

Genetic Variability, Heritability and Genetic Advance Studies for Different Traits of Tomato Genotypes/Hybrid

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Received 22 August 2022, Accepted 23 September 2022, Published 25 November 2022

ABSTRACT

A set of twenty genotypes of hybrid tomato were evaluated for studying of “Genetic variability, Heritability and Genetic advance studies for different traits of tomato Genotypes/hybrid”. The experiment was conducted in a Randomized Block Design with three replications during the *rabi* season, 2021 at Horticultural Research Farm, Department of Horticulture, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj. The data were recorded from five randomly selected plants for each genotype in all the replications for twenty characters. From the present investigation it is concluded that among 20 genotypes of tomato on the basis of mean performance 3 genotypes namely; Hybrid obtained by crossing Pant T-5 X Kashi Aman (HT-9), Angoorlata X Kashi Vishesh

(HT-2) and Azad T-6 X H-88-75-5 (HT-3) were found to be superior for fruit yield per plant and performed better for other desirable traits as compared to Kashi Abhiman. Analysis of variance showed the presence of significant variation among different genotypes for all characters studied. High GCV was recorded for vegetative and yield traits.

Keywords GCV, Heritability, Genetic advance, PCV, Tomato.

INTRODUCTION

Tomato, botanically known as *Solanum lycopersicum* L. or *Lycopersicon esculentum* Mill. belongs to family Solanaceae, is a diploid self-pollinated species with chromosome number $2n=2X=24$ (Karpechenko 1925). Tomato plants are dicots, and grow as a series of branching stems, with a terminal bud at the tip that does the actual growing. Tomato is native of Western South America (Vavilov 1924). Tomato is a warm season crop. The best fruit color and quality is obtained at a temperature range of 21-24°C.

Yield is a composite character and hinges upon number of component characters which are quantitatively inherited. As such before launching any breeding program, a rigorous knowledge of the nature and enormity of genetic variability and extent of interrelation between yield and other components is requisite. Estimation of genotypes to check out the existing variability is considered as pilot step in any

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crop improvement program. Variability for different traits in the source population is a prerequisite for crop improvement since all attempts of breeding and selection would be futile unless major portion of variability is heritable. Further, estimation of genetic advance and heritability would give the best picture of the extent of improvement expected from selection and reliability of selection based on phenotype (Falconer 1989).

MATERIALS AND METHODS

The experimental material for present investigation comprised of 20 genotypes/Hybrids of tomato (*Lycopersicon esculentum* Mill.) were obtained from sown at Horticultural Research Farm, Department of Horticulture, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj and IIVR. The experiment was conducted in Randomized Block Design comprising 20 (19 genotypes/Hybrids +1 check) with three replications during *rabi* 2021-22 with a spacing of 90 cm between the rows and 75 cm between the plants. The

observations were recorded on randomly selected five plants for vegetative and yield attributing characters.

Analysis of variance was calculated using the formula suggested by Fisher (1963) coefficient of variation including genotypic coefficient of variation and phenotypic coefficient of variation was calculated using the formula suggested by Burton (1952) Heritability (broad sense) was calculated using the formula suggested by Allard (1960) Genetic advance was calculated using the formula suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

From the above tables (Tables 1 and 2) and (Fig.1) figure we can say that the analysis of variance for all characters of tomato genotypes revealed presence of good extent of significant differences among the genotypes for all traits. Hence forth, the data for all 20 characters that showed sufficient amount of significant differences were subjected to further statistical analysis. These results were in agreement with the

Table 1. Analysis of variance (ANOVA) for 20 quantitative characters in tomato.

Characters	Mean sum of squares		
	Replication (df=2)	Treatment/ genotypes (df=19)	Error (df=38)
Plant height (cm)	33.88	1599.81**	57.78
Number of branches per plant	1.11	16.319**	0.56
Days to 1 st emergence of flower	4.97	34.18**	7.31
Days to 50% flowering	3.67	33.91**	9.25
Days to first fruit setting	20.38	33.69**	15.25
Days to first fruit picking	28.72	35.59**	14.36
Number of flowers per cluster	0.04	0.87**	0.20
Number of fruit set per cluster	0.02	1.09**	0.17
Number of flower clusters per plant	0.01	4.97**	0.47
Number of locules per plant	0.09	1.18**	0.16
Fruit length (cm)	0.06	1.39**	0.08
Fruit diameter (cm)	0.01	0.63**	0.023
Fruit weight (g)	7.51	284.42**	19.20
Number of fruits per plant	1.06	276.18**	12.46
Fruit yield per plant (kg/plant)	0.065	0.89**	0.04
Fruit yield per hectare (t/ha)	21.77	196.97**	8.91
TSS. (°Brix)	0.31	2.04**	0.11
Vitamin C (100 mg/g fruit)	0.36	7.66**	0.76
Acidity (%)	0.01	0.48**	0.01
Shelf life (days)	0.05	13.11**	0.26

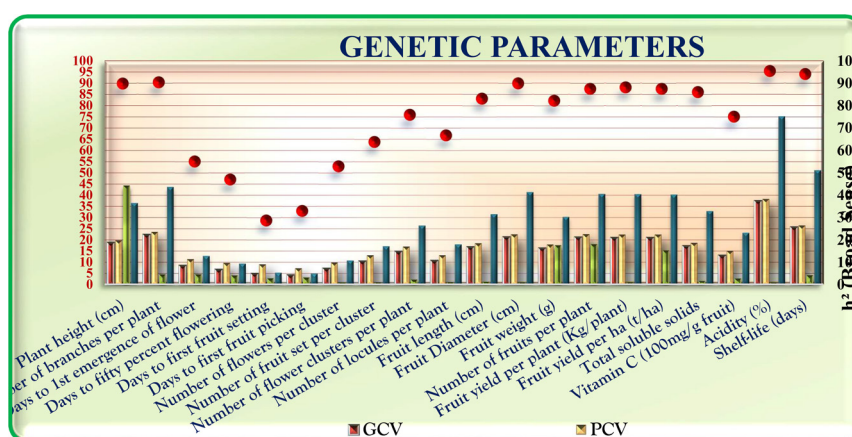
*, ** Significant at 5% and 1% respectively.

Table 2. Range, variability and genetic parameters for 20 quantitative characters of 20 tomato genotypes.

Sl. No.	Characters	Range	GCV (%)	PCV (%)	h ² (Heritability broad sense) (%)	GA (5% LOS)	GA as % mean
1.	Plant height (cm)	79.80-169.24	18.64	19.66	89.89	44.28	36.40
2.	Number of branches per plant	6.82-16.07	22.31	23.46	90.38	4.48	43.68
3.	Days to 1 st emergence of flower	30.66-42.89	8.37	11.28	55.04	4.57	12.79
4.	Days to 50% flowering	38.01-50.56	6.59	9.62	47.05	4.05	9.32
5.	Days to first fruit setting	46.02-58.60	4.81	8.98	28.71	2.73	5.31
6.	Days to first fruit picking	58.75-71.37	4.15	7.22	32.99	3.14	4.91
7.	Number of flowers per cluster	5.94-7.47	7.14	9.82	52.91	0.71	10.70
8.	Number of fruit set per cluster	4.32-6.40	10.38	13.01	63.74	0.91	17.07
9.	Number of flower clusters per plant	6.71-10.61	14.71	16.88	75.89	2.19	26.40
10.	Number of locules per plant	3.96-6.39	10.66	13.05	66.72	0.97	17.94
11.	Fruit length (cm)	2.77-5.19	16.74	18.36	83.10	1.24	31.43
12.	Fruit diameter (cm)	1.28-2.86	21.18	22.33	89.90	0.88	41.37
13.	Fruit weight (g)	41.09-77.39	16.19	17.86	82.15	17.55	30.23
14.	Number of fruits per plant	32.14-63.25	21.03	22.47	87.58	18.07	40.54
15.	Fruit yield per plant (kg/plant)	1.61-3.43	20.91	22.26	88.20	1.03	40.45
16.	Fruit yield per hectare (t/ha)	23.90-50.94	20.88	22.32	87.55	15.26	40.25
17.	TSS (°Brix)	2.83-6.23	17.2	18.54	86.02	1.53	32.86
18.	Vitamin C (100mg/g fruit)	9.58-15.62	12.94	14.93	75.05	2.70	23.09
19.	Acidity (%)	0.42-1.82	37.37	38.24	95.50	0.80	75.23
20.	Shelf life (days)	3.61-11.20	25.57	26.36	94.12	4.14	51.11

studies conducted by Singh and Cheema (2005), Ghosh *et al.* (2010), Shashikant *et al.* (2010), Kerketta and Bahadur (2019). Both High GCV and PCV was recorded for number of fruits per plant, acidity, fruit diameter, shelf life, fruit yield per plant and fruit yield per hectare which suggests that improvement in these characters might be gained to a reasonable extent. Both low GCV and PCV were recorded for

days to 50% flowering, days to first fruit setting, days to first fruit setting and number of flowers per cluster. While days to first flower emergence had low GCV but moderate PCV. Similar results for high GCV and PCV were concluded earlier by was earlier reported by Singh and Cheema (2005), Ghosh *et al.* (2010), Shashikant *et al.* (2010), Ahirwar *et al.* (2013), Patel *et al.* (2013) and Kerketta and Bahadur (2019). This

**Fig. 1.** Genetic parameters.

also suggests that improvement in these characters might be gained to a reasonable extent therefore, selection for these characters would be effective because response to selection is directly proportional to the variability present in the experimental material. In present study, high heritability (broad sense) estimates (60% and above) had been observed for plant height, number of branches per plant, number of flower clusters per plant, fruit length, fruit diameter, fruit weight, number of fruits per plant, fruit yield per plant, fruit yield per hectare, T.S.S., vitamin c content, acidity and shelf life. Therefore, these characters are predominantly governed by additive gene action and could be improved through individual plant selection owing to their high heritability values. Similar inferences were reported earlier by Singh and Cheema (2005), Ghosh *et al.* (2010), Shashikant *et al.* (2010), Dar *et al.* (2011), Ahirwar *et al.* (2013), Patel *et al.* (2013), and Kerketta and Bahadur (2019). High GCV along with high heritability was observed for number of fruits per plant, acidity, fruit diameter, shelf life, fruit yield per plant and fruit yield per hectare. This indicated that these traits are comparatively under less influence of environment hence forth, desirable for selection in breeding program. High estimates of heritability coupled with moderate genetic advance as % of mean was recorded for number of primary branches per plant, number of umbels per plant, seed yield per plant (g/plant), seed yield per plant (g/plant), seed yield per hectare (q/ha), and harvest index (%). While moderate estimates of heritability coupled with moderate genetic advance as % of mean was observed for days to first flower emergence and number of flowers per cluster. These traits are governed by additive gene action and thus can be improved through direct selection. This indicates closeness of respective σ_p^2 and σ_g^2 value thereby low environmental effect on expression of these characters. Such values may be attributed to the additive gene effects and direct selection for these traits would be fruitful. Thus, phenotypic selection may be effective for these characters. Similar inferences were drawn by reported earlier by Ghosh *et al.* (2010), Shashikant *et al.* (2010), Dar *et al.* (2011), Ahirwar *et al.* (2013) and Patel *et al.* (2013). High estimates of heritability coupled with high genetic advance as % of mean was recorded for all characters excluding days to 50% flowering, days to first fruit setting, days to first fruit picking only.

While moderate estimates of heritability coupled with moderate genetic advance as % of mean was observed for days to 1st emergence of flower, number of fruit set per cluster and number of locules per plant. These traits are governed by additive gene action and thus can be improved through direct selection.

CONCLUSION

It is concluded that among 20 genotypes of Tomato on the basis of mean performance 3 genotypes viz. Hybrid obtained by crosses Pant t-5 X Kashi Aman (HT9), Angoorlata X Kashi Vishesh (HT-2) and Azad T-6 X H-88-75-5 (HT-3) possessed maximum fruit yield per plant over the check variety Kashi Aman. Number of fruits per plant, acidity, fruit diameter, shelf life, fruit yield per plant and fruit yield per hectare exhibited high estimates of GCV and PCV and also high estimates of heritability (broad-sense). Therefore, these characters should be given priority during selection for improvement in tomato.

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