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Analysis of Genetic Variability, Heritability, and Genetic Advance for Yield-Associated Traits under High Temperature Stress in Tomato (Solanum lycopersicum L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The objective of this study was to examine the genetic variability, heritability, and genetic advancement in tomato plants (both parents and hybrids) in terms of their tolerance to high temperatures. The research was conducted at the ICAR-Indian Institute of Vegetable Research (ICAR-IIVR) in Varanasi during the summer season of 2024 (February-May). In this study, a total of 23 tomato genotypes comprising 8 parent varieties and 15 hybrid crosses were cultivated using a completely randomized block design (CRBD). The ANOVA analysis indicated a notable level of

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genetic variability present in the genotypes for the traits under investigation. Both the phenotypic and genotypic coefficient of variation showed a higher PCV for all traits examined in relation to their respective GCV, highlighting the significant impact of environmental factors on the results. Significant heritability and genetic advance were noted for various traits, including average fruit weight, fruit quantity per plant, fruit setting, plant yield, anther tip burning, plant height, seed count per fruit, stigma exertion, crop duration, and pollen viability, underscoring their potential for genetic improvement in future research endeavors. Our research findings indicate that these characters are influenced by the cumulative effects of genes, highlighting the potential effectiveness of employing a selection method to enhance their tolerance to high temperatures in tomato plants.

Keywords: Genetic variability; heritability; genetic advance; tomato; PCV; GCV.

1. INTRODUCTION

Tomato (Solanum lycopersicum L.) is highly regarded as the most important vegetable crop in India, holding a prominent position among various vegetables grown in the country [1]. It exhibits remarkable versatility for culinary applications. It is recognized globally as a "Protective food" due to its valuable mineral content, including calcium, phosphorus, and iron [2], as well as vitamins A, B, and C with small amounts of vitamin E [3] and the diet can be rich in antioxidants such as carotenoids (particularly lycopene and β -carotene), organic acids, and phenolic compounds. Tomato plays a crucial part in maintaining health and vitality. They possess antibiotic properties in their ripe fruits, making them highly beneficial for wound healing. Red ripe tomato contains a high-water content (93-94%). They are rich in lycopene ('renowned as the world's most powerful natural antioxidant') with concentrations of approximately 20-50 mg/100g of fruit weight in comparison with yellow varieties containing only 5 mg/100g [4]. In numerous countries, including India, tomato holds a prominent position, ranking second in significance after potato. In 2022, globally, 189.13mt of tomato were produced from 5.16mha, achieving an average yield of 36.60 tonnes per hectare according to FAOSTAT 2023. China leads in tomato production with 35.70%, with India following at 11.19%. India, ranking second after China's 67.53mt, produced 21.18mt from 0.84 million hectares at a productivity rate of 25.06 tonnes per hectare.

Given its significance as a key vegetable for local consumption and export markets, enhancing tomato productivity and desirable traits through genetic modification is crucial. To enhance the yield capacity of tomato, a systematic breeding strategy is necessary. Thorough examination and assessment of tomato genotypes are crucial for the ongoing and future enhancement of this crop in terms of agronomy and genetics. Additionally, evaluating genotypes is essential for any improvement initiative to comprehend genetic makeup and breeding potential of the existing genotypes [5]. The effectiveness of selection as a breeding technique in any crop improvement program depends on the extent of genetic variation for yield and its components [6].

The genetic variability within a quantitative trait can typically be divided into two key elements: additive variance, which is heritable, and nonadditive variance includes dominance and epistasis. Hence, it is crucial to separate the apparent variability in phenotypes into its heritable and non-heritable components using various parameters such as phenotypic and genotypic coefficients of variation, heritability, and genetic advance to better understand the underlying genetic mechanisms. In genetic studies, traits exhibiting a high genotypic coefficient of variation signify a considerable opportunity for targeted selection strategies. Analyzing the variability components in yield and its related traits helps us understand the impact of the environment on yield, considering that yield and its components are quantitative characteristics influenced by environmental factors [7]. Heritability gives insight into the level of genetic influence on the manifestation of a specific trait and the accuracy of the phenotype in forecasting its breeding worth and the degree to which a specific genetic trait can be passed down to future generations. A high heritability suggests that the observed variation is mainly due to genetic factors rather than environmental influences. However, the heritability value alone not indicate the level of genetic does improvement that would occur by selecting the best individuals [8.9]. By integrating heritability estimations with genetic advance, it becomes more efficient in evaluating the effectiveness of selecting superior individuals. Genetic advance, indicating the level of enhancement in a trait attained through targeted selection pressure,

plays a vital role in aiding breeders in determining an optimal selection strategy. When a characteristic exhibits both high heritability and substantial genetic advance, it indicates that the trait is strongly influenced by additive genetic factors, making it an optimal condition for selection.

Therefore, a thorough assessment of genetic resources is crucial for comprehending and estimating genetic diversity and heritability. Research on genetic parameters offers insights into the anticipated reaction of different traits to selection, aiding in the formulation of optimal breeding strategies. With this in mind, an effort was carried out to investigate the type and extent of genetic variation present in yield and its associated characteristics within the diverse tomato genotypes for high-temperature tolerance in the summer season.

2. MATERIALS AND METHODS

The study was conducted at the Vegetable Research Farm of ICAR-Indian Institute of Vegetable Research (ICAR-IIVR) in Varanasi in the summer of 2024. The experimental location is situated along the Ganges River, at 82.52°E longitude and 25.10°N latitude, at an elevation of 128.93 meters above mean sea level (MSL). The meteorological data for the season under study is showcased in Fig. 1. The eight diverse germplasms for different morphological traits were selected for this research. These 8 genotypes were used to create 15 crosses following a Line x Tester breeding design. The parents used in this study were VRT-06, EC-620402, Kashi Aman, Kashi Chayan, and Punjab Barkha Bahar-2 (PBB-2) as Lines; whereas, Superbug, Vaibhav, and EC-620386 were used as Testers. The genotypes were studied for 13 morphological, and yieldcontributing traits viz., crop duration (days), plant height (cm), pollen viability (%), anther tip burning (%), fruit setting (%), number of fruits per plant, average fruits weight (g), yield per plant (kg), fruit length (cm), fruit width (cm), number of seeds per fruit, and seed viability.

2.1 Statistical Analysis

ANOVA was performed to analyze the experimental design, separating the variance into treatments and replications following the method described by Panse and Sukhatme, [10]. The genotypic and phenotypic coefficients of variance were computed based on the approach by Burton & Devane [11] using the genotypic

and phenotypic variance estimates. The broad sense heritability (h2bs) was determined using the method suggested by Weber and Moorthy [12], and the Genetic advance as a percentage of the mean was categorized into three levels: low, moderate, and high, as detailed by Johnson et al. [13].

3. RESULTS AND DISCUSSION

The results from the ANOVA analysis in Table 1 indicated significant differences among the treatments for all thirteen traits. Fig. 1 displays the average performance and various genetic parameters such as PCV, GCV, heritability (h²), genetic advance (GA), and genetic advance as a percentage of the mean for the quantitative traits. The significant diversity among the genotypes highlights the presence of sufficient variability that can be effectively utilized through selection methods.

3.1 Mean Performance

Significant variations were noted between the lowest and highest mean values across all the characteristics examined (Table 2). The mean performanceamong thirteen traits ranged between yield per plant (0.94 kg) to crop duration (105.09 days) and remaining traits followed by plant height (94.93 cm), seed viability (63.36%), pollen viability (59.13%), number of seeds per fruit(56.61), fruit setting (52.93%), average fruit weight(51.36g), number of fruits per plant (29.79), anther tip burning (23.33%), stigma exertion (18.09%), fruit length (4.45cm), fruit width (4.28cm) showcasing their significant impact on the overall variability observed among the tomato genotypes. This highlights the potential for enhancing different desirable traits through direct selection as a near-term strategy. The broad spectrum of diversity obtained could be attributed to the inclusion of distinct genotypes in the research.

3.2 Analysis of Coefficient of Variation

There were significant variations among the genotypes concerning PCV and GCVas presented in Table 2. Across all traits examined, PCV exhibited a higher value compared to GCV, although with minor differences in some cases. The characteristics were not impacted by environmental factors, making selection based on phenotypic performance more dependable. The coefficients of variability differed in intensity from trait to trait (low, moderate, or high), indicating a substantial level of diversity.

| Table 1. ANOVA for 13 diverse morphological yield-associated characters in tomato (Solanum lycope | <i>ersicum</i> L.) genotypes |
|---|------------------------------|
|---|------------------------------|

| Characters | DF | Crop duration (days) | Plant height (cm) | Pollen viability (%) | Stigma exertion (%) | Anther tip burning (%) | Fruit setting (%) | Number of fruits/plants | Average fruit weight (g) | Yield/plan t (kg) | Fruit length (cm) | Fruit width (cm) | Number of seeds/fruits | Seed viability (%) |
|-------------|----|----------------------------|----------------------|----------------------------|---------------------------|------------------------------|-------------------------|----------------------------|-----------------------------|----------------------|-------------------------|------------------------|---------------------------|--------------------------|
| Replication | 2 | 22.22 | 34.01 | 19.96 | 1.63 | 5.39 | 20.71 | 3.83 | 4.14 | 0.01 | 2.05 | 1.46 | 23.00 | 33.32 |
| Treatment | 22 | 70.31** | 2742.12** | 233.40** | 69.31** | 153.79** | 377.09** | 594.68** | 383.93** | 0.57** | 0.43** | 0.59** | 664.08** | 69.82** |
| Error | 44 | 3.14 | 60.59 | 19.17 | 3.06 | 3.08 | 5.88 | 6.04 | 3.14 | 0.01 | 0.11 | 0.13 | 27.02 | 28.35 |
| Total | 68 | 25.43 | 927.36 | 88.50 | 24.45 | 51.91 | 126.41 | 196.42 | 126.36 | 0.19 | 0.27 | 0.32 | 233.01 | 41.91 |

Table 2. Genetic parameters of diverse morphological yield associated traits in tomato (Solanum lycopersicum L.) genotypes

| Characters | Mean | Minimum | Maximum | GCV (%) | PCV (%) | Heritability (%) | GA (%) | GA % over mean |
|--------------------------|--------|---------|---------|---------|---------|------------------|--------|----------------|
| Crop duration (Days) | 105.09 | 97.67 | 116.00 | 4.50 | 4.81 | 87.69 | 9.13 | 8.69 |
| Plant height (cm) | 94.93 | 60.00 | 150.00 | 31.49 | 32.54 | 93.65 | 59.60 | 62.79 |
| Pollen viability (%) | 59.13 | 39.21 | 74.57 | 14.29 | 16.10 | 78.84 | 15.46 | 26.14 |
| Stigma exertion (%) | 18.09 | 9.01 | 25.56 | 25.98 | 27.72 | 87.83 | 9.07 | 50.16 |
| Anther tip burning (%) | 23.33 | 10.20 | 33.63 | 30.38 | 31.30 | 94.23 | 14.17 | 60.75 |
| Fruit setting (%) | 52.93 | 34.77 | 78.98 | 21.02 | 21.51 | 95.46 | 22.39 | 42.30 |
| Number of fruit/plant | 29.79 | 10.87 | 55.73 | 47.02 | 47.74 | 97.01 | 28.42 | 95.41 |
| Average fruit weight (g) | 51.36 | 27.07 | 76.93 | 21.94 | 22.21 | 97.59 | 22.93 | 44.64 |
| Yield/plant (kg) | 0.94 | 0.30 | 1.66 | 46.11 | 47.20 | 95.44 | 0.87 | 92.80 |
| Fuit length (cm) | 4.45 | 3.83 | 5.43 | 7.40 | 10.47 | 49.89 | 0.48 | 10.76 |
| Fruit width (cm) | 4.28 | 3.17 | 5.20 | 9.11 | 12.40 | 54.02 | 0.59 | 13.80 |
| No. of seeds/fruit | 56.61 | 33.33 | 100.00 | 25.74 | 27.33 | 88.71 | 28.27 | 49.95 |
| Seed viability (%) | 63.36 | 55.67 | 71.67 | 5.87 | 10.25 | 32.78 | 4.38 | 6.92 |

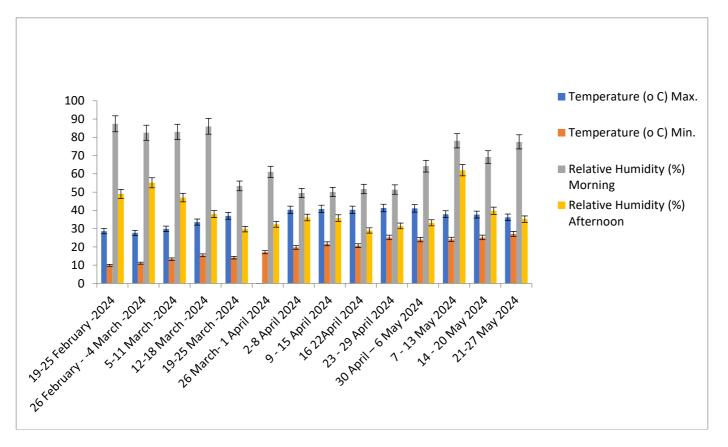


Fig. 1. Meteorological data during the experiment

3.3 Phenotypic Coefficient of Variation (PCV %)

The high PCV (>20%) was estimated for traits *viz.*, number of fruits per plant (47.74%) followed by yield per plant (47.20%), plant height (32.54%), anther tip burning (31.30%), stigma exertion (27.72%), number of seeds per fruit (27.33%), average fruit weight (22.21%), fruit setting (21.51%) whereas, medium PCV% (10-20%), reported in pollen viability (16.10%), fruit width (12.40%), fruit length (10.47%), seed viability (10.25%), while low PCV% (Less than 10%) observed only for crop duration (4.81%). A similar finding has been reported for plant height, number of fruits per plant, number of seeds per fruit [14], and average fruit weight [15].

3.4 Genotypic Coefficient of Variation (GCV %)

When evaluating phenotypic variability, it is crucial to differentiate between genetic and environmental factors. By focusing on genetic variability, we can accurately identify and isolate real genetic differences. The presence of a high genetic coefficient of variation (GCV) indicates greater potential for enhancing the specific trait under study.

The high GCV (> 20%) was estimated for traits viz., number of fruits per plant (47.02%) followed by yield per plant (46.11%), number of seeds per fruit (25.74%), plant height (31.49%), anther tip burning (30.38%), stigma exertion (25.98%), average fruit weight (21.94%), fruit setting (21.02%), whereas, medium GCV% (10-20%) only for pollen viability (14.29%), while low GCV% (< 10%) observed for fruit width (9.11%), fruit length (7.40%), seed viability (5.87%), and crop duration (4.50%). The PCV is observed higher than the GCV for all characters representing the influence of the environment on genotypes. Similar findings were also reported for traits like the number of fruits per plant, yield per plant, and plant height [14,16,17,18].

3.5 Heritability and Genetic Advance

Genetic coefficients of variation alone do not accurately estimate heritable variations; therefore, it is essential to determine heritability for a more reliable assessment of the potential improvement achievable through selection, as proposed by Burton & Devane [11]. The high heritability (> 60%) was estimated for average fruit weight (97.59%), followed by number of fruits per plant (97.01%), fruit setting (95.46%), yield per plant (95.44%), anther tip burning (94.23%), plant height (93.65%), number of seeds per fruit (88.71%), stigma exertion (87.83%), crop duration (87.69%), pollen viability (78.84%), whereas, moderate heritability (31-60%) reported in fruit width (54.02%), fruit length (49.89%), and seed viability (32.78%).

The high genetic advance (> 20%) disclosed the best performance for plant height (59.60%), number of fruits per plant (28.42%), number of seeds per fruit (28.27%), average fruit weight (22.93%), fruit setting (22.39%), whereas, moderate genetic advance (10-20%) observed for pollen viability (15.56%), anther tip burning (14.17%). while low genetic advance (less than 10%) was observed for crop duration (9.13%), stigma exertion (9.07%), seed viability (4.38%), yield per plant (0.87%), fruit width (0.59%), fruit length (0.48%).

High heritability, combined with notable genetic advances, was noted for characteristics likeplant height, number of fruits per plant, number of seeds per fruit, average fruit weight, and fruit setting. This suggests that these traits are influenced by additive gene effects and are dependable indicators for strategic selection purposes Panse [19]. High heritability coupled with genetic advance was reported [14] for average fruit weight, number of fruits per plant, plant height, and number of seeds per fruit [17] for plant height, average fruit weight, number of fruits per plant [16] for plant height, and average fruit weight in diverse tomato genotypes.

4. CONCLUSION

The analysis of variance showed that there was enough genetic variation present in the germplasm for different morphological yieldrelated traits. The estimates of genetic variability reveal the high value of the PCV for all selected traits compared to their respective GCV, indicating the effect of the environment. High heritability was recorded for all traits except seed viability, whereas a high genetic advance was recorded for traits like average fruit weight, number of fruits per plant, fruit setting, yield per plant, anther tip burning, plant height, number of seeds per fruit, stigma exertion, crop duration, and pollen viability. High heritability coupled with high genetic advance was observed for traits *viz.*, average fruit weight, number of fruits per plant, fruit setting, yield per plant, anther tip burning, plant height, number of seeds per fruit, stigma exertion, crop duration, and pollen viability. Overall, our study shows that these traits are under additive gene effects, and therefore they can be improved effectively by selecting these traits for improvement.

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Details of the AI usage are given below:

1.QuillBot. v15.406.19

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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