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Genetic variability studies for qualitative and quantitative traits in tomato (*Solanum lycopersicum* L.)

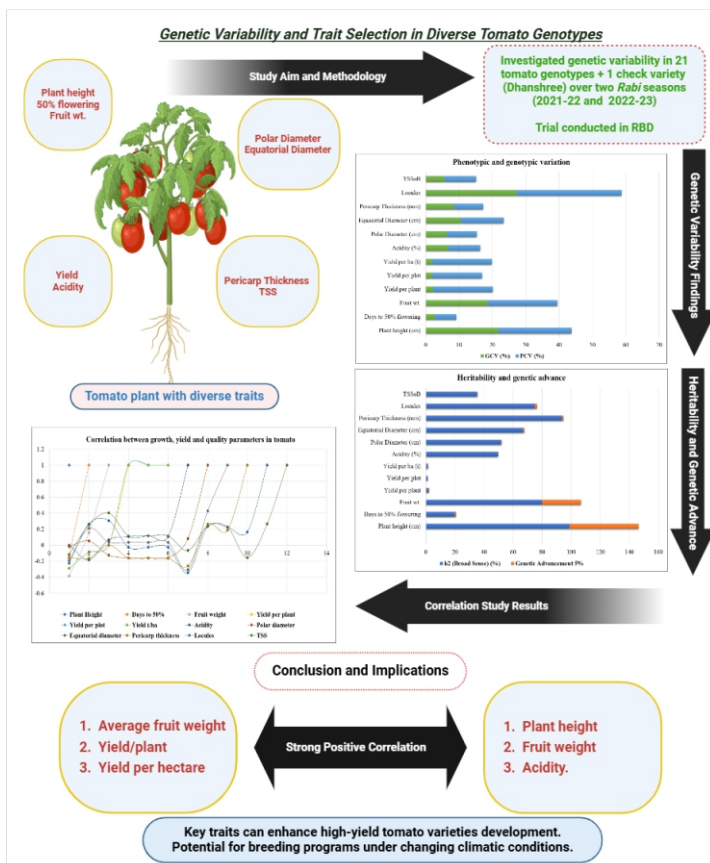
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## ABSTRACT

This study investigated the variability of 21 tomato genotypes, along with a check variety Dhanshree, for various growth, yield, and quality parameters over two growing seasons (Rabi 2021-22 and Rabi 2022-23) using a Randomized Block Design (RBD) with three replications. The findings revealed that phenotypic variation was generally greater than genotypic variation for most traits. High heritability estimates were noted for plant height, fruit weight, pericarp thickness, equatorial diameter, and number of the locules per fruit. The study faced challenges in accurately differentiating genetic variation from environmental influences due to the narrow genetic base of certain genotypes and fluctuating environmental conditions during the seasons. Despite these challenges, the research successfully identified key traits with high heritability and genetic variability. These results indicated that direct selection based on these traits could effectively identify superior tomato genotypes, providing valuable insights into genetic variability and heritability within the studied population.

**Keywords:** Heritability, tomato, traits, variability, correlation, genotype, and yield



## Graphical Abstract

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## INTRODUCTION

According to botanical research, the tomato (*Solanum lycopersicum* L.), a member of the *Solanaceae* family [4] originated in Peru, Ecuador, and other parts of South America [36, 21, 40]. Although it is a fruit that resembles a berry-type in nature, culinary professionals often use it as a vegetable because of its adaptability when using it for both fresh and cooked purposes [13].

In its raw state, it is high in nutrients and contains vitamins A, B, and C. It is primarily processed to manufacture ketchup and other foods [6]. In the human diet, tomato fruit provides a important source of vitamins B<sub>1</sub> and B<sub>6</sub> [41].

It also provides lycopene, which has beneficial health effects, in a novel way [7, 24]. To meet the needs of a large population, the impact on the environment and increasing tomato yield have been major areas of research worldwide [1]. Tomatoes are also farmed for specific processing purposes. Given the importance of tomato as an appealing vegetable in both the domestic and export consumer markets, it is critical to increase its productivity and desirable traits through gene exploitation [12, 16]. In this context, it is critical to identify traits and characteristics relevant to the improvement program.

Yield is a complex variable influenced by polygenic traits and their interactions. A study presents an association concept that could be used to develop selection techniques for varietal assessment of distinct growth and yield traits in order to improve yield and related components. For a successful selection improvement program, it is critical to assess the relative degree of association between different yield characters.

The appropriate understanding, combined with a wide range of genotype diversity, aids in identifying the most desirable genotypes, which are determined by the nature and breadth of genetic variability, as well as the degree of transmissibility of desirable characteristics [17]. When starting a prudent plant breeding program, a plant breeder must consider the effectiveness of selection into the degree of variability and

heritability contained in a crop species' gene pool for desirable traits. As a result, efforts were made to investigate the genetic diversity and heritability of numerous horticultural traits in tomato genotypes.

Genetic variability mechanisms such as  $h^2$  and genetic advance (GA) are critical biometric instruments for assessing population variation in order to make selections [2] and assessing tomato germplasms for improvement across a range of breeding systems [14]. Genetic variability influences plant selection, as evidenced by the higher PCV and GCV for yield and yield-related traits in tomatoes [20]. [5] Emphasise the need of understanding both the phenotypic and genotypic elements of tomato inheritance.

## Material and Methods

The current study was conducted in the Research Field, Tomato Improvement Scheme, MPKV, Rahuri, during *Rabi-2021-22* and *Rabi-2022-23*, with three replications of a check variety (Dhanshree) and 21 possible genotypes using Randomized Block Design (RBD). In this study, the following parameters were examined: plant height, days until 50% flowering, number of fruits per plant, fruit weight (g), yield per plant (kg), yield per plot (kg), yield per ha (t/ha), acidity (%), polar, equatorial diameter (cm), number of locules, pericarp thickness (mm) and total soluble solids (TSS).

**Table 1: List and source of potential genotypes in tomato**

Sr. No.	Accession ID Code	Country of Origin	Population type	Color of fruit	Fruit shape	Year of collection
1.	RHRT-20-01	India	Indet	Red	Round	2020
2.	RHRT-20-02	India	Semi. Indet	Red	Round	2020
3.	RHRT-20-03	India	Det.	Red	Round	2020
4.	RHRT-20-04	India	Indt	Red	Round	2020
5.	RHRT-20-05	India	Indet	Red	Round	2020
6.	RHRT-20-06	India	Indte	Red	Round	2020
7.	RHRT-20-07	India	Semi. indet	Red	Round	2020
8.	RHRT-20-08	India	Semi. indet	Red	Round	2020
9.	RHRT-20-09	India	Semi. indet	Red	Round	2020
10.	RHRT-20-10	India	Det.	Red	Round	2020
11.	RHRT-20-11	India	Semi. Det.	Red	Round	2020
12.	RHRT-20-12	India	Semi. indet	Red	Round	2020
13.	RHRT-20-13	India	Det.	Red	Round	2020
14.	RHRT-20-14	India	Semi. indet	Red	Round	2020
15.	RHRT-20-15	India	Det.	Red	Round	2020
16.	RHRT-20-16	India	Indet	Red	Round	2020
17.	RHRT-20-17	India	Det.	Red	Round	2020
18.	RHRT-20-18	India	Det.	Red	Round	2020
19.	RHRT-20-19	India	Semi. det	Red	Round	2020
20.	RHRT-20-20	India	Det.	Red	Round	2020
21.	RHRT-20-21	India	Det.	Red	Round	2020
	Dhanshree (c)	India	Det.	Orange Red	Round	--

A fundamental understanding of gene function is required for the crop development program to enhance certain attributes in the current study. The sandy loam soil at the testing site has excellent water-holding capacity and drainage. Before flowering, ten competitive plants from each entry in each replication were randomly selected, tagged, and several attributes were observed. The average values for these attributes were then employed in the statistical analysis.

The ANOVA was conducted using the procedures described by Panse and Sukhatme (1985) [34]. Based on an estimate of genotypic and phenotypic variation, the genotypic and phenotypic coefficients of variance were determined in accordance with Burton (1952) [10]. The broad sense heritability was estimated using Johnson's (1955) approach [22].

The broad sense heritability ( $h^2$ ) was estimated using the approach provided by Weber and Moorthy in 1952 [47]. Johnson *et al.* (1955) divided the genetic advance as a percentage of the mean into three categories: low, moderate, and high [22]. The statistical software OPSTAT Sheoran *et al.* (1998) was used for all statistical analyses [43]. Using mean data, variance analysis for several variables was performed to assess genetic variability between genotypes. Using Burton's formula Barton and DeVane 1950, the phenotypic and genotypic

coefficients of variability for each character were obtained [8].

## Results and Discussion

The current study examined genetic variability in tomatoes for both qualitative and quantitative features. Significant changes were observed in yield, yield-contributing characteristics, and quality traits. Plant height, equatorial diameter, pericarp thickness, and average fruit weight differed less between GCV and PCV, indicating that environmental factors had little effect on these traits' phenotypic expression (Haydar *et al.*, 2007). As a result, selection based on these features' phenotypic performance would be efficient in achieving significant genetic improvement. For the majority of the traits studied, the (PCV) Phenotypic Coefficient of Variation estimate was greater than the (GCV) Genotypic Coefficient of Variance (Table 2).

Plant height: Significant differences were found between the PCV (21.94%) and GCV (21.82%) [18].

Days to 50% flowering: This is an indicator of earliness and determines yield potential [42]. The PCV (6.37) is higher than the GCV (2.85), as was observed for all of the characters studied. Flowering in tomatoes always affects reproductive success in plants and has a significant impact on tomato yield. The fruit weight determines the crop's yield potential. Variability was observed in the phenotypic and genetic composition of the genotypes under study [37, 3].

Table 2: Analysis of variance (Mean Sum of Squares) for different characters in tomato

Sr. No.	Traits	Replication	Genotype	Error
1.	Plant height	0.34	14608.28**	105.17
2.	Days to 50% flowering	2.60	46.80**	53.40
3.	Fruit weight	102.42	6258.70**	965.63
4.	Yield per plant	0.26	1.00**	2.11
5.	Yield per plot	342.29	1311.60**	2730.05
6.	Yield per hectare	242.45	929.52**	1934.38
7.	Acidity	0.011	0.043	0.02
8.	Polar Diameter	2.47	3.57	1.69
9.	Equatorial Diameter	0.00	10.81**	3.06
10.	Pericarp Thickness	0.16	6.59	0.28
11.	Locules	3.20	24.30**	4.80
12.	TSS	0.05	2.57	1.94

\*\*Significant at 5% level of significance

**Yield per plant:** The (GCV) genotypic coefficient of variation was lower than the (PCV) phenotypic coefficient of variation observed for yield per plant (2.31, 17.85), indicating the presence of significant hereditary variability and confirming efficient trait selection. In variability studies, yield-contributing characters such as fruit weight, number of fruits per plant, and earliness positively increase yield levels [30, 3, 38]. Differences in genetic variability among genotypes were observed in yield per plot, as well as yield attributing characters.

The phenotypic coefficient of variation is greater than the genotypic coefficient of variation (14.96 vs. 1.97) [28, 42], indicating that such traits may be considered reliable selection indicators and are subject to additive gene effects.

**Yield tonne per hectare:** An increase in yield directly improves the variability traits, which are associated with number of fruits per plant, fruit weight and earliness at the genotypic level. For the yield tonne per hectare, it was discovered that the phenotypic coefficient of variation was greater than the genotypic coefficient of variation. (17.85, 2.04) [15, 42]. The results revealed that the PCV values were higher than the GCV values, indicating that the characters are more sensitive to changes in their surroundings. Tomato yield is a multigenic trait heavily influenced by environmental factors [46]. As a result, genetic selection based on these characters' phenotypic performance would be beneficial in significantly increasing these traits in genotypes [3, 11].

**Acidity:** Increased acidity is a desirable cooking quality. The current findings revealed that the phenotypic coefficient of variation was greater than the genotypic coefficient of variation for both (9.60, 6.77). TSS and acidity interact to produce flavour and taste in tomatoes, and this interaction varies by maturity stage [44].

**Polar and equatorial diameter:** For the tomato genotypes studied, the phenotypic coefficient of variation (8.94 & 6.43, 12.89 & 10.54) outweighed the genotypic coefficient of variation for the parameters polar and equatorial diameter. Its wide heritability ranges (51.80 & 66.90) revealed differences in the genotype's genetic diversity [44].

**Pericarp thickness, locules and TSS:** Among the several genotypes under investigation, the character's degree of genetic variability differs. It was observed that for pericarp thickness (8.80, 8.52), number of locules (31.45, 27.29), and TSS (9.50, 5.65), respectively, the phenotypic coefficient of variation (Table 3 fig. 1) was greater than the genotypic coefficient of variance [18].

**Heritability:** Evaluating heredity in conjunction with genetic advancement would be more effective in predicting the efficacy of selecting the best genotype. Heritability measurements are useful for predicting a genotype's response to selection. When breeders use heritability estimates, they can better allocate resources to select desired traits and maximise genetic gain with the least amount of time and effort. [22] divided heritability into three categories: low (less than 30%), medium (30-60%), and high (more than 60%). Plant height (98.93%), fruit weight (80.00%), equatorial diameter (66.90%), pericarp thickness (93.80%) and number of locules (75.00%) all indicated a broad sense of heredity (>60%) (Table 3 fig. 1). This suggested that simple selection for these traits could result in improvement. Days until 50% flowering, yield per plant, yield per plot, and yield per hectare all had a low heritability (0-30%). The low heritability implies that the environment had a greater influence on the expression of traits. As a result, progeny testing and family-based selection techniques are more effective and efficient for future improvement [39, 27, 31, 23, 29, 9].

**High heritability with high genetic advance:** A heritability estimate that takes genetic advancement into account is more precise and significant than one that considers each parameter separately. Plant height, fruit weight, and locule number were all calculated as percentages of the mean [26, 35, 33]. This suggested that the features were either additive gene effects or were simply inherited in nature and governed by a small number of key genes [27].

Furthermore, there is significant potential for improving essential traits through direct selection for plant height (98.93% and 44.71%), fruit weight (80.00% and 34.36%), and number of locules (75.0% and 48.77%). The percent mean of estimates for these characters indicated that they were less affected by environmental factors, implying that additive gene action dominates the expression of these characters (Table 3 fig. 1) [35, 33].

**Heritability and low genetic advance:** It was noted that the genetic progress and low heritability as a percentage above the mean was observed for days to 50 per cent flowering (20.06% and 2.63%), yield per plant (1.70 and 0.62), yield per plot (1.30% and 0.48%), yield per ha (1.30% and 0.48%), Acidity (49.80% and 9.85%), Polar diameter (51.80% and 9.54%), equatorial diameter (66.90% and 17.76%), pericarp thickness (93.80% and 17.02%), locules (75% and 48.77%), Total Soluble Solids (35.40% and 6.93%) the non-additive gene expression governs these characters [45, 23].

Table 3: Estimates of the genetic advancement, heritability, components of variation, mean and range for tomato growth, yield and quality parameters

Sr. No.	Traits	Range		General Mean	GCV (%)	PCV (%)	h2 (Broad Sense) (%)	Genetic Advancement 5%	Gen Adv as per cent Mean 5%
		Min	Max						
1.	Plant height	73.28	145.21	106.39	21.82	21.94	98.93	47.57	44.71
2.	Days to 50% flowering	28.00	32.00	30.20	2.85	6.37	20.06	0.79	2.63
3.	Fruit weight	44.52	97.86	78.39	18.65	20.86	80.00	26.9	34.36
4.	Yield per plant	1.63	2.21	1.90	2.31	17.85	1.70	0.62	0.79
5.	Yield per plot	68.60	79.63	68.54	1.97	14.96	1.30	0.01	0.48
6.	Yield ton per hectare	49.33	67.03	57.69	2.04	17.85	1.30	0.27	0.48
7.	Acidity	0.45	0.58	0.51	6.77	9.60	49.80	0.05	9.85
8.	Polar Diameter	4.50	5.60	4.94	6.43	8.94	51.80	0.47	9.54
9.	Equatorial Diameter	6.30	5.00	5.56	10.54	12.89	66.90	0.98	17.76
10.	Pericarp Thickness	4.90	6.48	5.73	8.52	8.80	93.80	0.97	17.02
11.	Locules	2.00	5.00	3.30	27.29	31.45	75.00	1.60	48.77
12.	TSS	3.97	4.78	4.30	5.65	9.50	35.40	0.29	6.93

Table 4: Estimation of correlation between growth, yield and quality characters in tomato

Characters	Plant height	Days to 50%	Fruit weight	yield/plot	yield/plant	Yield t/ha	Acidity	Polar dia.	Equatorial dia.	Pericarp thickness	Locules	TSS
Plant height	1											
Days to 50% flowering	-0.1273	1.00										
Fruit weight	-0.3854	0.1552	1.00									
Yield per plant	-0.2901	-0.0879	0.3897**	1.00								
Yield per plot	-0.2911	-0.0875	0.3918**	0.9999	1.00							
Yield ton per hectare	-0.2911	-0.0876	0.3919**	0.9999	1.00	1.00						
Acidity	0.3799**	-0.1841	0.0652	0.1071	0.1176	0.1076	1.00					
Polar diameter	-0.0187	0.0520	-0.1250	-0.1592	-0.1591	-0.1591	0.0823	1.00				
Equatorial diameter	-0.1913	0.2105	0.0371	0.0348	0.0338	0.0338	-0.3076	0.4275	1.00			
Pericarp thickness	-0.1584	-0.1631	-0.3773**	-0.1620	-0.1634	-0.1634	-0.2590	0.2632	0.1876	1.00		
Locules	-0.2249	0.2637	0.3060	-0.0267	-0.0264	-0.0264	-0.3443	0.2339	0.2239	0.1650	1.00	
TSS	-0.1166	0.2525	0.4024	0.1134	0.1138	0.1138	-0.066	0.2349	0.2258	-0.1566	0.2660	1.00

\*\* Significant at 5% level of significance

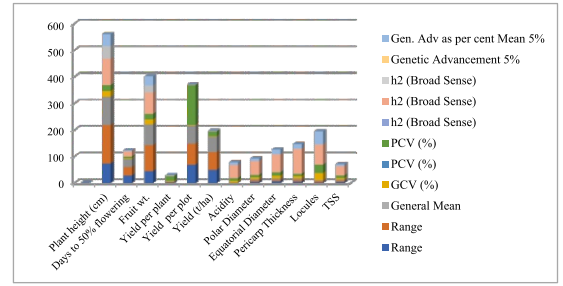


Fig. 1: Estimates of the genetic advance, heritability, components of variation, mean and range for tomato growth, yield and quality metrics in tomato.

For all yield-related parameters investigated, the mean sum of squares attributable to treatments was found to be highly significant at the 5% level of significance, indicating that the genotypes under study had a significant degree of variability. Fruit weight (0.1552), yield per plant (0.3897), yield per plot (0.9999), and yield tonne per hectare (0.9999) were all positively correlated with yield per plant (Table 4). It concludes that selection would be beneficial in increasing tomato yield under field conditions. Previous research has also demonstrated that selecting such traits in the intended direction increases tomato yield [32, 25].

**Conclusion**

The present research was carried to study the existence of hereditary variability for the quantitative, and qualitative traits among the diverse genotypes of tomato. These genotypes can be further tested to improve or develop genotypes to mitigate the suitability for varying weather conditions. The genetic enhancement of tomato crop needs to reveal the availability of inherited traits and genetic nature of genotypes. Due to the existence of wider genetic diversity present in genotypes, these genotypes can be improved by selection and hybridization program. Heritability governs the gene action nature among the genotypes resemblance to additive and non-additive action. A major role was played by additive gene action for effective selection. For some of the traits under investigation, the percentage of moderate to high GCV along with moderate to high heritability and genetic advancement clearly indicated the presence of dominant additive gene action. The results of the correlation analysis demonstrated a substantial positive association between the average fruit weight, acidity and increase in plant height, as well as yield per plant and yield ton per hectare. As a result, these traits can be recognized as key factors influencing tomato production. Both direct and indirect selection may be useful in developing tomato varieties with high yields so that breeding programs can be further enhanced through tomato selection.

**Future scope of the study**

The identified genetic variability among tomato

genotypes can guide breeding programs aimed at developing high-yielding and weather-resilient varieties. Traits with moderate to high GCV, heritability and genetic advancement can be targeted for selection and hybridization to enhance desirable characteristics. Additive gene action can be exploited for effective selection to improve quantitative and qualitative traits. Correlation analysis highlights key traits such as average fruit weight, plant height and yield per plant, which can serve as selection criteria for yield improvement. The findings can contribute to developing climate-resilient tomato varieties that ensure sustainable production under diverse environmental conditions. This study serves as a foundation for further research into the genetic enhancement of tomato using both direct and indirect selection approaches.

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**Authors' contribution:** The experiment was conceptualized and designed by A. V. Chandanshive, executed the experiment and performed data analysis. S. D. Gaikwad, P. N. Sonavane and D. R. Bankar wrote the manuscript under the supervision of A. V. Chandanshive.

**Research content:** The research content of the manuscript is original and has not been published elsewhere.

**Conflict of interest:** The authors declare no conflict of interest.

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