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Assessment of Genetic variability, Heritability and Genetic Advance among the various Genotypes of Tomato (*Solanum lycopersicum* L.) under Northern Hilly Region of Kashmir

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ABSTRACT: A field experiment was carried out, in which twenty seven genotypes were evaluated to estimate the genetic variability, heritability and genetic advance for the various traits. The experiment was laid out in a Randomized Block Design (RBD) with three replications. The highest phenotypic and genotypic coefficients of variability were observed for number of primary branches plant^{-1} followed by fruit yield (q/ha), seed weight fruit^{-1} (mg), titrable acidity (%) and juice to pulp ratio. High heritability (bs) was shown by all the traits with maximum genetic advance (percent of mean) for number of primary branches plant^{-1} followed by fruit yield (q/ha), titrable acidity (%), juice to pulp ratio, seed weight fruit^{-1} (mg), plant height (cm), total soluble solids (%), days to first flowering, 1000 seed weight (g), average fruit weight (g). The characters which have exhibited high heritability coupled with genetic advance may be selected for the future breeding programme, because they were governed by additive gene action.

Keywords: Phenotypic and genotypic coefficient of variability, Genetic advance, Heritability, Tomato.

INTRODUCTION

Tomato is the most important vegetable crops grown in entire world. Tomato is an important member of the family solanaceae. The probable ancestor of tomato is *Solanum lycopersicum* var. *cerasiforme* Bailey. It is originated in wild form with in the Peru Equador region of Andes (South America) and it is cultivated in almost every corner of the planet (Robertson and Labate 2007). Tomato is a self pollinated crop, but cross-pollination also occurs upto some extent. It is a warm season vegetable crop reasonably tolerant to heat and drought. It is an important source of like sauce, ketchup, puree and paste could be made from it.

The area and production of tomato has been increasing constantly over the years. India shown second position in area and production of tomato after china. In India major tomato producing states are Madhya Pradesh, Karnataka, Andhra Pradesh, Tamil Nadu and Gujarat. During 2019-20, India produced 20.51 million metric tonnes of tomato in an area of about 0.81 million hectares Average productivity of the crop is 16.1 metric tonnes (NHB, 2nd Advance estimates, 2019-20).

The success of breeding programme depends on the amount of variability present in the germplasm. The variability can be partitioned into heritable and non-heritable component *viz.*, phenotypic and genotypic coefficients of variation, heritability and genetic advance on which selection can be effectively worked out. Heritability defines the proportion of genotypic variance to the phenotypic variance. So, the breeders can select best variety for a particular trait. High heritability coupled with maximum genetic advance could provide efficient selection criteria in segregating generations (Johnson *et al*., 1955). Genetic advance denotes the improvement in the mean genotypic values of selected families over base population and thus helps the plant breeder to select the progenies or offspring's in the earlier generation itself.

MATERIALS AND METHODS

The present experiment was conducted at Vegetable Experimental Farm of Division of Vegetable Science, SKUAST-K, Shalimar during summer 2018. The experimental plot is located at 34° N of latitude and 74.89° E of longitude. The climate is mostly temperate and characterized by mild summers. The high rainfall is received in the months March and April. Randomized Block Design (RBD) is followed and the genotypes were replicated thrice. The details of genotypes along with their source are presented in Table 1. The experimental plot consists of 27 treatments in each replication, such that there are 81 treatments (genotypes) in total. The spacing followed for the row to row and plant to plant is 60 × 35 cm. Standard cultural and plant protection practices were followed to attain a healthy crop. The magnitude of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) existing in a trait was worked out by the formula given by Burton (1952). Genotypic variance and phenotypic variances are calculated using the method suggested by Johnson *et al.* (1955): Heritability (broad sense) is estimated as per the procedure developed by Johnson *et al.* (1955); Hanson *et al.* (1956). Genetic advance at 5% selection intensity was calculated by using the formula given by Lush (1949).

Quality characters

Total soluble solids (%). The total soluble solids (TSS) contents of the fruits were measured with the help of hand refractometer. Red ripen Tomato fruits are used for the collection of juice. A small drop of juice was placed over the prism of digital refractometer and was recorded in percentage.

Titrable acidity(%). Acid content of the extracted juice was determined by titrating 5 ml of juice against N/10 NaOH using Phenolphthalein as an indicator. Acidity was expressed in term of anhydrous citric acid (A.O.A.C.1960) per 100 ml of tomato juice.

Juice to pulp ratio. A composite sample of 500g of fruit was taken from the randomly selected plants from each replication and crushed thoroughly in an electrically operated juice extractor. The extract was filtered through dry muslin cloth and the filtrate was collected in the weighed beaker. The weight of juice along with the beaker was recorded and juice content was calculated as

Juice content = (juice + beaker) weight-beaker weight

Pulp content was calculated as

Pulp content = fruit weight-juice weight

Juice to pulp ratio was calculated as

Juice to pulp ratio = juice content/pulp content.

RESULTS AND DISCUSSION

A. Genetic variability

The mean performance of 27 genotypes for eleven characters exhibited a wide range of variations and the mean performances were observed for all the traits (Table 3). Analysis of variance was carried on various yield and yield contributing traits for studying the variation. Variance due to genotypes were 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 maximum to the phenotypic variations for all the traits studied (Table 3). The analysis of variance revealed significant mean square estimates for all the characters indicating sufficient genetic difference among the genotypes. The variation in the genotypes would be helpful in the development of superior varieties in further breeding programme.

The plant height ranged from 47.66 cm to 90.90 cm comprising mean value was 72.95 cm. The number of primary branches in different genotypes ranged from 1.83 to 7.50 with average value was 4.94. The highest and lowest values for the trait days to first flowering are18.23 days and 27.93 days comprising the mean value of 22.23 days. Days to fruit set ranged from 26.86 days to 35.26 days with the mean value of 31.11. The range of average fruit weight varies from 50.33 g to 72.66 g with the grand mean value of 61.01 g. From the Table 2 it is observed that the range of 1000 seed weight varies between 2.43 g to 3.76 g. The general mean was obtained as 3.00 g. The variation for the seed weight fruit^{-1} is ranged from 1.10 mg to 2.33 mg with the mean value of 1.56 mg. fruit yield (q/ha) ranged from 124.66 q to 362.66 q with the general mean of 211.86 q. Total soluble solid (%) ranged from 3.20 % to 6.23 % with the mean value of 4.46%. The highest and lowest titrable acidity was observed between 0.46 % and 0.16 %. The general mean for this trait was 0.28 %. The highest and lowest values for the trait juice to pulp ratio was recorded as 0.71 and 0.27. The general mean for this trait was 0.50.

The coefficient of genotypic and phenotypic variability is helpful to measure the extent of genetic variability present in particular trait. The highest genotypic as well as phenotypic coefficient of variability values are observed for number of primary branches plant^{-1} (32.19 %) followed by fruit yield (q/ha) (27.86 %), titrable acidity (23.38 %), seed weight fruit^{-1}(23.37 %), juice to pulp ratio (22.62 %) whereas 1000 seed weight (15.06 %), total soluble solids (14.65 %), plant height (14.59 %), days to first flowering (13.90 %) average fruit weight (10.01 %) were shown moderate coefficient of variability while days to fruit set (7.04 %) had shown the lowest coefficients of variation (Table 3a). The investigation revealed that the phenotypic variation was high as compared to genotypic variation for all the traits studied indicating the influence of environment and it was found maximum for number of primary branches per plant, fruit yield (q/ha). It was also found that yield contributing traits recorded higher phenotypic co-efficient of variation when compared to genotypic co-efficient of variation indicating considerable environmental influences whereas less influence on quality traits. Results obtained in present investigation are in agree with the findings of Dar and Sharma (2011); Venkadeswaran *et al.* (2020).

B. Heritability and Genetic advance

Genetic variability could be due to additive, dominance and epistatic gene action. In the present study, the broad sense heritability estimates were high for all the traits of interest and it ranged from 81.00 to 99.70. Estimates of heritability in broad sense (h^2_{bs}) for eleven traits are shown in Table 3b. High heritability was recorded for all the traits and the maximum heritability was recorded for fruit yield (q/ha) followed by plant height, days to first flowering, juice to pulp ratio, days to fruit set, average fruit weight, total soluble solids, titrable acidity, number of primary branches per plant, seed weight per fruit and 1000 seed weight respectively. Such high values of heritability implies that it may be due to environment influence and selection based on phenotypic performance would be reliable. In traits with high heritability, genotypic variance is more than environmental variance and these characters could be considered and exploited for selection in earlier generations. Whereas, in the traits with low heritability, influence of environmental factors is strong for their expression and genotype selection based on these characters may be postponed to the later generations.

The results are in agreement with the findings of Mohammad *et al.* (2012).

Highest genetic advance as per cent of mean was recorded for number of primary branches per plant (62.47) followed by fruit yield (q/ha) (57.30), titrable acidity (46.33), juice to pulp ratio (46.00), seed weight fruit^{-1} (44.82), plant height (29.76), total soluble solids (29.28), days to first flowering (28.34), 1000 seed weight (27.93), average fruit weight (21.25), while days to fruit set (14.30) shown moderate genetic advance in per cent of mean. The presence of high heritability in broad sense along with high genetic advance in percent of mean are recorded for fruit yield (q/ha), juice to pulp ratio and number of primary branches plant-1, indicating that these traits maybe controlled by additive gene action. High heritability with low genetic advance was reported for average fruit weight and days to fruit set which implies that it is controlled by non-additive gene action. Results obtained in present investigation are in agreement with the findings of Mehta and Asati (2008); Mohamed *et al.* (2012); Ahirwar *et al.* (2013); Arup *et al.* (2014).

Table 1: List of genotypes of tomato (*Solanum lycopersicum* L.).

Sr. No.	Genotype/variety	Source
1.	Kashi Hemanth	IIVR (Varanasi)
2.	Kashi Amrit	IIVR (Varanasi)
3.	Kashi Sharad	IIVR (Varanasi)
4.	Kashi Vishesh	IIVR (Varanasi)
5.	Kashi Chayan	IIVR (Varanasi)
6.	Kashi Aman	IIVR (Varanasi)
7.	Kashi Anupam	IIVR (Varanasi)
8.	TOLCV-16	IIVR (Varanasi)
9.	TOLCV-28	IIVR (Varanasi)
10.	TOLCV-32	IIVR (Varanasi)
11.	VRT-01	IIVR (Varanasi)
12.	VRT-19	IIVR (Varanasi)
13.	VRT-13	IIVR (Varanasi)
14.	Sel-7	IIVR (Varanasi)
15.	Jawahar-99	IIVR (Varanasi)
16.	2016/TOVDVAR-12	AICRP, IIVR (Varanasi)
17.	2016/TODVAR-11	AICRP, IIVR (Varanasi)
18.	2016/TODVAR-1	AICRP, IIVR (Varanasi)
19.	2016/TODVAR-3	AICRP, IIVR (Varanasi)
20.	2016/TODVAR-10	AICRP, IIVR (Varanasi)
21.	2016/TODVAR-5	AICRP, IIVR (Varanasi)
22.	2016/TODVAR-2	AICRP, IIVR (Varanasi)
23.	2015/TODHYB-4	AICRP, IIVR (Varanasi)
24.	2015/TODBYB-1	AICRP, IIVR (Varanasi)
25.	Roma	SKUAST-K, Shalimar
26.	Shalimar Hybrid Tomato-1	SKUAST-K, Shalimar
27.	Marglobe	SKUAST-K, Shalimar

Table 2: Analysis of variance for different characters in tomato (*Solanum lycopersicum* L.)

Sr. No.	Character	Mean sum of squares		
		Replication	**Treatment**	**Error**
d.f		2	26	52
1.	Plant height (cm)	0.8492	342.5798**	2.3381
2.	No. of primary branches plant^{-1}	0.8981	7.9230**	0.3212
3.	Days to first flowering	0.2949	28.8820**	0.2001
4.	Days to fruit set	0.0538	14.5454**	0.1353
5.	Average fruit weight (g)	0.3456	128.1661**	2.4226
6.	1000-seed weight (g)	0.0237	0.6623**	0.0480
7.	Seed weight per fruit (mg)	0.1225	0.4230**	0.0206
8.	Fruit yield (q/ha)	4.8625	10466.3775**	11.7693
9.	Total soluble solids (%)	0.0509	1.3094**	0.0270
10.	Titrable acidity (%)	0.0001	0.0140**	0.0003
11.	Juice to pulp ratio	0.0004	0.0387**	0.0003

** significant at 5%.

Table 3a: Estimates of mean, range, genotypic and phenotypic coefficients of variability for different characters in Tomato (*Solanum lycopersicum* L.).

Sr. No.	Characters	Mean	Range	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)
1.	Plant height (cm)	72.95	47.66-90.90	14.59	14.74
2.	Number of primary branches plant^{-1}	4.94	1.83-7.50	32.19	34.17
3.	Days to first flowering	22.24	18.23-27.93	13.90	14.04
4.	Days to fruit set	31.11	26.86-35.26	7.04	7.14
5.	Average fruit weight (g)	61.01	50.33-72.66	10.61	10.91
6.	1000 Seed weight (g)	3.00	2.43-3.76	15.06	16.74
7.	Seed weight fruit^{-1} (mg)	1.56	1.10-2.33	23.37	25.11
8.	Fruit yield (q/ha)	211.86	124.66-362.66	27.86	27.91
9.	Total soluble solids (%)	4.46	3.20-6.23	14.65	15.11
10.	Titrable acidity (%)	0.28	0.16-0.46	23.38	24.31
11.	Juice to pulp ratio	0.50	0.27-0.71	22.62	22.91

Table 3b: Estimates of phenotypic variance, genotypic variance, heritability (bs) and genetic advance (as percent of mean) for different characters in Tomato (*Solanum lycopersicum* L.).

Sr. No.	Characters	Genotypic variance (gv) ($\sigma g^{2)}$)	Phenotypic variance (pv) ($\sigma p^{2)}$)	Heritability (bs)%	Genetic advance (as percent of mean)
1.	Plant height (cm)	113.41	115.75	98.00	29.76
2.	Number of primary branches plant^{-1}	2.53	2.85	88.70	62.47
3.	Days to first flowering	9.56	9.76	97.90	28.34
4.	Days to fruit set	4.80	4.93	97.30	14.30
5.	Average fruit weight (g)	41.91	44.33	94.50	21.25
6.	1000 Seed weight (g)	0.20	0.25	81.00	27.93
7.	Seed weight fruit^{-1} (mg)	0.13	0.15	86.60	44.82
8.	Fruit yield (q/ha)	3484.86	3496.63	99.70	57.30
9.	Total soluble solids (%)	0.42	0.45	94.10	29.28
10.	Titrable acidity (%)	0.005	0.005	92.50	46.33
11.	Juice to pulp ratio	0.013	0.013	97.50	46.00

CONCLUSIONS

The information generated from this study can be exploited for further breeding programme in tomato. The highest phenotypic as well as genotypic coefficient of variation were observed for all genotypes in number of primary branches plant^{-1} followed by fruit yield (q/ha), fruit yield plot^{-1}, titrable acidity, seed weight fruit^{-1}, Juice to pulp ratio whereas 1000 seed weight, total soluble solids, days to first flowering and average fruit weight were showed moderate coefficient of variability. The presence of high heritability in broad sense along with high genetic advance in percent of mean are recorded for fruit yield (q/ha), juice to pulp ratio and number of primary branches plant^{-1}.

FUTURE SCOPE

Those traits which exhibited high phenotypic and genotypic coefficients of variability as well as high heritability in broad sense and high genetic advance as percent mean are largely governed by additive gene action and hence there is further scope for effective improvement through selection.

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Conflict of Interest. None.

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