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EXPLORING THE GENETIC POTENTIAL FOR ENHANCING NUTRITIONAL QUALITY AND YIELD IN TOMATO: HERITABILITY AND GENETIC ADVANCE INSIGHTS TOMATO BREEDING

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ABSTRACT

The present investigation was conducted during the autumn-winter season of 2023–24 at the Main Experimental Research Station, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India, to assess the genetic variability among 25 tomato (*Solanum lycopersicum* L.) genotypes using 16 quantitative traits. The field experiment was laid out in a randomized block design with three replications. The study aimed to explore the genetic potential of tomato genotypes for improving yield and nutritional quality traits, with emphasis on heritability and genetic advance. Analysis of variance (ANOVA) revealed highly significant differences among genotypes for all studied traits, indicating substantial genetic variability across phenological, morphological, yield, and quality parameters. Mean performance analysis identified promising genotypes such as NDT-22-1 for high yield potential and NDT-22-7 for superior fruit size. Noteworthy variation was also observed in quality traits, particularly lycopene content and ascorbic acid, highlighting their potential for nutritional enhancement. Heritability estimates ranged from 39.82% (days to first fruit harvest) to 95.77% (lycopene content), suggesting strong genetic control over several traits. High genetic advance coupled with high heritability was observed for traits such as fruit yield per plant, lycopene content, and average fruit weight, indicating their suitability for direct phenotypic selection. Conversely, traits with lower heritability may require alternative breeding strategies. The findings emphasize the significant scope for genetic improvement in tomato and provide valuable insights for breeding programs aimed at developing high-yielding and nutritionally superior cultivars.
***Keywords*:** Genetic Variability, Nutritional Quality, ANOVA, Heritability, Genetic Advance.

Introduction

Feeding the rapidly expanding global population has emerged as one of the most critical challenges of the 21st century, as it exerts immense pressure on finite natural resources (Airoboman & Onobhayedo, 2022). The escalating demand for food, coupled with resource limitations, calls for urgent and innovative strategies to ensure sustainable food security (D'Esposito et al., 2021).

Tomato (*Solanum lycopersicum* L.) a member of the Solanaceae family, is widely grown and consumed around the world, earning its reputation as a vital component of the human diet and often labeled as a "protective food." It is one of the most significant vegetables used in processing industries. India currently holds the fourth position globally in terms of tomato cultivation area (Kumar *et al.,* 2023). South Mexico is the center of origin of tomato (Campos *et al.,* 2021).

According to the Food and Agriculture Organization of the United Nations (FAO), the global tomato production in 2022 was approximately 186.1 million metric tones, making it one of the most widely cultivated vegetable crops worldwide. China was the leading producer with 68.2 million tones, followed by India with 20.7 million tones, and other major contributors including Turkey, the United States, and Egypt. In India, tomato is cultivated extensively across various agro-climatic zones and holds significant importance in both fresh market and processing sectors (FAO, 2024).

The evaluation of tomato germplasm is essential for the agronomic improvement and genetic advancement of the crop, both under current and future cultivation scenarios (Ramzan *et al.,* 2014). Tomato yield is a quantitatively inherited trait influenced by multiple genes and is highly susceptible to environmental fluctuations (Wang *et al.,* 2021). To enhance yield performance, plant breeders have increasingly utilized advanced hybridization strategies aimed at developing high-yielding tomato cultivars.

Genetic variability parameters, including heritability (h^2) and genetic advance (GA), are essential biometric tools for quantifying population diversity and enabling effective selection in crop improvement programs (Akhter *et al.,* 2021). These metrics are particularly significant in evaluating tomato germplasm for targeted genetic enhancement through systematic breeding strategies. In this context, (Javed *et al.,* 2022) reported elevated phenotypic and genotypic coefficients of variation (PCV and GCV) for yield and related traits in tomato genotypes, highlighting the crucial role of genetic variability in guiding breeding decisions. Conventional breeding methods have long been utilized in tomato to generate genetic variability, which is a key factor in the success of breeding programs aimed at developing high-yielding genotypes. The effectiveness of these strategies is largely determined by the magnitude and nature of variability in yield-contributing traits. Therefore, estimating genetic parameters such as PCV, GCV, broad-sense heritability (h^2), and genetic advance (GA%) is crucial for making informed selection decisions. The ultimate goal in tomato breeding is to develop varieties with superior yield potential.

Materials and Methods

Experimental Site and Conditions

The experiment was conducted during the autumn-winter season of 2023–24 at the Main Experimental Research Farm, College of Horticulture, ANDUA&T, Kumarganj, Ayodhya, Uttar Pradesh, India (24.56°N, 81.84°E; 113 m AMSL). The site experiences a humid subtropical climate with ~1200 mm annual rainfall. During the crop period, temperatures ranged from 5.3°C to 40.9°C. The soil was sandy loam, slightly alkaline (pH 8.5), and low in organic matter.

Plant Material and Experimental Design

Twenty-five tomato genotypes, comprising released varieties, breeding lines, landraces and a check Kashi Aman with diverse traits, were obtained from ANDUA&T, Kumarganj, Ayodhya. The trial followed a randomized block design (RBD) with three replications. Each plot consisted of two rows 60 cm apart with plants spaced at 45 cm within rows. Observations were taken on 5 plants in each replication. Standard agronomic practices were uniformly followed to ensure optimal growth.

Statistical Analysis

Analysis of variance (ANOVA) was performed as per (Panse and Sukhatme 1967). Genotypic and phenotypic coefficients of variation (GCV, PCV) were calculated following (Burton and Devane 1953). Broad-sense heritability (h^2) was estimated using the method of (Weber and Moorthy 1952), and genetic advance as percent of mean was assessed based on (Johnson *et al.,* 1955).

Results and Discussion

The present study assessed the extent of genetic variability, heritability, and genetic advance among 25 tomato genotypes for 16 quantitative traits. The data were derived from ANOVA, mean performance, and genetic variability analyses (Tables 1-3), and were supplemented by graphical illustrations to visualize genotypic differences (Figure 1-3).

Analysis of variance (ANOVA)

The ANOVA revealed highly significant differences among the 25 tomato genotypes for all sixteen traits, as indicated by the treatment mean squares (Table 1). This confirms the presence of substantial genetic variability in phenological, morphological, quality, and yield traits, offering a strong foundation for effective selection and improvement in tomato breeding.

Trait-Wise Assessment of Genotypic Means

The mean performance of 25 tomato genotypes, including the check variety 'Kashi Aman', exhibited wide variability across all evaluated traits (Table 2).

Phenological traits showed marked differences. Days to 50% flowering ranged from 31.33 days (NDT-22-10) to 46.67 days (NDT-22-1 and NDT-22-26), with a mean of 40.76 days. Early flowering genotypes are advantageous as they tend to mature earlier, thereby escaping several abiotic stresses that commonly affect crop performance. Such genotypes are often associated with high yield potential, which is influenced by a combination of vigorous early vegetative growth, efficient nutrient and water use, stable photosynthetic and respiratory activity, greater biomass accumulation before anthesis, and effective mobilization of assimilates toward seed development. These integrated physiological and metabolic traits ultimately contribute to enhanced yield performance (Shavrukov *et al.,* 2017). Similarly, days to first fruit harvest varied from 67.33 days (NDT-22-12) to 85.67 days (NDT-22-26), with an average of 78.25 days, reflecting variability in crop maturity duration.

Vegetative traits also exhibited significant variation. Plant height ranged from 54.32 cm (NDT-22-29) to 91.78 cm (NDT-22-20), with a mean height of 73.82 cm. The number of primary branches per plant ranged between 3.27 (NDT-22-25) and 7.30 (NDT-22-20), averaging 5.07 branches. These differences in vegetative growth highlight the diversity in plant architecture, which can influence canopy development and light interception. The results obtained are in agreement with the findings of (Pradeep Kumar *et al.,* 2001) and (Gonzalez-Cebrino *et al.,* 2011).

Fruit morphological traits demonstrated wide variability. Polar fruit diameter ranged from 3.02 cm (NDT-22-24) to 6.79 cm (NDT-22-10), with a mean of 4.70 cm, while equatorial diameter ranged from 3.15 cm (NDT-22-22) to 6.52 cm (NDT-22-15), averaging 4.60 cm. Pericarp thickness varied from 2.57 mm (NDT-22-23) to 5.73 mm (NDT-22-27), with a mean of 3.72 mm. The number of locules per fruit ranged from 2.00 (in genotypes like NDT-22-9,-10, -13, -14, -17, -25) to 5.67 (NDT-22-20), with a mean of 3.69. These variations highlight potential targets for fruit firmness, structure, and processing quality.

Yield-contributing traits were notably diverse. Average fruit weight ranged from 31.53 g (NDT-22-24) to 80.20 g (NDT-22-7), with a mean of 60.76 g. The number of fruits per plant ranged from 15.67 (NDT-22-17) to 26.78 (Kashi Aman), averaging 21.32 fruits. Fruit yield per plant varied between 0.68 kg (NDT-22-24) and 1.94 kg (NDT-22-12), with a mean of 1.32 kg. Fruit yield per plot ranged from 4.13 kg (NDT-22-16) to 10.67 kg (NDT-22-13), averaging 8.16 kg. Fruit yield per hectare ranged from 114.76 q/ha (NDT-22-16) to 291.69 q/ha (NDT-22-1), with a mean of 231.68 q/ha, reflecting substantial yield potential among genotypes. The results obtained are in agreement with the findings of (Singh et al., 2010), (Pemba sherpa *et al.,* 2014) and (Venkadeswaran *et al.,* 2020).

Quality attributes also showed meaningful variation. TSS content ranged from 3.52°Brix (NDT-22-25) to 6.22°Brix (NDT-22-20), with a mean of 4.94°Brix. Ascorbic acid content varied between 12.54 mg/100g (NDT-22-29) and 23.68 mg/100g (NDT-22-16), averaging 17.71 mg/100g. Lycopene content ranged from 2.78 mg/100g (NDT-22-20) to 6.46 mg/100g (NDT-22-16), with a mean of 4.80 mg/100g. These findings indicate the nutritional richness and quality differentiation among the genotypes.

Overall, genotypes such as NDT-22-1 (high yield potential) and NDT-22-7 (large fruit size) emerged as promising candidates for future breeding programs. The observed phenotypic diversity provides valuable resources for hybridization and trait-specific improvement.

Heritability

Broad-sense heritability (h^2) estimates (Table 3) varied considerably across traits, reflecting differences in genetic control. An effective breeding program to improve quantitative traits needs reliable h^2 estimates (Mohamed *et al.,* 2012).

Heritability values ranged from 39.82% for days to first fruit harvest to 95.77% for lycopene content. Traits such as lycopene content (95.77%), fruit yield per hectare (94.48%), average fruit weight (93.32%), fruit yield per plot (91.56%), primary branches per plant (92.80%), pericarp thickness (91.48%), ascorbic acid (90.84%), equatorial diameter (90.38%), and locules per fruit (90.33%) recorded heritability above 90%, suggesting strong genetic control with minimal environmental influence. These traits showed a higher magnitude of PCV than those of their GCV, showing the more substantial impact of the environment on the appearance of that trait (Kuru Dosegnaw, 2021; Kulus, 2022).

Moderately high heritability (70–90%) was observed for polar diameter (89.38%), fruit yield per plant (87.63%), TSS content (86.06%), fruit per plant (83.49%), plant height (74.42%), and days to 50% flowering (75.60%), indicating that both genetic and environmental factors influence trait expression. Selection for these traits can be effective under stable environments.

In contrast, days to first fruit harvest showed relatively low heritability (39.82%), indicating a higher influence of environmental variability. For such traits, improvement may require multi-location trials and indirect selection strategies.

Genetic Advance and Prospects for Selection Gain

Genetic advance as a percentage of the mean (GA %) (Table 3) is an essential biometric parameter that helps to determine the effectiveness and potential of selection in a breeding program (Pooja *et al.,* 2022). A high magnitude of genetic advance, when coupled with high heritability estimates, provides a more dependable prediction of genetic gain through selection (Eppakayala *et al.,* 2021).

In the present study, locules per fruit (64.37%), fruit yield per plant (56.53%), fruit yield per hectare (52.42%), fruit yield per plot (50.13%), average fruit weight (47.54%), primary branches per plant (45.77%), and lycopene content (45.63%) showed higher genetic advance as a % of the mean coupled with high h^2, which is more valuable than h^2 alone in predicting the resultant effects during the selection of the best genotype (Shankar *et al*., 2013). Higher genetic advance with a higher h^2 for average fruit weight (g) strongly confirmed that additive gene action is present, and the selection of genotypes for the improvement of average fruit weight (g) would be highly effective (Mahebub *et al.,* 2021).

Moderate GA% values were observed for pericarp thickness (41.82%), equatorial diameter (37.01%), polar diameter (35.69%), and ascorbic acid content (33.74%). Traits with moderate genetic advance coupled with the higher h^2 indicated the need for single plant selection to improve the genotypes.

Conversely, days to 50% flowering (19.52%), plant height (19.35%), TSS content (28.13%), fruits per plant (26.33%), and days to first fruit harvest (6.90%) exhibited lower GA% despite moderate to high heritability. The further crossing is obligatory to create desired variations if both components are low in traits (Behera *et al.,* 2020).

Contribution of Traits to Genetic Divergence

Figure 3 illustrates the percentage contribution of various quantitative traits to the total genetic divergence among 25 tomato genotypes. Days to 50% flowering contributed the most (9.47%), followed by days to first fruit harvest (8.90%), and plant height (8.42%), indicating their significant role in genotype differentiation. Yield-related traits such as fruit yield per plant (7.95%), fruit yield per plot (7.72%), and fruit yield per hectare (6.06%) also exhibited notable contributions. Additional influential traits included number of locules per fruit (7.18%), number of primary branches (6.26%), polar diameter (6.30%), equatorial diameter (5.63%), pericarp thickness (5.30%), number of fruits per plant (5.10%), and average fruit weight (5.06%). Traits with relatively lower contributions included ascorbic acid content (4.86%), lycopene content (3.09%), and TSS content (2.68%). These results suggest that traits with higher contributions should be prioritized in selection and breeding programs aimed at improving yield and related characteristics in tomato.

Conclusion

The present investigation revealed significant genetic variability among 25 tomato genotypes for yield and quality traits, underscoring their potential for genetic improvement. Traits such as fruit yield per plant, average fruit weight, locules per fruit, and lycopene content, which exhibited high heritability coupled with high genetic advance, are governed by additive gene action and can be effectively improved through direct selection. For traits with lower heritability and genetic advance, alternative breeding strategies like recurrent selection and hybridization may be more suitable. The identified superior genotypes offer valuable genetic material for developing high-yielding and nutritionally enriched tomato cultivars.

Table 1 : Analysis of variance (ANOVA)

S. No.	Character	Mean sum of squares		
		Replication (df = 2)	Treatment (df = 24)	Error (df = 48)
1.	Days to 50% Flowering	0.21	65.53**	6.36
2.	Days to First Fruit Harvest	3.36	77.81**	26.07
3.	Plant Height (cm)	4.22	216.03**	22.21
4.	No. of Primary Branches/Plant	0.06	4.22**	0.11
5.	Polar Fruit Diameter (cm)	0.002	2.316**	0.088
6.	Equatorial Fruit Diameter (cm)	0.010	2.344**	0.080
7.	Pericarp Thickness (mm)	0.047	1.931**	0.058
8.	No. of Locules/Fruit	0.214	4.581**	0.158
9.	Average Fruit Weight (g)	15.52	647.00**	15.07
10.	No. of Fruits/Plant	0.02	28.45**	1.76
11.	TSS Content (°Brix)	0.003	1.669**	0.086
12.	Ascorbic Acid (mg/100g)	0.01	28.72**	0.93
13.	Lycopene Content (mg/100g)	0.039	3.588**	0.052
14.	Fruit Yield/Plant (kg)	0.019	0.468**	0.021
15.	Fruit Yield/Plot (kg)	0.47	13.32**	0.40
16.	Fruit Yield (q/ha)	49.49	11250.78**	214.91

*, ** significant at 5% and 1% level, respectively

Table 2 : Mean performance of 25 tomato genotypes for 16 quantitative characters

S.N.	Genotypes	Days to 50% flowering	Days to first fruit harvest	Plant height (cm)	No. of primary branches/plant	Polar fruit diameter (cm)	Equatorial fruit diameter (cm)	Pericarp thickness (mm)	No. of locules /fruit	Average fruit weight (g)	No. of fruits /plant	TSS content (Brix)	Ascorbic acid (100mg/fruit)	Lycopene content (mg/100gm)	Fruit yield/plant (Kg)	Fruit yield/plot (kg)	Fruit yield (q/ha)
1	NDT-22-1	46.67	84.33	76.84	6.82	4.72	5.34	3.55	4.67	77.67	23.81	4.95	16.73	4.57	1.85	10.50	291.69
2	NDT-22-2	43.33	79.67	69.78	5.91	3.95	3.43	3.12	5.33	79.85	22.16	5.68	14.17	5.39	1.77	9.30	269.50
3	NDT-22-3	34.00	69.67	75.14	4.74	4.80	4.20	4.18	5.00	49.60	25.14	4.37	16.75	4.75	1.25	8.09	224.83
4	NDT-22-4	45.33	83.33	83.77	7.09	4.28	4.89	2.80	3.67	61.13	21.00	4.17	19.06	6.28	1.23	10.56	285.46
5	NDT-22-5	39.33	72.33	74.02	6.66	4.87	5.15	3.07	4.33	58.00	24.70	4.68	22.58	3.53	1.43	9.66	281.27
6	NDT-22-7	32.67	70.33	70.09	3.78	5.27	4.88	4.04	4.00	80.20	20.87	5.45	15.57	6.29	1.67	10.13	281.50
7	NDT-22-9	41.67	78.67	76.02	4.51	5.92	3.76	2.78	2.00	68.53	23.74	5.20	19.29	4.74	1.63	9.27	274.53
8	NDT-22-10	31.33	72.67	81.58	6.07	6.79	4.06	3.29	2.00	76.62	21.23	3.80	20.40	3.55	1.62	9.36	283.31
9	NDT-22-12	32.33	67.33	75.54	6.33	4.47	4.18	4.09	4.33	78.00	24.83	5.90	14.69	4.46	1.94	10.37	288.08
10	NDT-22-13	43.00	79.67	81.08	4.38	6.59	3.64	2.69	2.00	66.33	26.63	3.97	15.56	2.87	1.77	10.67	287.15
11	NDT-22-14	34.33	70.33	87.50	5.11	5.66	3.85	3.64	2.00	47.27	18.76	3.80	18.00	5.51	0.89	6.87	177.69
12	NDT-22-15	40.67	80.67	68.92	6.16	4.94	6.52	4.66	5.33	63.93	20.91	4.70	21.97	4.76	1.34	8.37	223.26
13	NDT-22-16	44.67	82.00	72.37	4.33	4.28	5.23	3.77	3.00	44.80	18.14	4.68	23.68	6.46	0.85	4.13	114.76
14	NDT-22-17	39.33	79.33	69.10	4.05	4.19	4.89	3.75	2.00	48.67	15.67	5.70	19.69	3.55	0.76	7.63	214.94
15	NDT-22-20	43.67	82.33	91.78	7.30	5.21	6.09	5.30	5.67	59.27	18.10	6.22	13.34	2.78	1.07	5.73	148.24
16	NDT-22-21	37.67	75.33	71.41	5.03	4.56	5.14	4.23	4.67	46.53	16.97	4.78	18.16	3.47	0.79	4.90	136.12
17	NDT-22-22	45.33	82.33	68.51	4.38	3.67	3.15	4.12	4.33	41.40	22.46	5.22	13.42	6.14	0.93	4.63	122.00
18	NDT-22-23	41.00	77.33	65.72	3.56	3.77	3.43	2.57	3.00	43.13	17.92	4.58	17.05	4.64	0.84	5.40	163.32
19	NDT-22-24	44.33	82.67	80.03	4.86	3.02	3.63	2.73	3.33	31.53	19.56	5.18	18.49	4.13	0.68	5.17	140.83
20	NDT-22-25	39.67	78.00	75.92	3.27	4.38	4.53	3.60	2.00	45.53	23.12	3.52	16.58	5.56	1.05	8.53	236.96
21	NDT-22-26	46.67	85.67	56.68	3.77	4.96	4.56	4.38	3.00	76.73	23.06	5.62	23.29	4.83	1.77	10.03	278.73
22	NDT-22-27	40.00	78.33	66.88	4.04	4.81	5.16	5.73	4.33	75.15	20.75	4.38	18.40	6.40	1.63	10.27	285.21
23	NDT-22-28	43.00	83.00	72.28	5.24	3.88	4.85	3.12	5.33	60.93	18.49	5.33	17.97	4.52	1.13	6.94	280.55
24	NDT-22-29	43.33	80.67	54.32	3.90	4.68	6.02	4.21	4.00	79.20	18.21	5.52	12.54	5.24	1.44	8.76	258.38
25	Kashi Aman (check)	45.67	80.33	80.31	5.58	3.91	4.35	3.62	3.00	58.87	26.78	6.00	15.37	5.52	1.58	8.77	243.63
	Mean	**40.76**	**78.25**	**73.82**	**5.07**	**4.70**	**4.60**	**3.72**	**3.69**	**60.76**	**21.32**	**4.94**	**17.71**	**4.80**	**1.32**	**8.16**	**231.68**
	Min	31.33	67.33	54.32	3.27	3.02	3.15	2.57	2.00	31.53	15.67	3.52	12.54	2.78	0.68	4.13	114.76
	Max	46.67	85.67	91.78	7.30	6.79	6.52	5.73	5.67	80.20	26.78	6.22	23.68	6.46	1.94	10.67	291.69
	SE(d)	2.06	4.17	3.85	0.27	0.24	0.23	0.20	0.32	3.17	1.08	0.24	0.79	0.19	0.12	0.52	11.97
	C.D.	4.15	8.41	7.76	0.54	0.49	0.47	0.40	0.65	6.39	2.19	0.48	1.59	0.38	0.24	1.04	24.14
	C.V.	6.19	6.53	6.38	6.42	6.32	6.16	6.48	10.76	6.39	6.22	5.92	5.46	4.76	11.02	7.72	6.33

Table 3 : Estimation of phenotypic and genotypic coefficients of variation, heritability, genetic advance and genetic gain for various traits in tomato

Character	Mean	Min	Max	GCV (%)	PCV (%)	Heritability (H^2%)	Genetic Advance	Genetic Advance as % of Mean
Days to 50% flowering	40.76	31.33	46.67	10.9	12.53	75.6	7.95	19.52
Days to first fruit harvest	78.25	67.33	85.67	5.31	8.41	39.82	5.4	6.9
Plant height (cm)	73.82	54.32	91.78	10.89	12.62	74.42	14.28	19.35
Primary branches/plant	5.07	3.27	7.3	23.06	23.94	92.8	2.32	45.77
Polar fruit diameter (cm)	4.7	3.02	6.79	18.32	19.38	89.38	1.68	35.69
Equatorial fruit diameter (cm)	4.6	3.15	6.52	18.9	19.88	90.38	1.7	37.01
Pericarp thickness (mm)	3.72	2.57	5.73	21.23	22.19	91.48	1.56	41.82
No. of locules/fruit	3.69	2	5.67	32.88	34.59	90.33	2.38	64.37
Average fruit weight (g)	60.76	31.53	80.2	23.89	24.73	93.32	28.88	47.54
No. of fruits/plant	21.32	15.67	26.78	13.99	15.31	83.49	5.61	26.33
TSS content (°Brix)	4.94	3.52	6.22	14.72	15.87	86.06	1.39	28.13

Ascorbic acid (mg/100g)	17.71	12.54	23.68	17.18	18.03	90.84	5.97	33.74
Lycopene content (mg/100g)	4.8	2.78	6.46	22.63	23.13	95.77	2.19	45.63
Fruit yield/plant (kg)	1.32	0.68	1.94	29.32	31.32	87.63	0.74	56.53
Fruit yield/plot (kg)	8.16	4.13	10.67	25.43	26.58	91.56	4.09	50.13
Fruit yield (q/ha)	231.68	114.76	291.69	26.18	26.93	94.48	121.45	52.42

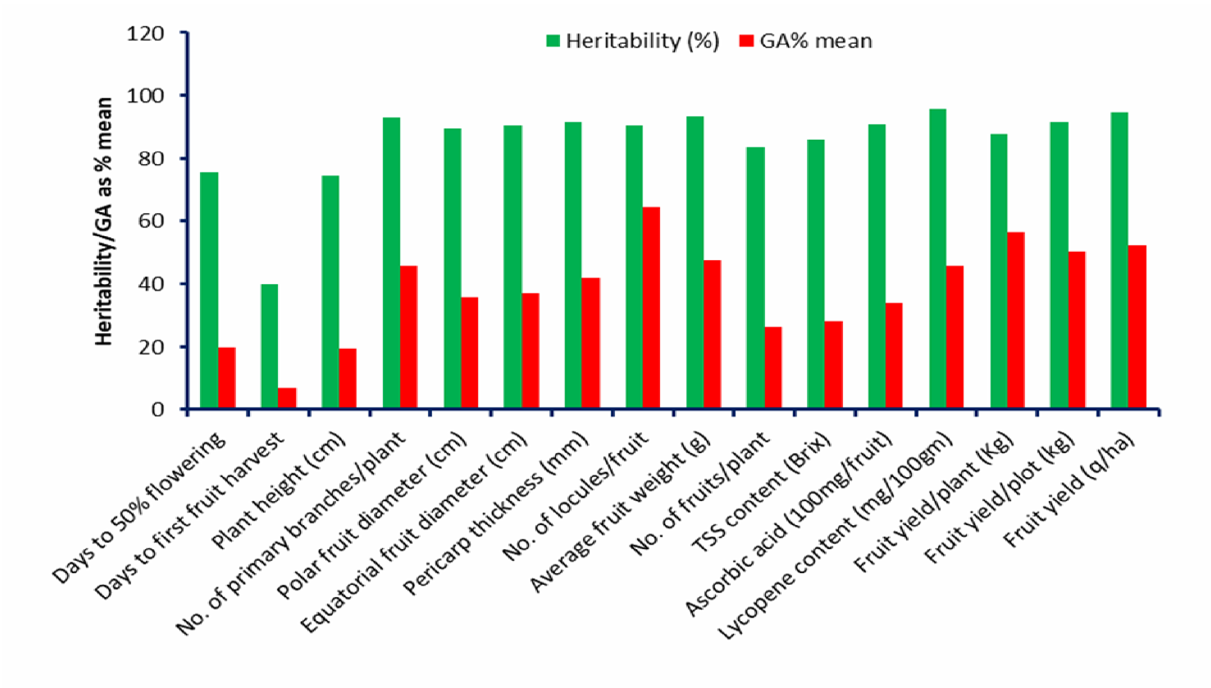

Fig. 1: Bar graph showing Heritability (%) and Genetic Advance as % of mean for quantitative traits in tomato genotypes.

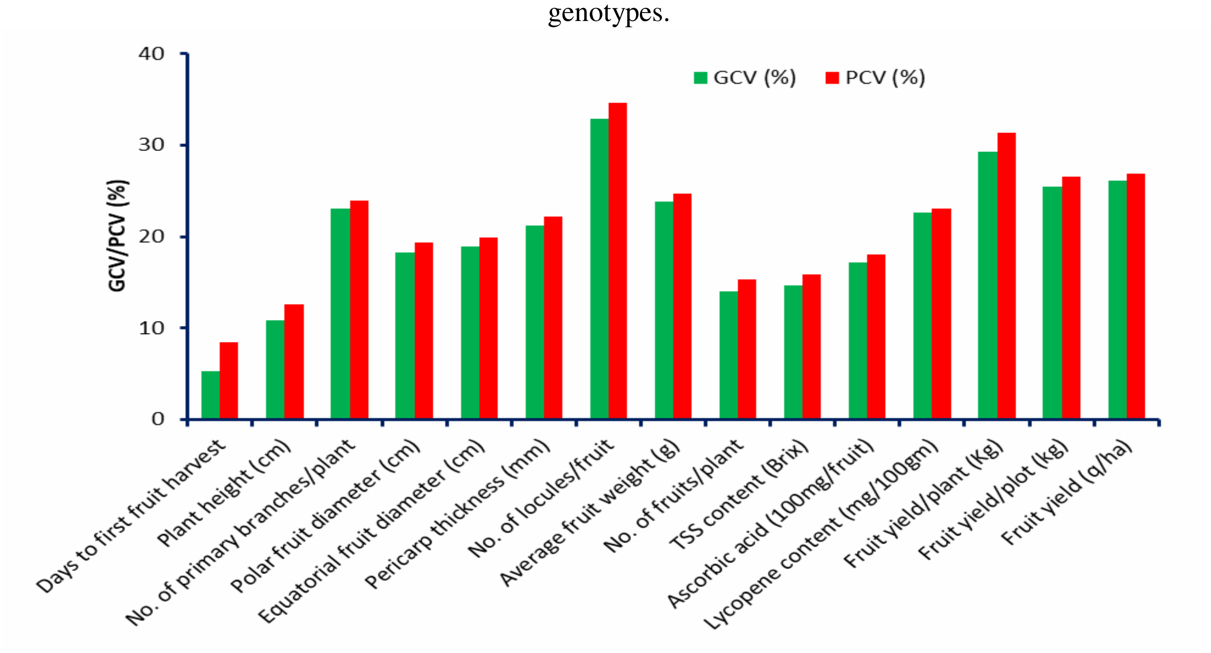

Fig. 2: Bar graph showing Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) for different traits in tomato genotypes.

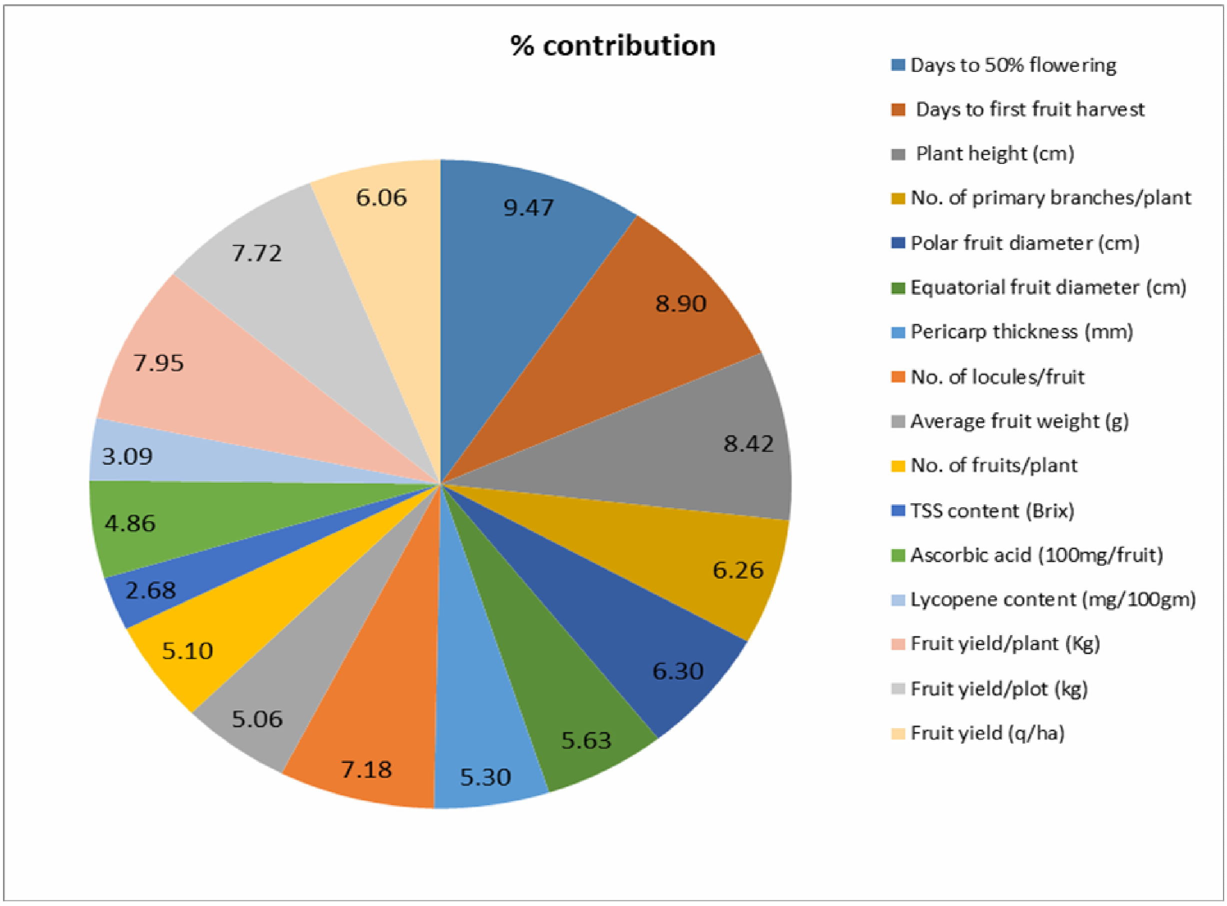

Fig. 3: Pie chart depicting percent contribution of each quantitative trait to genetic divergence in tomato genotypes.

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