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## Genetic variability, heritability and genetic advance for yield and yield contributing traits in Tomato (*Solanum lycopersicum* L.)

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### Abstract

Sixteen tomato genotypes were tested in order to quantify variability, heritability, and genetic progress in yield and yield contributing characteristics. The magnitude of the phenotypic coefficient of variation (PCV) was greater than the size of the genotypic coefficient of variation (GCV) for all traits. High PCV, GCV, and Heritability were observed, along with high genetic advance as a percentage of mean for both fruit yield/plant (kg) and fruit yield (kg/plot), number of clusters/plants, plant height (cm), number of primary branches/plants, number of fruits/plants, locule number, average fruit weight (g), and number of flower/clusters. These estimates demonstrated high heritability (broad sense) values were high for all traits viz, number of cluster/plants, plant height (cm), average fruit weight (g), number of fruits per plant, fruit yield (kg/plot), fruit yield per plant (kg), days to 50% flowering, polar diameter (mm), days to first fruit setting, days to first flowering, fruit equatorial diameter (mm), number of primary branches per plant, days to first fruit harvest, locule number. Highest estimate of genetic advance was noted in plant height (cm) followed by number of clusters per plant.

**Keywords:** Tomato, variability, heritability, genetic advance, GCV and PCV

### Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most significant vegetable crops grown worldwide due to its great adaptability, high yielding capacity, and suitability for a multitude of uses in both fresh and processed food industries. This species is native to South America, likely Peru and Ecuador, but it was domesticated in Mexico for the first time. In many countries it is considered as “poor man’s orange” because of its attractive appearance and nutritive value while in England, it is known as the “love of apple”. Tomato is also a significant component of the cocktail known as “Blood Marry” (Meena *et al.*, 2014) [22]. Tomato belongs to a family Solanaceae, with other important crops such as pepper, eggplant and potato. It is a significant warm-season self-pollinated vegetable farmed for both fresh and processed markets (Das *et al.*, 2011) [12]. It is a self-pollinated diploid with twelve pairs of chromosomes ( $2n=2x=24$ ). The evolutionary classification of the Solanaceae family was recently modified, and the genus *Lycopersicum* was reintegrated into the genus *Solanum* with its new nomenclature (Peralta *et al.*, 2008) [24]. It is an herbaceous, annual to perennial crop plant with bisexual flowers that is sexually propagated. Tomato is a day neutral plant that is largely self-pollinated with some cross-pollination. Tomatoes are classified as determinate or indeterminate, and they can be cultivated in open fields or greenhouses. The *Solanum* genus contains over 3000 species, with tomatoes being the most lycopene-producing of them all. It is a good source of lycopene and ascorbic acid, as well as antioxidants and chemo-protective compounds, and hence qualifies as a functional food (Akhtar and Hazra 2013; Maurya *et al.* 2022) [3, 21]. Section *lycopersicum* includes the only cultivated tomato species, *Solanum lycopersicum*, as well as a dozen more wild cousins (Kalloo 2012) [17]. Tomatoes are one of the most important vegetable crops grown around the world. It is ranked second among vegetable crops and seventh overall. In India, it is next only to potato and onion among vegetables in terms of production. The crop has gained popularity among farmers due to its short duration, high yield potential, high profitability,

and economic feasibility, as well as its strong nutritional and protective properties (Chauhan *et al.*, 2014) [8]. The current studies focus on these characteristics, as well as other factors researched by other researchers. As a result, the study will go a long way towards identifying desirable genotypes suitable for distribution as an open pollinated cultivar or involving favourable genotypes in the development of hybrids fit for the vegetable production system widespread in Madhya Pradesh. The crop is farmed in the country on an area of 0.841 million hectares, yielding 20.34 million metric tonnes with an average national productivity of 24.36 metric tonnes per hectare (Anonymous, 2022) [4]. India ranks second in area (11280 thousand ha) and production (204613 MT) next to China, while its productivity (25.6 ton/ha) is quite lower many of the major producing countries. Andhra Pradesh is the largest producer of tomatoes in India. Tomatoes are another common vegetable in M.P, with an area of 46.27 thousand ha, a production of 1011MT, and a productivity of 21.85 tons/ha (Anonymous, 2022) [4]. The main tomato producing states in India include Andhra Pradesh, Madhya Pradesh, Karnataka, Telangana, and Gujarat. Tomato includes minerals, vitamins, and phytochemicals, they are an important part of the human diet. Tomatoes are high in vitamins (A and C), minerals (Ca, P, and Fe), and are a powerful antioxidant that can help prevent cancer and heart disease. It's output has skyrocketed because to its numerous applications, including fresh for salad, cooked as vegetables, and processed in a variety of forms such as soup, sauces, ketchups, preserves, paste, and puree. Tomato's red pigment is currently regarded as the "World's most powerful antioxidant". It also plays an important role in boosting poor people's nutrition resources when compared to meat, milk, fruits, and other high-priced food goods (Saleem *et al.*, 2013) [27]. It is classified as a 'Protective food' because it contains lycopene and flavonoids, which have specific nutritional and antioxidant qualities (Sepat *et al.*, 2013) [28]. In the human diet, tomatoes and their derivatives are the principal source of lycopene and other antioxidants. Tomatoes' antioxidants, notably lycopene, beta-carotene, ascorbic acid, vitamin E, phenolic compounds, and flavonoids, are responsible for their health advantages (Frusciante, 2007) [14]. Lycopene is an important dietary component since it reduces the risk of a variety of cancers and heart attacks (Dorgan *et al.*, 1998; Clinton, 2005) [13, 9]. As a result, an attempt was made to investigate the genetic diversity, heritability, and genetic gain among several tomato genotypes for various horticultural parameters.

### Materials and Methods

In the autumn-winter season of 2022-23, sixteen tomato genotypes were grown. The field experiment was conducted at ITM University's Vegetable Research Farm (CRC-1), School of Agriculture, Department of Horticulture, Gwalior (MP). It is located in India's Grid area at 26° 21' N latitude and 78° 20' E longitude, with an elevation of 211.5 m above sea level. It may be found southwest of Gwalior. Tomato genotypes were planted in the nursery bed as part of the experimental material. Tomato seedlings were transplanted in a Randomized Block Design with three replications. In our trial, we transplanted thirty-day-old seedlings on raised beds at a 5050 cm spacing to optimize crop growth. The details of the plant materials are presented in Table 1.

**Table 1:** List of tomato genotypes used in field trail.

S.N.	Genotypes	Source
01	Pusa Gaurav	IIVR, Varanasi
02	Pusa Ruby	IIVR, Varanasi
03	Punjab Chhuhara	IIVR, Varanasi
04	Money Maker	IIVR, Varanasi
05	CO-3	IIVR, Varanasi
06	H-24	IIVR, Varanasi
07	EC-620424	IIVR, Varanasi
08	EC-620444	IIVR, Varanasi
09	Deep Deshi	Local collection
10	Rishi	Local collection
11	Deshi Red	Local collection
12	NF-54	Local collection
13	ZS-21	Local collection
15	Pusa Sadabahar	IIVR, Varanasi
15	Kashi Sharad	IIVR, Varanasi
16	Pusa Sheetal	IIVR, Varanasi

Nineteen yield and yield attributing traits and quality parameters were recorded. Plant height (cm), number of primary branches/plant, days to first flowering, days to 50% flowering, days to first fruit harvest, average fruit weight (g), fruit polar diameter (mm), fruit equatorial diameter (mm), number of locules, pericarp thickness (mm), number of flowers/cluster, flower cluster/plant, number of fruits/cluster, number of fruits/plant, fruit yield/plant (g), fruit yield (kg/plot) Total soluble solids (TSS), total titrable acidity (TTA), and pH of the fruits were among the quality criteria measured. Comstock and Robinson's 1952 technique was used to calculate the genotypic and phenotypic coefficients of variance (GCV and PCV). Similarly, heritability was evaluated using Lush's 1940 approach, and genetic advance prediction was obtained using Lush's (1949) methodology and revised by Johnson *et al.* in 1955 [16].

### Results and discussion

The recorded data on all quantitative characters were subjected to analysis of variance to test whether there was significant variation among the genotypes. Analysis of variance has been presented in Table 2. It shows that the mean square due to the genotypes were highly significant for all the characters suggesting significant variability among all the traits under study and indicates the presence of ample scope for selection.

The genetic variability estimates for several qualities such as genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance, and genetic advance as a percentage of mean (Table 3). The coefficient of genotypic and phenotypic variability is a useful measure for measuring the degree of variation in a particular trait. They can also be used to compare the degree of variability among different quantitative features. The magnitude of the phenotypic coefficient of variation (PCV) was greater than the size of the genotypic coefficient of variation (GCV) for all traits (Table 3). Higher values of PCV compared to GCV was reported by Ahirwar *et al.* (2013) [2], Kumar *et al.* (2016) [18] and Pandey *et al.* (2018) [23], Maurya *et al.* (2022) [21]. According to Dar and Sharma (2011) [11], the greater PCV values in comparison to the GCV values indicated that there was some influence of environment on all of the qualities under consideration.

Sivasubramanian and Madhavamenon (1973) [29] defined GCV and PCV as low when less than 10%, moderate when 10-20%, and high when greater than 20%. Estimates of high genotypic variance were recorded for both fruit yield per plant and fruit yield (kg per plot), number of clusters per plant, plant height (cm), number of primary branches per plant, number of fruits per plant, locule number, average fruit weight, number of flower per cluster; whereas, days to first flowering, polar diameter, days to first fruit setting,

days to 50% flowering, pericarp thickness, fruit equatorial diameter, days to first fruit harvest, total soluble solids, showed moderate genotypic variation, whereas pH, total titrable acidity showed low genotypic variation. Dar and Sharma (2011) [11] previously observed high GCV and PCV values for fruit number per plant and overall yield, whereas Prema *et al.* (2011) [25] saw the same for fruit polar and equatorial diameter, as well as fruit TSS.

**Table 2:** Analysis of variance (mean squares) for nineteen characters in 16 tomato genotypes

Source of Variation	Replication	Treatment	Error	Total
DF	2	15	30	47
Days to first flowering	9.77	107.21**	1.59	35.65
Days to first fruit setting	1.75	109.55**	1.48	35.99
Days to 50% flowering	3.52	126.04**	1.14	41.10
Days to first fruit harvest	20.77	529.22**	10.26	176.33
Average fruit weight (g)	18.83	962.23**	3.52	310.14
Fruit equatorial diameter (mm)	3.35	150.26**	2.49	49.69
Polar diameter (mm)	5.34	228.71**	2.87	75.05
Locule number	0.02	3.20**	0.08	1.07
Pericarp thickness (mm)	0.14	1.78**	0.20	0.71
Number of flowers/clusters	0.32	7.33**	0.32	2.55
Number of cluster / plants	6.85	2782.60**	4.23	891.06
Number of fruits /plants	9.65	410.10**	2.12	132.65
Number of primary branches/plants	0.03	14.61**	0.27	4.84
Plant height (cm)	60.34	4514.19**	7.99	1448.36
Total Soluble Solids	0.141	0.943**	0.100	0.371
Total Titrable Acidity	0.078	0.066**	0.014	0.034
pH	0.033	0.535**	0.069	0.216
Fruit yield / plant (Kg)	0.11	3.32**	0.02	1.08
Fruit yield (Kg/plot)	29.88	849.19**	4.72	275.30

\* and \*\* depict significance at  $p \leq 0.05$  and  $p \leq 0.01$  respectively;

Critical selection qualities are heritability and genetic advancement. Estimating heritability is especially important when genotypic coefficients of variation provide information on the variance present across genotypes for a certain trait. The proportion of a trait's variability that can be handed down to children is referred to as heritability. Johnson *et al.* (1955) [16] classed heritability estimates as low (less than 30%), moderate (30-60%), or high (greater than 60%). The heritability of all variables evaluated in this study was found to be high, indicating a predominance of additive gene activity.

This observation is consistent with the findings of Ara *et al.* (2009), Agarwal *et al.* (2014) [1], and Bhandari *et al.* (2017) [6], who reported similar results in previous studies. When heritability estimates are accompanied by the genetic advance, it becomes more accurate to predict genetic gains through selection (Johnson *et al.* 1955) [16]. Johnson *et al.* (1955) [16] also proposed a classification of genetic advance as a percentage of mean, with low (less than 10%), moderate (10-20%), and high (greater than 20%) categories.

High heritability combined with high genetic progress shows that additive gene action has a significant influence, making selection successful in such instances. High heritability mixed with little genetic progress, on the other hand, shows non-additive gene activity, rendering selection ineffectual. Low heritability combined with high genetic progress suggests additive gene effects in trait inheritance, but significant environmental influence on trait expression, rendering early-generation selection ineffectual. In such instances, though, selection in later generations may be effective. If both low heritability and poor genetic progress

are seen, the trait is driven mostly by environmental variables, rendering selection ineffectual.

Burton and De Vane (1953) [7] reported that, when combined with heritability estimates, genetic coefficients of variability can be used to forecast the degree of improvement feasible by selection. High heritability values (in the broad sense) were observed in this study for all traits, including number of clusters per plant (99.54%), plant height (99.47%), average fruit weight (98.91%), number of fruits per plant (98.46%), fruit yield (kg/plot) (98.35%), fruit yield per plant (98.34%), days to 50% flowering (97.33%), polar diameter (96.33%), days to first fruit setting (96.05%), days to first flowering (95.67%), fruit equatorial diameter (95.19%), number of primary branches per plant (94.63%), days to first fruit harvest (94.40%), and locule number (93.16%). (Table 3).

Heritability was high for all the traits under study suggesting predominance of additive gene action for the traits. Kumar *et al.* (20018) [23], Ara *et al.* (2009), Agarwal *et al.* (2014) [1], Bhandari *et al.* (2017) [6] and Maurya *et al.* (2022) [21] also reported similar findings earlier. The estimate of genetic advance is combined with heritability, it leads to more accurate predictions of genetic gain under selection reported by Johnson *et al.* (1955) [16]. Highest estimate of genetic advance was recorded in plant height (79.63%) followed by number of cluster per plant (62.55%), whereas, average fruit weight (36.62%), fruit yield kg/plot (34.28%), days to first fruit harvest (26.32%), showed moderate genetic advance and number of fruits/plant (23.84%), polar diameter (17.54%), fruit equatorial diameter (14.11%), days to 50% flowering (13.11%), days to first fruit setting (12.12%), days to first flowering (11.96%), number of primary branches per plant (4.38%), number of flower per cluster (2.95%), fruit



yield per plant (2.14%), locule number (2.03%), pericarp thickness (1.27%), total soluble solids (0.94%), pH (0.68%), total titrable acidity (0.20%) showed lowest estimate of genetic advance. Golani *et al.* (2007) [15] previously showed

high heritability for fruit weight, number of locules/fruit, and fruit production. Rai *et al.* (2016) [26] discovered strong heritability with high genetic gain for fruit yield per plant, average fruit weight, and number of fruits per plant.

**Table 3:** Estimates of range, grand mean, phenotypic, genotypic, environmental, coefficients of variation, heritability in broad sense ( $h^2_{bs}$ ) and genetic advance in per cent of mean ( $\bar{GA}$ ) for nineteen characters in tomato genotypes

Characters	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to first flowering	30.40	20.33	42.67	35.21	36.80	95.67	11.96	39.33	19.52	19.96
Days to first fruit setting	35.81	25.67	47.33	36.02	37.51	96.05	12.12	33.83	16.76	17.10
Days to 50% flowering	39.79	27.67	53.33	41.63	42.78	97.33	13.11	32.95	16.22	16.44
Days to first fruit harvest	103.08	77.00	117.33	172.99	183.25	94.40	26.32	25.54	12.76	13.13
Average fruit weight (g)	67.20	33.87	97.00	319.57	323.09	98.91	36.62	54.50	26.60	26.75
Fruit equatorial diameter (mm)	50.89	40.08	61.47	49.26	51.75	95.19	14.11	27.72	13.79	14.14
Polar diameter (mm)	48.83	37.09	70.47	75.28	78.15	96.33	17.54	35.92	17.77	18.10
Locule number	3.62	2.07	5.53	1.04	1.12	93.16	2.03	56.00	28.16	29.18
Pericarp thickness (mm)	5.02	3.69	6.43	0.53	0.73	71.98	1.27	25.24	14.44	17.02
Number of flowers/cluster	7.03	5.33	12.33	2.34	2.65	88.03	2.95	42.05	21.76	23.19
Number of clusters/plant	78.14	28.73	155.00	926.12	930.36	99.54	62.55	80.04	38.95	39.03
Number of fruits/plant	38.38	17.57	53.67	135.99	138.11	98.46	23.84	62.11	30.38	30.62
No of primary branches/plant	6.89	3.33	10.50	4.78	5.05	94.63	4.38	63.64	31.76	32.64
Plant height (cm)	100.80	39.87	179.33	1502.07	1510.05	99.47	79.63	78.99	38.45	38.55
Total Soluble Solids	4.45	3.03	5.20	0.28	0.38	73.67	0.94	21.06	11.91	13.88
Total Titrable Acidity	1.55	1.37	1.83	0.02	0.03	54.53	0.20	12.90	8.48	11.48
pH	4.32	3.73	5.33	0.16	0.22	69.34	0.68	15.66	9.13	10.96
Fruit yield/plant (Kg)	2.59	0.95	4.01	1.10	1.12	98.34	2.14	82.82	40.54	40.88
Fruit yield (Kg/plot)	41.38	15.20	64.08	281.49	286.21	98.35	34.28	82.82	40.54	40.88

## Conclusion

Therefore, based on the results of the current study, it can be inferred that a high genetic variability for various fruit quality and biochemical traits was produced using a variety of tomato genotypes, indicating the existence of a significant opportunity for these genotypes to be improved for these traits through selection and hybridization. Furthermore, for all characters under study, moderate to high GCV, high heritability, and moderate to high genetic advance as a percentage of mean were reported, indicating a predominance of additive gene action and ample opportunity for the improvement of the concerned traits through selection.

## Author contribution

DM and PD conceptualized and prepared the manuscript. VJ critically supplemented the manuscript. SY and SD assisted in preparing the manuscript. All authors read the final version of the manuscript, provided necessary suggestions and approved it for publication.

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