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Genetic Studies in Cherry Tomato (*Solanum lycopersicum* L. var. *Cerasiforme*) Germplasm Lines under West Garo Hills, Meghalaya

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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

Cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*) germplasm maintained in West Garo Hills, Meghalaya, represents a useful source of morphological variability for selection. The present investigation evaluated 15 germplasm lines during 2023 at the Demonstration unit, Biotech KISAN Hub, Tura, using a randomised block design with three replications. Twenty-two horticultural characters were assessed to estimate phenotypic and genotypic coefficients of variation, broad-sense heritability and genetic advance. Analysis of variance revealed highly significant differences among the germplasm lines for the characters studied, indicating substantial variability. Phenotypic coefficients of variation were higher than the corresponding genotypic coefficients for all characters. Fruit weight recorded the highest phenotypic coefficient of variation (39.16%), while fruit yield per plant recorded the highest genotypic coefficient of variation (36.72%). The lowest phenotypic coefficient of variation was observed for days to first fruit harvest (4.43%), whereas the lowest genotypic coefficient of variation was also recorded for days

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to first fruit harvest (3.62%). Broad-sense heritability ranged from 28.73% to 94.54%, with the highest estimate for pericarp thickness. Genetic advance as a percentage of the mean ranged from 6.11 to 71.43%, with the highest value for fruit yield per plant. The observed combination of variability, heritability and genetic advance indicates useful scope for selection of promising cherry tomato germplasm under West Garo Hills conditions.

Keywords: Germplasm; cherry tomato; variation; heritability; genetic advance.

1. Introduction

Tomato (*Solanum lycopersicum* L.) is one of the important summer-season vegetable crops of the family Solanaceae, has a chromosome number of 2n = 24, and is also known as a protected fruit. According to Swarup (2014), tomato is considered to have about 90 genera, which have been divided into two subfamilies, Solanoideae and Cestroidaea, and the genus Lycopersicon belongs to the subfamily Solanoidae. Within the sub-Solanoidae, the genus *Lycopersicon* belongs to the largest tribe, Solaneae, under which 18 genera are present; the largest is *Solanum*, the smallest is *Lycopersicon*, and both are closely related genera. According to Rick *et al*. (1976), all tomato species originated in western South America. Ramya *et al*. (2016) stated that cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*) is regarded as a botanical variety of cultivated tomato and is considered to be the probable ancestor of cultivated tomatoes. Cherry tomatoes are beneficial to human health because they are rich in vitamin C, which helps maintain the immune system, and potassium, which is vital for the proper functioning of the heart and muscles. They also contain vitamins A and K, manganese and magnesium. The colour of cherry tomato is due to the presence of the pigment lycopene, which is a potent antioxidant that may help protect against cellular damage, certain cancers and heart diseases. Other antioxidants, such as beta-carotene and melatonin, also contribute to their anti-carcinogenic effects. Cherry tomato is gaining popularity worldwide and is usually grown under protected structures. According to Kobryn and Hallmann (2005), demand for cherry tomato has increased in the market due to recognition of its high quality and good taste. Prema *et al*. (2011) reported that cherry tomatoes have gained considerable popularity worldwide because of favourable characteristics such as vitamin A and C content, high TSS, better taste and low calorie content, and their ability to set fruit even at high temperatures.

Considering the popularity, potential and prospects of the crop, there is an urgent need for its improvement to develop superior varieties that are well suited to the specific region and specific purposes. Therefore, it is necessary to determine the prospects and potential of cherry tomatoes, and steps should be taken to improve the crop by assessing cultivated species for desirable characters under different agro-climatic conditions. This will also aid in obtaining and recording comprehensive information on the existing genetic variability in the region for various important characters. Evaluation of different morphological characters and their associations is of immense importance because it leads to a better understanding of the nature and extent of variability among different germplasm lines. Greater diversity among germplasm lines provides greater opportunities for the selection of desired types.

Recent analyses of cultivated tomato germplasm have demonstrated substantial genetic diversity, reinforcing the value of systematic germplasm characterization for breeding-oriented selection (Tripodi et al., 2024; Xu et al., 2024).

The breeding value of diverse cherry-type and related tomato germplasm has also been demonstrated through the development of genetically diverse populations for trait association and pre-breeding applications (Arrones et al., 2024).

Recent genotype evaluations have further reported appreciable variability and heritability for yield-related tomato traits, supporting the continued use of these parameters in selection-oriented studies (Preetham et al., 2026).

Genotype-dependent responses of tomato germplasm under defined environmental stress also support the need to evaluate germplasm under specific growing conditions (Sivakumar & Basha, 2023).

In the West Garo Hills region of Meghalaya, several landraces and cherry tomato germplasm lines are available, with considerable variability in various morphological traits, and are grown and maintained by local farmers using their indigenous methods.

Despite the presence of locally maintained cherry tomato germplasm in West Garo Hills, systematic information on genetic variability, heritability, and genetic advance for key horticultural traits under this specific environment remains limited.

1.1 Objective

To characterise and identify the potential cherry tomato germplasm from this region, the present investigation was undertaken to determine genetic variability, heritability and genetic advance in cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*) germplasm lines under West Garo Hills, Meghalaya.

2. Materials and Methods

The research was conducted during 2023 at the demonstration unit, Biotech KISAN Hub, Tura, Meghalaya. Tura is located at 25°31’ N latitude and 90° 13’ E longitude, at an altitude of 527 m above MSL. The experiment comprised 15 cherry tomato germplasm lines obtained from various locations in West Garo Hills District, Meghalaya, India. The experiment was conducted in an RBD with three replications. Seeds were sown on 3rd February 2023. A spacing of 60X60 cm was maintained between rows and between plants. The first fruits were harvested on 25th April 2023, and the final harvest was conducted on 15th May 2023. For proper crop growth, the recommended cultural practices of the Indian Council of Agricultural Research were adopted during the growing

season. Data were collected from five randomly selected plants for the following characters: stem thickness (ST) (cm), measured at the fruiting stage using a measuring tape; plant height (PH) (cm), calculated as the average of five randomly selected plants from ground level to the tip of the main stem before the last harvest; number of primary branches per plant ($NOPBP^{-1}$), recorded as the average of five randomly selected plants at the end of the blooming period; number of secondary branches per plant ($NOSBP^{-1}$), also calculated as the average of five randomly selected plants at the end of the blooming period; number of days to 50% flowering (DTFPF) in the field, observed as the total number of days from the date of transplanting to the date when at least 50% of the plants in the field showed fully bloomed flowers; total number of flower clusters per plant ($NOFCP^{-1}$), recorded as the average of 5-10 plants at the blooming stage; total number of flowers per flower cluster ($NOFFC^{-1}$), obtained by calculating the average of five randomly selected flower clusters during the blooming period; days to first fruit set (DTFFS), counted as the number of days from the date of transplanting to the date of first fruit set; total number of fruits per cluster (NOFC-1), obtained by calculating the average of five randomly selected clusters at the marketable stage; total number of fruits per plant (NOFP-1), obtained by calculating the average of five plants at the early maturity stage; days to first fruit maturity (DTFFM), recorded as the number of days from transplanting to the date when plants attained physical maturity (turning stage); days to first fruit harvest (DTFFH), calculated as the number of days from transplanting to the harvesting of the first fruit at the breaker stage; total number of locules per fruit ($NOLF^{-1}$), obtained by calculating the average of five randomly selected fruits at the early maturity stage; fruit length (FL) (cm), measured after harvesting using a Vernier caliper from the stem end to the blossom end, to one decimal place, at the mature stage; fruit breadth (FB) (cm), measured after harvesting at the widest diameter of cross-sectioned fruits, to one decimal place, at the mature stage using a Vernier caliper and scale; fruit weight (FW) (g), obtained by calculating the average weight of 5 fruits at the early maturity stage; total number of seeds per fruit ($NOSPF^{-1}$), recorded by observing five mature fruits selected from the germplasm lines; 1000-seed weight (TSW) (g), observed by extracting the seeds to measure fresh weight, after which the seeds were sun-dried and one hundred dried seeds were weighed; peduncle length (PDL) (cm), obtained by calculating the average of 5 randomly selected fruits at the marketable stage; pericarp thickness (PT) (mm), recorded as the average of 5 fruits from an equatorial section using a Vernier caliper near the maturity stage; days to last fruit harvest (DTLFH), obtained by calculating the number of days from sowing/transplanting to the harvest of the last marketable fruit; and fruit yield per plant (FYP^{-1}) (g), obtained by calculating the average collective yield of all pickings from the same five selected plants at the early maturity stage.

The phenotypic coefficient of variation and genotypic coefficient of variation for each character in the present experiment were studied using the formula proposed by Burton (1952). According to Sivasubramaniam and Madhava Menon (1973), PCV and GCV were characterised as low (0–10%), moderate (10–20%) and high (>20%). Broad-sense heritability was assessed according to Burton and DeVane (1953). Genetic advance at 5% selection intensity was calculated using the formula given by Johnson *et al*. (1955).

3. Results and Discussion

Knowledge of the genetic variability of yield components is important in a crop improvement programme. The greater the extent of genotypic variability, the greater the possibility of improving a given character. Understanding heritability coupled with genetic advance helps in drawing important conclusions for effective selection based on the phenotypic performance of germplasm. A broad-sense heritability estimate from a test provides information on the comparative extent of genetic and environmental variation in the germplasm pool. Knowledge of heritability coupled with the expected genetic advance of a trait is important for assessing the scope for improvement of a character through selection.

In this experiment, fifteen cherry tomato germplasm lines were assessed for genetic variability, heritability and genetic advance as a percentage of the mean. The ANOVA findings revealed highly significant differences among the 15 germplasm lines for 22 horticultural traits, as shown in Tables 1 and 2. Significant variation was observed for all characters, indicating scope for selection and breeding improvement in cherry tomato. It can also be observed from the experimental results presented in Table 3 that phenotypic variability is not entirely consistent because it includes genotypic and environmental components, along with genotype-by-environment interaction mechanisms. Furthermore, the phenotypic appearance of a crop is affected by additive gene effects, which are heritable, as well as dominant and epistatic effects, which are non-heritable, with no interaction between alleles. According to Rashid *et al*. (2020), it is necessary to divide the observed variability into phenotypic and genotypic coefficients of variation, which helps identify the extent of variability present in different characters. Knowledge of genetic variability in yield and related traits is important in crop improvement programmes.

3.1 Coefficient of Variation

Phenotypic coefficient of variation was highest (>20) for FW (39.16), followed by FYP^{-1} (38.89), PT (30.34), $NOPBP^{-1}$ (29.14), $NOSBP^{-1}$ (27.75), $NOLF^{-1}$ (23.95) and ST (20.22), signifying the existence of ample variation in these parameters in this experiment. PCV was moderate (10-20) for PDL (19.08), $NOFP^{-1}$ (18.37), PH (18.13), TSW (15.60), $NOSPF^{-1}$ (14.29), $NOFFC^{-1}$ (14.09), FL (13.56) and FB (13.10). The lowest PCV values were obtained for DTFFH (4.43), followed by DTFFM (4.73), DTLFH (4.75), DTFFS (6.93), $NOFC^{P-1}$ (7.70) and $NOFC^{-1}$ (9.36).

GCV was highest (>20) for FYP^{-1} (36.72), followed by FW (36.33), PT (29.50) and $NOPBP^{-1}$ (22.28), signifying the presence of ample variation for these traits in the present investigation. GCV was moderate for PDL (18.17), $NOFP^{-1}$ (17.82), PH (17.36), ST (17.73), $NOFFC^{-1}$ (13.36), $NOLF^{-1}$ (13.18), $NOSPF^{-1}$ (12.94), FB (11.16), FL (11.09) and $NOSBP^{-1}$ (14.86). DTFFH exhibited the lowest GCV (3.62), followed by DTLFH (3.98), DTFFM (4.55), DTFFS (6.28), $NOFC^{P-1}$ (6.85), DTFPF (7.53), $NOFC^{-1}$ (8.57) and TSW (9.81).

Table 1. Analysis of variance for 22 horticultural characters of Cherry Tomato

Source of variation	Degree of freedom	Mean square										
		ST	NOPBP^{-1}	NOSBP^{-1}	DTFPF	NOFCP^{-1}	DTFFS	NOFC^{-1}	NOFFC^{-1}	NOFP^{-1}	DTFFM	DTFFH
Replication	2	0.01	0.80	8.82	2.02	0.04	0.46	0.05	0.86	0.81	0.46	7.02
Genotype	14	0.09	15.37	58.11	27.35	0.45	26.32	0.61	33.27	1546.43	39.29	33.40
F value		10.99	5.22	2.20	14.55	12.27	14.82	16.52	27.73	49.01	37.01	7.05

Table 2. Analysis of variance for 22 horticultural characters of Cherry Tomato

Source of variation	Degree of freedom	Mean square										
		FL	FB	FW	PDL	PT	NOLF^{-1}	NOSPF^{-1}	TSW	PH	DTLFH	FYP^{-1}
Replication	2	0.01	0.01	0.09	0.01	0.01	1.06	13.08	0.14	23.87	4.82	970.52
Genotypes	14	0.12	0.12	10.87	1.13	0.90	0.86	276.31	0.11	604.79	74.31	163429.66
F Value		7.08	8.93	19.55	30.22	52.96	2.30	14.69	2.96	33.96	8.11	25.60

Table 3. Estimates of different genetic parameters for 22 horticultural characters in cherry tomato

Characters	PCV (%)	GCV (%)	H^2 (b) (%)	GA (%)
ST	20.22	17.73	76.91	32.04
NOPBP^{-1}	29.14	22.28	58.46	35.10
NOSBP^{-1}	27.75	14.86	28.73	16.41
DTFPF	8.32	7.53	81.87	14.04
NOFCP^{-1}	7.70	6.85	78.98	12.54
DTFFS	6.93	6.28	82.16	11.73
NOFC^{-1}	9.36	8.57	83.80	16.17
NOFFC^{-1}	14.09	13.36	89.90	26.11
NOFP^{1}	18.37	17.82	94.11	35.62
DTFFM	4.73	4.55	92.30	9.01
DTFFH	4.43	3.62	66.85	6.11
FL	13.56	11.09	66.97	18.71
FB	13.10	11.16	72.56	19.59
FW	39.16	36.33	86.08	69.18
PDL	19.08	18.17	90.69	35.65
NOSPF^{-1}	14.29	12.94	82.03	24.16
NOLF^{-1}	23.95	13.18	30.29	14.95
TSW	15.60	9.81	39.52	12.71
PT	30.34	29.50	94.54	59.10
PH	18.13	17.36	91.65	34.24
DTLFH	4.75	3.98	70.34	6.89
FYP^{-1}	38.89	36.72	89.13	71.43

ST-Stem thickness (cm); NOPBP-^{1}- Number of primary branch; NOSBP^{-1}- Number of secondary branches; DTFPF-days to 50% flowering; NOFCP^{-1}- Number of flower cluster per plant; DTFFS- Days to first fruit set; NOFC^{-1}- Number of fruits per cluster; NOFFC^{-1}- Number of flowers per flower cluster; NOFP: Number of fruits per plant; DTFFM- Days to first fruit maturity; DFFH- Days to first fruit harvest; FL- Fruit length (cm); FB- Fruit breadth (cm); FW- Fruit weight (g); PDL- Peduncle length (cm); NOSPF^{-1}- Number of seeds per fruit; NOLPF^{-1}- number of locules per fruit; TSW- 1000 seed weight (g); PT- Pericarp thickness (mm); PH- Plant height (cm); DLFH- Days to last fruit harvest; FYP^{-1}- Fruit yield per plant (g)

The PCV was higher than the corresponding GCV for all parameters in the present investigation, indicating that environmental factors affected their expression to some extent. In line with these findings, Brar *et al*. (2000) and Kaushal *et al.* (2017) reported higher PCV than GCV for number of fruits per plant, average fruit weight, plant heightand fruit yield per plant, respectively, in tomato.

3.2 Heritability

Broad-sense heritability (h2bs) was high for most traits, with values ranging from 28.73% to 94.54%. High heritability was shown by PT (94.54%), followed by $NOFP^{-1}$ (94.11%), DTFFM (92.30%), PH (91.65%), PDL (90.69%), $NOFFC^{-1}$ (89.90%), FYP^{-1} (89.13%), FW (86.08%), $NOFC^{-1}$ (83.80%), DTFFS (82.16%), $NOSPF^{-1}$ (82.03%), DTFPF (81.87%), $NOFC^{P-1}$ (78.98%), ST (76.91%), FB (72.56%), DTLFH (70.34%), FL (66.97%) and DTFFH (66.85%). The results indicate that these characters were not greatly affected by environmental conditions and that selection based on phenotypic performance would be reliable. Moderate heritability was recorded for $NOPBP^{-1}$ (58.46%), TSW (39.52%) and $NOLF^{-1}$ (30.29%), while the least heritable trait was $NOSBP^{-1}$ (28.73%). Thus, most characters had moderate to high broad-sense heritability estimates.

Reddy *et al*. (2013) reported broad-sense heritability ranging from 36.60 for days to last fruit harvest to 99.70 for number of fruits per cluster in tomato. Kaushal *et al.* (2017) observed high heritability in tomato for fruit weight (97.37%), number of fruits per plant (94.93%) and pericarp thickness (PT) (94.15%).

3.3 Genetic Advance

Genetic advance as a percentage of the mean ranged from 6.11 to 71.43. The highest genetic advance as a percentage of the mean was recorded for FYP^{-1} (71.43), followed by FW (69.18), PT (59.10), PDL (35.65), $NOFP^{-1}$ (35.62), $NOPBP^{-1}$ (35.10), PH (34.24), ST (32.04), $NOFFC^{-1}$ (26.11), $NOSPF^{-1}$ (24.16), FB (19.59), FL (18.71), $NOSBP^{-1}$ (16.41), $NOFC^{-1}$ (16.17), $NOLF^{-1}$ (14.95), DTFPF (14.04), TSW (12.71), $NOFC^{P-1}$ (12.54), DTFFS (11.73), DTFFM (9.01), DTLFH (6.89) and DTFFH (6.11).

High heritability coupled with genetic advance as a percentage of the mean was recorded for PT (94.54% and 59.10), PH (91.65% and 34.24%), PDL (90.69% and 35.65%), $NOFFC^{-1}$ (89.90% and 26.11%), FYP^{-1} (89.13% and 71.43%), FW (86.08% and 69.18%), $NOFC^{-1}$ (83.80% and 16.17%) and $NOSPF^{-1}$ (82.03% and 24.16%), clearly indicating scope for improvement through simple selection for these traits.

Reddy *et al.* (2013) also reported high heritability along with high genetic gain for plant height, number of clusters per plant, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, fruit length, fruit weight and fruit yield per plant. Khanom *et al.* (2008) reported the highest heritability for individual fruit weight, followed by number of days to first flowering and number of seeds per fruit.

High heritability and low genetic advance were recorded for DTFFM (92.30% and 9.01*%),* $NOFC^{-1}$ (83.80% and 16.17%), DTFFS (82.16% and 11.73%) and DTFPF (81.87% and 14.04%).

Hussain et al. (2021) reported high heritability and low genetic advance for number of primary branches per plant (1% and 0.68%), fruit length (1% and 0.89%) and fruit diameter (1% and 0.94%). High heritability along with low genetic advance results from non-additive gene action, and selection would be ineffective in early generations. However, selection in later generations might be effective in such cases (Dwary *et al.*, 2023).

4. Conclusion

The analysis of variance showed highly significant differences among the germplasm lines for all characters studied, indicating the presence of sufficient variability for each trait among the germplasm lines. The results indicated considerable variability among the cherry tomato germplasm lines for traits such as yield, fruit weight and number of fruits per plant. The present investigation found high estimates of heritability coupled with high genetic advance (as a percentage of the mean), indicating the predominance of additive gene effects in the control of these traits and suggesting that selection for these traits would be effective in cherry tomato improvement programmes. The study also suggests that progress through selection could be made towards higher yield. Therefore, based on the results and discussion, the germplasm lines have considerable potential for combining the elite allelic resources present in these cherry tomato germplasm lines through an efficient breeding and selection approach to obtain higher-yielding recombinants with desirable quality characters.

5. Limitation

This investigation was conducted during a single growing season at one location in West Garo Hills using 15 cherry tomato germplasm lines. Consequently, the estimated variability, heritability and genetic advance reflect the germplasm and environmental conditions evaluated in this experiment. Multi-season and multi-location evaluation would be required to assess the consistency of trait expression and the stability of selection responses across environments.

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Declaration of AI Use

This manuscript was prepared through the combined contributions of all author(s), including contributions to the study design, data, content development, results, interpretation, and related scholarly work. The author(s) acknowledge the use of Grammarly and ChatGPT to assist with grammar checking, language refinement, reference formatting. These AI-assisted tools were not used as authors and did not replace the intellectual contributions or scholarly judgment of the author(s). All AI-assisted outputs, including content, references, and interpretations, were carefully reviewed, revised, verified, and approved by the author(s). The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that they have no known competing financial interests or non-financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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