing was maintained at 60cm X 60 cm in a plot of 3m X 3m size. Standard cultural practices were adopted involving repeated ploughing to obtain good tilth of soil followed by adequate fertilization and irrigation in adequate quantities at the right time. The observations on various characters were recorded on five randomly selected plants in each treatment/genotype of replication and average was taken for the Plant height (cm), No. of primary branches per plant, Days to 50% flowering, No. of fruits per plant, No. of fruits per plant, Fruit length (cm), Fruit width (cm), Pericarp thickness (cm), Total soluble solids (ºBrix), No. of locules per fruit, Average fruit weight (g), Vegetative biomass (kg), Fruit biomass (kg), Total plant biomass (kg), Fruit yield per plant (g) and Fruit yield per hectare (q/ha). The study utilized specific methods for statistical analysis of the mean data [14] and calculation of heritability, genetic advance, and genetic gain [15, 16]. Heritability in general terms and genetic improvement as a proportion of recommendations were calculated by formulations provided by reference [36, 37]. Statistical analysis was carried out using the SAS program [39].

3. RESULTS AND DISCUSSION

The present study evaluated several genotypes for their yield potential per hectare. The results indicate that VR-20 exhibited the highest yield among the tested genotypes, with a value of 595.11 q/ha. DVRT-2 and Pant-T-7 followed with yields of 539.27 q/ha and 530.35 q/ha, respectively. CTS-04-01 exhibited the lowest yield per hectare, with a value of 225.31 q/ha followed by DT-2 demonstrated a higher yield of 347.58 q/ha (Table 2). The present study investigated the trend of vegetative biomass in relation to yield. The results indicate that vegetative biomass exhibited a similar trend to that of yield. The study revealed that the highest degree of variation was observed in fruit yield per plant, ranging from 834.48 to 2204.11g. This was followed by fruit yield per hectare, which ranged from 225.31 to 595.11 q/ha. Plant height also exhibited significant variation, ranging from 45.26 to 118.07 cm. Lastly, the average fruit weight displayed a range of 31.60 to 91.86 g (Table 2). The characters which exhibited high variation are considered suitable by breeders as it provides sufficient variability that can be utilized in a breeding program. Similar results were reported by Manna and Paul [17], Kumar et al. [18], Patel et al. [19], Chadha and Bhusan [20], Sidhva et al [21], Khapte and Jansirani [22].

The present study aimed to determine the genotypic coefficient of variation (GCV) for various morphological and yield-related traits in a population of plants. The results revealed that several traits exhibited a high GCV, indicating significant genetic variability among the individuals (Table 3). Specifically, the number of branches per plant (21.81), plant height (27.28), fruit length (34.96), fruit width (30.59), pericarp thickness (21.93), number of locules per fruit (21.66), average fruit weight (22.39), total soluble solids (30.51), vegetative biomass (23.88), fruit biomass (23.63), total biomass (21.14) and fruit yield (20.25) were found to have a high GCV. These findings suggest that these traits may be under strong genetic control and could be targeted for improvement through selective breeding or other genetic manipulation techniques. Further research is needed to explore the underlying genetic mechanisms responsible for the observed variability and to develop strategies for enhancing these traits in the population. The genotypic coefficient of variation (GCV) for two important traits, namely number of fruits per plant and days to 50% flowering (Table 3). The GCV values were estimated to be 13.03 and 7.07 for number of fruits per plant and days to 50% flowering, respectively. The observed GCV for number of fruits per plant indicates moderate genetic variability among the studied genotypes, while the low GCV for days to 50% flowering suggests limited genetic variability for this trait. These findings provide valuable insights into the genetic potential of the studied genotypes for these traits, which can be utilized in future breeding programs aimed at improving crop productivity and yield. Similar trends are observed in Singh [23], Sharma et al. [24], Ghosh et al. [25] and Singh et al. [26].

The phenotypic coefficient of variation (PCV) in various plant traits of interest. The results indicated that PCV was high in several characters, including the number of branches per plant (7.88), plant height (27.33), fruit length (35.45), fruit width (31.90), pericarp thickness (22.05), number of locules per fruit (21.73), average fruit weight (22.48), total soluble solids (31.42), vegetative biomass (24.24), fruit biomass (23.66), total biomass (21.21), fruit yield per plant (20.77), and fruit yield per hectare (20.77). These findings suggest that these traits are highly variable and may be influenced by both genetic and environmental factors. The results revealed that the PCV for the number of fruits per plant was moderate (13.49), indicating a considerable degree of variation in this trait among the individuals. On the other hand, the PCV for days to 50% flowering was found to be low (7.88), suggesting a relatively low level of variation in this trait. The higher value of PCV as compared to GCV indicates that the expression of characters is influenced by environmental factors, however the narrow difference between PCV and GCV indicated that they were relatively stable in regard to environmental variation.

The heritability values of various traits were determined in this study. The results showed that the heritability value for days to 50% flowering was 80.35%, while the heritability value for plant height was approximately 99.60%. These findings suggest that plant height is highly heritable, while days to 50% flowering is moderately heritable (Table 3). The results indicate that all characters exhibited high heritability, suggesting that they are minimally influenced by environmental factors. These findings suggest that selection based on phenotype may be a reliable method for this population. The present study reports the genetic advance as a percentage of mean for various traits in the studied population. The values obtained for this parameter ranged from 13.05% for days to 50% flowering to 71.01% for fruit length, indicating a medium to high degree of genetic variability in the population. The genetic gain for plant height, average fruit weight, and fruit yield were 56.09%, 45.92%, and 40.68%, respectively. The results of the study indicate that there were low estimates of genetic advance observed for all the remaining characters. High values of heritability, GCV and genetic gain indicate additive gene effects and thus characters showing them provide ample scope for efficient selection and reproduce greater selection values [29]. The results are in line with Chadha and Bhusan [20], Sidhva et al. [21], Khapte and Jansirani [22], Kumar et al. [27] and Prajapati et al. [28].

High heritability coupled with high GCV, and genetic gain was observed for plant height, average fruit weight and fruit yield. This might be due to additive gene action conditioning and in such cases, amelioration can be done by simple methods. High heritability, high genetic advance along with high GCV and PCV were reported for characters such as fruit weight and plant height [17, 29, 30, 31]. Average fruit weight in tomato noted high heritability with high GCV and genetic gain [18]. If additive gene action is responsible for heritability, then high genetic gain would occur, or low genetic gain will occur due to non-additive gene action. Similar observations on tomatoes were also reported by other researchers in their respective studies [32, 33, 34, 35].

Table 1. Analysis of Variance for 15 characters of 14 genotypes of tomato

Character/ Source	Do	Plant height (cm)	No. of primary branches per plant	Days to 50% flowering	No. of fruits per plant	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	Total soluble solids (ºBrix)	No. of locules per fruit	Average fruit weight (g)	Vegetative biomass (kg)	Fruit biomass (kg)	Total plant biomass (kg)	Fruit yield per plant (g)	Fruit yield per hectare (q/ha)
Replication	2	3.51	0.03	3.59	1.42	0.02	0.01	0.00	0.03	0.00	0.67	0.00	0.00	0.00	8271.15	602.96
Treatment	13	1352.71**	4.76**	22.52**	41.76**	6.88**	5.03**	0.03**	4.80**	1.32**	538.43**	0.09**	0.58**	0.90**	351516.24**	25625.53**
Error	26	1.80	0.09	1.69	0.99	0.06	0.14	0.00	0.09	0.00	1.56	0.00	0.00	0.00	5999.51	437.36

Table 2. Mean performance for 15 characters of 14 genotypes of tomato

S. No.	Varieties	Plant height (cm)	Number of primary branches per plant	Days to 50% flowering	Number of fruits per plant	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	Total soluble solids (ºBrix)	Number of locules per fruit	Average fruit weight (g)	Vegetative biomass (kg)	Fruit biomass (kg)	Total plant biomass (kg)	Fruit yield per plant (g)	Fruit yield per hectare (q/ha)
1	CTS-04-01	118.07	4.46	37.33	26.40	3.46	5.01	0.44	4.46	2.48	31.60	0.59	0.94	1.54	834.48	225.31
2	KS-229	45.26	5.53	34.00	21.53	3.77	3.33	0.52	5.26	2.94	66.20	0.80	1.77	2.58	1425.38	384.85
3	VR-20	64.19	7.46	36.33	29.53	3.83	3.39	0.65	1.53	3.82	74.66	0.68	2.41	3.09	2204.11	595.11
4	VTG-88	68.36	3.46	37.00	28.86	1.92	2.02	0.39	4.60	2.91	53.60	0.98	1.94	2.93	1547.02	417.69
5	ATL-02-	87.30	6.33	33.00	30.20	2.73	3.45	0.41	3.46	2.42	61.40	0.75	2.37	3.13	1855.1	500.87

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6	KS-227	77.75	7.26	34.00	32.36	3.94	5.77	0.49	5.53	2.61	58.46	0.61	1.98	2.59	1892.19	510.89
7	DVRT-2	51.62	6.60	36.66	21.73	5.82	4.32	0.55	2.53	3.57	91.86	1.09	2.19	3.28	1997.30	539.27
8	C0-3	87.96	6.60	41.00	29.33	3.98	3.39	0.59	3.20	4.13	54.40	0.51	1.53	2.04	1596.71	431.11
9	PANT-T-7	96.02	5.50	34.66	35.46	3.89	3.00	0.45	4.46	2.47	55.36	0.84	2.36	3.20	1964.28	530.35
10	PANT-T-8	50.65	4.46	37.66	27.33	5.89	3.62	0.55	5.33	4.25	61.60	0.89	1.99	2.88	1683.19	454.46
11	VRFTS-5	75.69	5.53	39.00	29.40	6.87	4.87	0.75	2.46	2.25	54.73	0.56	1.66	2.23	1610.18	434.75
12	DT-2	72..09	4.26	40.66	25.46	7.02	3.84	0.50	4.53	3.24	50.53	0.65	1.13	1.78	1287.36	347.58
13	VRFTS-2	106.68	5.26	38.66	28.20	4.03	6.89	0.35	5.53	2.52	65.40	0.80	2.01	2.81	1844.70	498.06
14	CTS-05-03	87.14	7.34	41.66	30.26	3.20	5.51	0.39	4.53	3.29	56.63	0.53	1.74	2.27	1713.72	462.70
	Grand Mean	**77.77**	**5.72**	**37.2**	**28.29**	**4.31**	**4.17**	**0.50**	**4.10**	**3.06**	**59.74**	**0.73**	**1.86**	**2.59**	**1675.41**	**452.36**
	SEM±	**0.77**	**0.17**	**0.75**	**0.57**	**0.14**	**0.21**	**0.006**	**0.17**	**0.03**	**0.72**	**0.01**	**0.01**	**0.02**	**44.71**	**12.07**
	C.D. 5%	**2.25**	**0.51**	**2.18**	**1.67**	**0.42**	**0.63**	**0.01**	**0.51**	**0.08**	**2.09**	**0.05**	**0.03**	**0.07**	**129.99**	**35.09**
	C.D. 1%	**3.04**	**0.69**	**2.95**	**2.25**	**0.57**	**0.85**	**0.02**	**0.70**	**0.11**	**2.83**	**0.06**	**0.04**	**0.10**	**175.73**	**47.44**

Table 3. Range, grand mean, phenotypic and genotypic coefficient of variation (PCV and GCV), heritability (h^2), genetic advance (GA) and genetic advance as per cent of mean for 15 characters of 14 genotypes of tomato.

Character	Range	Grand mean	PCV	GCV	Heritability (%)	Genetic advance	GA as % of mean (%)
Plant height (cm)	45.26-118.07	77.77	27.33	27.28	99.60	43.62	56.09
Number of primary branches per plant	3.46-7.46	5.72	22.46	21.81	94.27	2.49	43.63
Days to 50% flowering	33-41.66	37.26	7.88	7.07	80.35	4.86	13.05
Number of fruits per plant	21.53-35.46	28.29	13.49	13.03	93.20	7.33	25.91
Fruit length (cm)	1.92-7.02	4.31	35.45	34.96	97.24	3.06	71.01
Fruit width (cm)	2.02-6.89	4.17	31.90	30.59	91.96	2.52	60.44
Pericarp thickness (cm)	0.35-0.75	0.50	22.05	21.93	98.90	0.22	44.94
Total soluble solids (ºBrix)	1.53-5.53	4.10	31.42	30.51	94.25	2.50	61.01
Number of locules per fruit	2.25-4.25	3.06	21.73	21.66	99.39	1.36	44.49
Average fruit weight (g)	31.60-91.86	59.74	22.48	22.39	95.14	27.43	45.92
Vegetative biomass (kg)	0.51-1.09	0.73	24.24	23.88	94.03	0.35	48.45
Fruit biomass(kg)	0.94-2.41	1.86	23.66	23.63	93.79	0.90	48.63
Total plant biomass (kg)	1.54-3.28	2.59	21.21	21.14	96.35	1.12	43.41
Fruit yield per plant (g)	834.48-2204.11	1675.41	20.77	20.25	95.05	681.57	40.68
Fruit yield per hectare (q/ha)	225.31-595.11	452.36	20.77	20.25	95.05	184.02	40.68

4. CONCLUSION

The results of the study suggest that both CTS-04-01 and VR-20 genotypes exhibit promising potential for high fruit yield. The outcomes of the GCV (genotypic coefficient of variation) and PCV (phenotypic coefficient of variation) analyses have provided clear indications that all the characters, with the exception of days to 50% flowering and number of fruits per plant, which exhibited low and medium values, respectively, are viable options for inclusion in yield enhancement programs. The heritability of various characters in a population revealed that all characters exhibited high heritability, suggesting that the phenotypic expression of these characters can be relied upon for breeding programs.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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