

ISSN Online: 2617-4707 NAAS Rating: 5.29 IJABR 2025; 9(7): 668-670 www.biochemjournal.com Received: 19-04-2025 Accepted: 22-05-2025

ISSN Print: 2617-4693

Awaneesh Pratap Singh

M.Sc. Student, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

CN Ram

Professor and Head, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

Ashish Kumar Singh

Assistant Professor,
Department of Vegetable
Science, Acharya Narendra
Deva University of Agriculture
& Technology, Kumarganj,
Ayodhya, Uttar Pradesh, India

Nimit Singh

Research Scholar, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya, Utter Pradesh, India

Himani Shukla

M.Sc. Student, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

Shivangini Paswan

M.Sc. Student, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

Corresponding Author: CN Ram

Professor and Head, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

Genetic evaluation for variability, heritability and genetic advance in tomato (Solanum lycopersicum L.) genotypes

Awaneesh Pratap Singh, CN Ram, Ashish Kumar Singh, Nimit Singh, Himani Shukla and Shivangini Paswan

DOI: https://www.doi.org/10.33545/26174693.2025.v9.i7i.4814

Abstract

Tomato (*Solanum lycopersicum* L.) a crop of significant importance in india, exhibits extensive genetic diversity, making it a prime candidate for genetic enhancement. The present study was conducted during the rabi season of 2023-2024 at the Vegetable Research farm Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, using 34 diverse tomato genotypes in a Randomized Block Design (RBD) with three replications. Significant differences among genotypes were observed for 12 quantitative traits, and 4 qualtitative traits, indicating the presence of substantial genetic variability. Traits such as lycopene content, no. of fruits per plant, no. of locule per fruit and fruit yield showed high genotypic and phenotypic coefficients of variation. High heritability estimates were recorded lycopene content, no. of fruit per plant, no. of locule per fruit, suggesting additive gene action and effectiveness of direct selection. Genotypes NDT-23-19 followed by NDT-23-1, NDT-23-3 were outperformed the standard check (Kashi Aman) in yield indicating their potential utility in future breeding programs aimed at yield enhancement. The results underscore the importance of exploiting genetic variability for the genetic improvement of tomato.

Keywords: Tomato, genetic variability, heritability, genetic advance, PCV, GCV, yield improvement

1. Introduction

"The tomato (Solanum lycopersicum L., 2n=2X=24) belongs to the genus Solanum and the family Solanaceae. It is vital source of nutrition due to its rich content of vitamins, minerals, proteins, and antioxidants (Ravi et. al., Kumar et. al. 2017) [8]. Tomatoes grow on 8.50 lakh hectares of land in India, yielding 208.2 lakh tons and 24.49 t/ha of productivity. With an area of 1.19 lakh hectares and a production of 34.98 lakh tons, Madhya Pradesh leads India, while Karnataka comes in second with an area of 0.78 lakh hectares and a production of 24.43 lakh tons. Tomato production in Uttar Pradesh is 9.40 lakh tons, with an area of 0.23 lakh hectares. (1st Advance estimate, Statistics, Ministry of Agriculture and Farmer welfare, Govt. of India, 2023-24). The plant's genetic composition and the growing environment have a major influence on the phenotypic expression of its characteristics. Additionally, any quantitative attribute's genetic variance includes both non-additive and additive variance, as well as dominance and epistasis (non-allelic interaction). Thus, using suitable parameters such as genotypic and phenotypic coefficient of variation, heritability, and genetic advancement, it becomes imperative to separate the observed phenotypic variability into its heritable and non-heritable components. Furthermore, the efficiency of selection can be predicted using genetic advancement. The degree of transmissibility of desirable traits and the type and extent of genetic variability determine how effective selection is. (Golani et al., 2007) [4].

2. Materials and Methods

The site of investigation was Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.), The experimental field had sandy loam soil, low in organic matter, nitrogen, medium in phosphorous, potash, and slightly alkaline in nature with pH 8.5.

The mechanical composition of soil was 60.9 percent, 27.8 percent silt and 11.3 percent clay. The experiment was conducted in Randomized Block Design with three replications during autumn-winter season in 2023-24 to assess the performance of 34 genotypes. Each treatment consisted of twelve plants in two rows, having spacing of 60 x 50 cm with net plot size of 3.0×1.2 m². According to Panse and Sukhatme (2000) [7] analysis of variance (ANOVA) was performed for each character, heritability, and variance components were calculated using the methods of Johnson *et al.* (1955) [5], and Burton and Devane (1953) [2], respectively.

3. Results and Discussion

"Any crop species needs genetic variability for a breeding program to be successful, and before starting an improvement program, The data recorded on sixteen traits from the experiment were subjected to analysis of Variance. Mean squares due to treatments were highly significant for all the traits (Table 1. indicating therefore significant differences among the genotypes with respect to the traits under study. In other words, the performances of the genotypes with respect to these characters were statistically different; suggesting that, there exists ample scope for selection in the available germplasm of tomato.

Days to 50% flowering exhibited a high variability among the traits studied, ranging from 27.00 to 36.00 in NDT-23-6 and NDT-23-28, respectively, with a general mean of 31.89. mean days to first fruit harvest was 82.23 which range from 78.33 (NDT-23-16) to 87.33 (NDT-23-33). Mean plant hight was 96.18 which range from 59.67 (NDT-23-5) to 137.00 (NDT-23-17), mean poler fruit diameter was 4.79 which range from 3.60 (NDT-23-26) to 5.70 (NDT-23-27), mean equatorial fruit diameter was 5.51 which range from 3.30 (NDT-23-26) to 7.50 (NDT-23-24), mean no. of locules per fruit was 4.21 which range from 2.67 (NDT-23-29) to 6.33 (NDT-23-11,24), mean pericarp thickness was 5.38 which range from 2.50 (NDT-23-19) to 7.20 (NDT-23-2), mean average fruit weight was 90.66 which range from 70.53 (NDT-23-24) to 103.30 (NDT-23-21), mean no. of fruits per plant was 13.5 which range from 8.33 (NDT-23-26) to 18.67 (NDT-23-1), mean no. of primary branches per plant was 5.15 which range from 3.67 (NDT-23-11) to 7.00 (check Kashi Aman), mean TSS was 4.05 which range from 2.40 (NDT-23-31) to 5.70 (NDT-23-16), mean lycopene content was 2.29 which range from 0.80 (NDT-23-7) to 5.53 (NDT-23-29), mean titrable acidity was 0.39 which range from 0.27 (check Kashi Aman) to 0.57 (NDT-23-27), mean ascorbic acid was 20.57 which range from 17.30 (NDT-23-14) to 24.57 (check Kashi Aman), mean fruit yield per plant (kg) was 1.13 which range from 0.83 (NDT-23-30) to 1.43 (NDT-23-19), and mean fruit yield (q/ha) was 338.99 which range from 249.13 (NDT-23-26) to 428.86 (NDT-23-19).

3.1 Genotypic and Phenotypic Coefficient of variation

The estimates of genotypic and phenotypic coefficients of variations for seventeen characters of tomato germplasm have been presented in Table 4.3. The estimates of phenotypic coefficients of variations (PCV) were higher than genotypic coefficients of variations (GCV) for all the characters. The highest phenotypic (>20%) as well as genotypic coefficients of variation were observed in the case of lycopene content (GCV 39.37% and PCV 39.98%) followed by number of fruits per plant (GCV 25.48% and

PCV 26.06%), number of locules per fruit (GCV 23.55% and PCV 24.33%) Fruit yield (q/ha) (GCV 19.85% and PCV 20.65%), fruit yield/plant(kg) (GCV 19.73% and PCV 20.52%), plant height (GCV 19.36% and PCV 20.40%), pericarp thickness (GCV 18.95% and PCV 19.68%).

Moderate (10-20%) estimates of PCV and GCV were estimated for TSS (GCV 18.40% and PCV 19.38%), titrable acidity (GCV 17.92% and PCV 18.81%) number of primary branch per plant (GCV 16.34% and PCV 17.43%), equatorial fruit diameter (GCV 15.29% and PCV 16.32%) poler fruit diameter (GCV13.22 and PCV 14.67).

The phenotypic and genotypic coefficients of variations were lower (<10%) for average fruit weight (GCV 8.82 and PCV 10.34), days to 50% flowering (GCV 6.72% and PCV 7.10%), ascorbic acid (GCV 6.22% and PCV 8.44%) and days to first fruit harvest (GCV 2.13% and PCV 2.76%), low GCV and PCV for these traits indicated that there was less variation for this trait.

Table 1: Analysis of variance (mean sum squares) genotypes for twelve quantitative and four qualitative characters in tomato

Parameter	Replication	Treatment	Error
DF	2	33	66
Days to 50% flowering	4.30	14.32**	0.53
Days to first fruit harvest	3.36	11.27**	2.08
Plant height (cm)	31.44	1078.27**	38.45
Polar fruit diameter (cm)	0.463	1.295**	0.093
Equatorial fruit diameter (cm)	0.889	2.226**	0.099
No. of locules per fruit	0.030	3.010**	0.066
Pericarp thickness (mm)	0.960	3.201**	0.081
Average fruit weight (g)	25.31	215.73**	24.00
No. of fruits per plant	11.25	76.94**	1.17
No. of primary branches per plant	3.46	2.22**	0.10
TSS (0 Brix)	0.311	1.727**	0.060
Lycopene content (mg/100 g)	0.154	2.457**	0.025
Titrable acidity (%)	0.001	0.015**	0.000
Ascorbic acid (mg/100 g)	1.429	6.289**	1.382
Fruit yield per plant (kg)	0.341	0.373**	0.010
Fruit yield (q/ha)	2884.80	33931.15**	906.22

Similar, results have been reported by Bhandari et al. (2017), they observed number of seed per fruit (PCV 36.38% and GCV 35.22%), total number of fruits per plant (PCV 35.84% and GCV 35.37%), fruit yield (PCV 35.07% and GCV 34.69%), average fruit weight (PCV 31.25% and GCV 30.89%), number of locules per fruit (PCV 26.07% and GCV 23.12%), number of fruit per cluster (PCV 23.32% and GCV 21.36%), number of primary branches per plant (PVC 21.07% and GCV 19.57%), number of flower per cluster (PCV 19.58% and GCV 18.60%), plant height (PCV 18.18% and GCV 16.85%), days to 50% flowering (PCV 12.06% and GCV 9.65%) demonstrating a wide range of genetic variability for these traits.

3.2 Heritability and Genetic advance

To determine how much an individual attribute had improved, heritability was calculated in relation to genetic advancement. Very high estimates of heritability (>80%) were recorded for thirteen characters i.e. lycopene content (97.02%) followed by number of fruits per plant (95.58%), pericarp thick ness (92.76), fruit yield per plant (kg) (92.52%), fruit yield (q/ha) (92.39%), titrable acidity (90.77%), TSS (90.20), plant hight (90.02%), days to 50% flowering (89.73), number of primary branch per plant (87.89%), equatorial fruit diameter (87.73%). However high

heritability (60-80%) was recorded for one character *i.e.* Average fruit weight (72.70%) and moderate heritability (40-60%) was recorded for two character *i.e.* ascorbic acid (54.21%) and days to first fruit harvest (59.55) there is not lower heritability (<40%) was recorded in estimated in all 16 characters. The highest value of genetic advance in percent of the mean was shown by lycopene content (79.89%).

Similar results were also reported by Cholin *et al.* (2021c) ^[3]. High heritability coupled with high genetic advance in percent of mean were recorded for polar diameter (95.4% and 42.66%), average fruit weight (94.3% and 72.04%), fruit firmness (94.3% and 26.24%), fruit pH (91.4% and 31.99%), plant spread (84.8% and 27.07%) indicating that these traits were little influenced by environment. Thus, it requires low selection intensity for improvement.

Table 2: Estimate of range, grand mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance and percent of mean for sixteen characters in tomato germplasm.

Characters	Mean	Min	Max	GCV (%)	PCV (%)	Heritability (%)	GA% mean
Days to 50% flowering	31.89	27.00	36.00	6.72	7.10	89.73	13.12
Days to first fruit harvest	82.23	78.33	87.33	2.13	2.76	59.55	3.38
Plant height (cm)	96.18	59.67	137.00	19.36	20.40	90.02	37.83
Polar fruit diameter (cm)	4.79	3.60	5.70	13.22	14.67	81.15	24.53
Equatorial fruit diameter (cm)	5.51	3.30	7.50	15.29	16.32	87.73	29.50
No. of locules per fruit	4.21	2.67	6.33	23.55	24.33	93.67	46.95
Pericarp thickness (mm)	5.38	2.50	7.20	18.95	19.68	92.76	37.60
Average fruit weight (g)	90.66	70.53	103.30	8.82	10.34	72.70	15.49
No. of fruits per plant	13.5	8.33	18.67	25.48	26.06	95.58	51.31
No. of primary branches/plant	5.15	3.67	7.00	16.34	17.43	87.89	31.56
TSS (0 Brix)	4.05	2.40	5.70	18.40	19.38	90.20	36.01
Lycopene content (mg/100 g)	2.29	0.80	5.53	39.37	39.98	97.02	79.89
Titrable acidity (%)	0.39	0.27	0.57	17.92	18.81	90.77	35.17
Ascorbic acid (mg/100 g)	20.57	17.30	24.57	6.22	8.44	54.21	9.43
Total Fruit yield/plant (kg)	1.13	0.83	1.43	19.73	20.52	92.52	39.10
Fruit yield (q/ha)	338.99	249.13	428.86	19.85	20.65	92.39	39.30

4. Conclusion

Knowledge of genetic variability assessed via estimation of coefficient of variation, heritability (broad sense) and genetic advance, in importance trait Growth and yieldrelated traits such as fruit yield(q/ha), tomato genotype NDT-23-19 (428.86) followed by NDT-23-1(421.43), NDT-23-3(418.88) and NDT-23-20 (377.42) were found significant over best check Kashi Aman (356.74). Genotypic (GCV) and phenotypic (PCV) coefficients of variation were high for lycopene content (GCV 39.37%, PCV 39.98%), no. of fruits per plant (GCV 25.48%, PCV 26.06%). Broadsense heritability was high for lycopene content, no. of fruits per plant, no. of locule per fruit, pericarp thickness, fruit yield per plant, fruit yield (q/ha) titrable acid, TSS. Genetic advance as percent of mean (GAM) was highest for yield per hectare (39.30%) and plant height (37.83%). This indicates that tomato fruit production would eventually be increased via selection that mostly focused on fruit weight, no. of fruit per plant, fruit yield per plant (kg) and fruit yield (q/ha). These results offer a solid foundation for focused enhancement in tomato via hybridization and selective selection.

5. References

- Bhandari HR, Srivastava K, Reddy GE. Genetic variability, heritability and genetic advance for yield traits in tomato (*Solanum lycopersicum* L.). Int J Curr Microbiol Appl Sci. 2017;6(7):4131-4138.
- 2. Burton GW, De Vane EH. Estimated heritability in tall replicated clonal material. Agron J. 1953;45(3):474-478.
- 3. Cholin S, Raghavendra S. Assessment of genetic variability in tomato (*Solanum lycopersicum* L.) for yield and yield attributing traits. Pharm Innov J. 2021;10(1):399-403.

- 4. Golani IJ, Mehta DR, Purohit VL, Pandya HM, Kanzariya MV. Genetic variability, correlation and path coefficient studies in tomato. Indian J Agric Res. 2007;41(2):146-149.
- 5. Johnson HW, Robinson HF, Comstock RE. Genetic and environmental variability in soybean. Agron J. 1955;47(3):314-318.
- 6. Ministry of Agriculture & Farmers Welfare. Area and production of horticulture crops for 2023-24 (1st advance estimates) [Internet]. 2023 [cited 2025 Jul 14]. Available from:
 - https://agriwelfare.gov.in/en/StatHortEst
- 7. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 4th ed. New Delhi: Indian Council of Agricultural Research; 2000.
- 8. Ravi M. History of tomato (Poor man's apple). IOSR J Humanit Soc Sci. 2017;22:31-34.