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## Study of genetic variability, heritability and genetic advance for yield and yield contributing traits in tomato (*Solanum lycopersicum* L.)

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### Abstract

The present research programme, Genetic variability, heritability and genetic advance for yield and yield attributes in tomato (*Solanum lycopersicum* L.), was carried out at Hill Millet Research Station, Waghai, The Dangs, NAU. Rabi season 2021-22. Fifty genotypes of tomato were evaluated in Randomized Block Design with three replications. The analysis of variance revealed highly significant variation among the genotypes for all the characters studied indicating considerable amount of variability among the genotypes. High GCV and PCV were observed for plant height, average fruit weight, total number of fruits per plant, total soluble solids, vitamin c. This indicates the existence of broad genetic base, which would be amenable for further selection. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, average fruit weight (g), total number of fruits, yield per plant (kg/ha), total yield (t/ha), TSS and vitamin C content.

**Keywords:** Variability, GCV, PCV, heritability, genetic advance, tomato

### Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most important and widely grown vegetable in the worldwide. It is most popular vegetable of Solanaceae family because to its higher adaptability, high yield potential and short duration crop hence area under tomato cultivation is increasing day by day. It has a diploid genome with 24 chromosome and a genome size of 950 Mb. (Michaelson *et al.* 1995) [19] encoding approximately 35,000 genes that are largely sequestered in contiguous euchromatic regions. Tomato has its primary centre of diversity in a narrow belt along the Andean region of Ecuador and Peru. Tomato fruits are good source of total sugar (reducing sugar and non reducing sugar), beta-carotene and lycopene contain which helps to maintain the human health. In world, it ranks second in importance after potato, but tops the list of processed vegetables (Chaudhary, 1996) [4]. This crop is an excellent source of income for small and marginal farmers as well as contributes to the nutrition of the consumer (Singh *et al.*, 2010) [15]. Agro-statistics include India as second highest tomato producers in the world after China. In 2021-22, the growing area reached 8.40 M ha, resulting in a total production of about 20.33 M tons and In Gujarat, tomato cultivated in 0.53 M ha with a total 1.48 M tons. Tomato yield is a multigenic trait and is greatly affected by environmental factors. The components of genetic variability like GCV, PCV,  $h^2$  (Broad sense heritability) and genetic advance (GA) are essential biometric tools for assessing dissimilarity in population for making a selection and evaluating tomato germplasm for improvement through breeding techniques. The nature and degree of genetic variability in a crop is of paramount importance improvement in yield and related characters as well to select the most potential parents for making the hybridization programme successful. The success of breeding programme depends on the extent of genetic variability present in the available germplasm. The coefficient of variation expressed in at phenotypic (PCV) and genotypic (GCV) levels have been compared for variability observed among different traits. The GCV indicates the amount of genetic variability present in character, while the heritability estimates aid in determining the relative amount of heritable portion of variation for those characters. The heritability estimates in broad sense would be reliable if accompanied with genetic advance.

**Materials and Methods**

The present experiment was carried out during *Rabi* season, 2021-22 at Rambhas Farm, Hill Millet Research Station, Waghai, Navsari Agricultural University. The experiment was carried out at Randomized Block Design (RBD) with 3 replications. A total 30 genotypes were used in this study. Total experimental area was 973.35 m<sup>2</sup>. The spacing was 90 cm and 60 cm between rows and plants respectively and total 12 plants planted in line (10 +2 boarder plant). Fertilizer rate of 150:60:60 NPK kg/ha was applied. The seeds were grown during the November month and transplanted after 45 days into main field. Random plant selection (five plants) was made from each replication for each genotype to record the data for each parameter. Plant height, average fruit weight, number of fruits per plant, yield per plant (kg/ha), total yield (t/ha). Total soluble solid content was determined with the help of Pocket Refractometer. The vitamin C i.e., ascorbic acid content was determined by Dye method as detailed by

Rangana (1986) [13]. The analysis of variance for design of experiment was done for partitioning the variance into treatments and replications. Phenotypic and genotypic coefficients of variation were calculated by using the following formulae suggested by Burton and Devane (1953) [2]. The broad sense heritability (h<sup>2</sup>) was calculated using the method proposed by Webber and Moorthy (1952) [18]. Genetic advance and genetic advance as per cent over mean for each character was predicted by the formula given by Johnson *et al.* (1955) [6].

**Results and Discussion**

The analysis of variance for all the characters under study are presented in Table 1. The mean sum of squares for genotypes was found to be significant for all characters *viz.*, plant height (cm), average fruit weight (g), number of fruits per plant, yield per plant (kg/ha), total yield (t/ha), total soluble solids (<sup>0</sup>Brix) and vitamin C content (mg/100g).

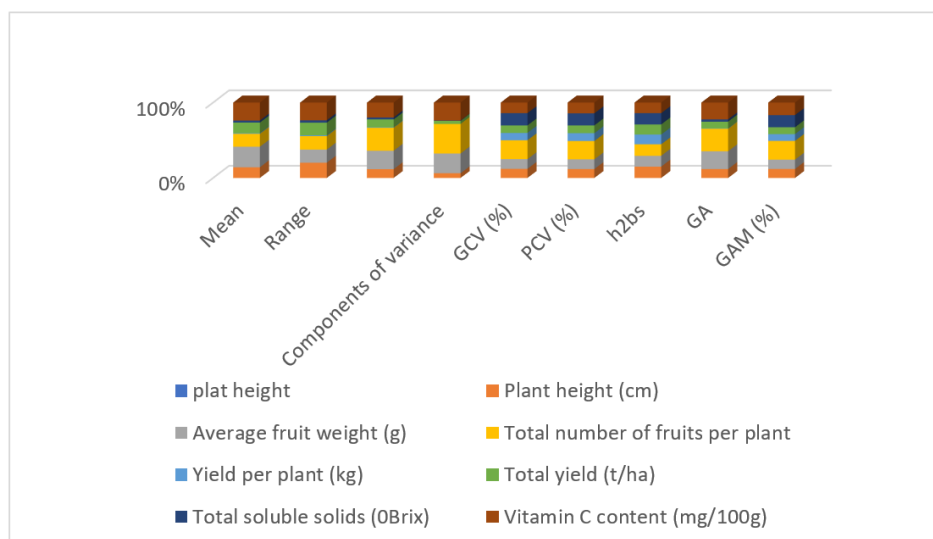
**Table 1:** Analysis of variance for various characters in tomato

Source of variation	Mean sum of squares						
	Plant height (cm)	Average fruit weight (g)	Total number of fruits per plant	Yield per plant (kg/ha)	Total yield (t/ha)	Total soluble solids ( <sup>0</sup> Brix)	Vitamin C content
Replication (2)	0.77	84.58	44.02	0.38	132.75	0.027	2.23
Genotype (29)	98.31**	432.74**	605.09**	0.21**	74.98**	6.74**	402.99**
Error (58)	2.83	32.21	6.77	0.03	12.15	0.20	38.77
S. Em ±	1.37	4.63	2.12	0.15	2.84	0.37	5.08
C.D. at 5%	2.75	9.27	0.30	0.30	5.69	0.74	10.17

**Table 2:** Estimates of genetic parameters in tomato genotypes

Sr. No.	Characters	Range	Mean	σ <sup>2</sup> g	σ <sup>2</sup> p	σ <sup>2</sup> e	GCV (%)	PCV (%)	h <sup>2</sup> <sub>bs</sub> (%)	GAM (%)
1	Plant height (cm)	16.70-37.10	25.29	31.82	32.77	0.94	22.30	22.63	97.1	45.28
2	Average fruit weight (g)	14.36-77.53	48.28	133.50	144.24	10.73	23.92	24.87	92.6	47.22
3	Total number of fruits per plant	14.80-96.60	30.47	199.43	201.69	2.25	46.34	46.60	98.9	94.93
4	Yield per plant (kg)	0.75-1.79	1.35	0.06	0.07	0.01	18.22	19.91	83.7	34.35
5	Total yield (t/ha)	13.93-33.22	25.08	20.94	24.99	4.05	18.24	19.93	86.3	34.40
6	Total soluble solids ( <sup>0</sup> Brix)	2.60-8.40	4.87	2.17	2.24	0.07	30.24	30.72	96.9	61.34
7	Vitamin C content (mg/100g)	19.40-62.50	42.31	121.40	134.33	12.92	26.03	27.38	90.4	63.351

σ <sup>2</sup> g = Genotypic variance	PCV (%) = Phenotypic coefficient of variation
σ <sup>2</sup> p = Phenotypic variance	h <sup>2</sup> <sub>bs</sub> (%) = Heritability (broad sense)
σ <sup>2</sup> e = Environmental variance	GA = Genetic advance
GCV (%) = Genotypic coefficient of variation	GAM (%) = Genetic advance as per cent of mean



**Fig 1:** GCV (%), PCV (%), Heritability (%), Genetic advance and Genetic advance as per cent of mean (%) of various characters of tomato

For all the traits studied, PCV was slightly higher than GCV, this indicates that these characters were not much influenced by environmental factors. Hence, selection based on phenotypic performance will be more reliable. These results were in accordance with the findings of Taiana *et al.* (2015)<sup>[17]</sup> in tomato. High GCV and PCV were observed for the plant height (cm), average fruit weight (g), number of fruits per plant, Total soluble solids and vitamin C content. Therefore, it is suggested that these traits were true representative of their genotype and selection based on these characters should be more reliable. Similar results were also observed by Hetal *et al.* (2016)<sup>[5]</sup>, Kerketta and Bahadur (2019)<sup>[8]</sup>, Anuradha *et al.* (2020)<sup>[1]</sup>, Kavya *et al.* (2021)<sup>[9]</sup>, Pooja *et al.* (2022)<sup>[12]</sup>. Moderate GCV and PCV was observed for the characters like yield per plant (kg/ha) and total yield (t/ha). Coefficient of variation indicates only the extent of variability present in the genotypes for different traits, but for the prediction of response to selection, heritability estimates are useful. Considering heritability in broad sense along with genetic advance may reveal the prevalence of specific components (additive or non-additive) of genetic variance and thus, help in judging the effectiveness of selection for the trait more accurately (Johnson *et al.* 1955)<sup>[6]</sup>. High heritability (>60%) coupled with high genetic advance (>20%) was observed for plant height (cm), average fruit weight (g), total number of fruits, yield per plant (kg/ha), total yield (t/ha), TSS and vitamin C content. The traits under this experiment, exhibited high heritability and GAM revealed the presence of predominant additive interactions of the genetic components. Therefore, any selection technique may be applied for developing stable genotypes for these characters. Similar to our results, high heritability with genetic advance was advocated by Kaushik *et al.* (2011)<sup>[7]</sup>, Patel *et al.* (2013)<sup>[11]</sup>, Anuradha *et al.* (2020)<sup>[1]</sup>, Sushma *et al.* (2020)<sup>[16]</sup>, Kavya *et al.* (2021)<sup>[9]</sup>.

### Conclusion

The analysis of variance revealed highly significant difference among genotypes for all the traits concluding wide range of variability present in the experiment materials for all the characters. The characters with high GCV and PCV proved the presence of wide variation and hence further crop improvement can be done by selection of these individual traits. High heritability coupled with high GAM indicates that these characters are controlled by additive gene effect and are less influenced by environmental factors. Therefore, direct selection would be effective technique for further improvement for these characters.

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