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Evaluation of genetic diversity of cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*) germplasm under West Garo Hills, Meghalaya

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Abstract

Vegetables, encompassing a variety of edible plant parts such as leaves, stems, fruits, roots, and bulbs, are vital components of the human diet due to their rich nutritional profile. Among them, tomato (*Solanum lycopersicum* L.), particularly the cherry tomato variety (*S. lycopersicum* var. *cerasiforme*), holds significant economic and dietary importance worldwide. Cherry tomato is noted for its small, nutrient-rich fruits, high adaptability to diverse climates, and potential as a genetic reservoir for breeding. Given its increasing global demand, genetic improvement of cherry tomato is essential for enhanced yield, stress tolerance, and nutritional value. This study aimed to evaluate the genetic divergence among 15 cherry tomato genotypes collected from the West Garo Hills of Meghalaya using Mahalanobis D² statistics. The genotypes were grouped into two clusters, with Cluster II showing greater internal genetic variability and Cluster I demonstrating superior traits for yield and fruit weight. Key contributors to genetic divergence included the number of fruits per cluster, fruits per plant, and earliness traits. The analysis highlighted considerable genetic variability among the genotypes, which is crucial for effective selection in breeding programs. Traits with higher contributions to divergence particularly those related to yield and earliness should be prioritized in future hybridization strategies. The findings support the importance of evaluating genetic parameters and character associations to guide the selection of parental lines. The study emphasizes the need for continued assessment and conservation of local cherry tomato germplasm for sustainable crop improvement.

Keywords: Tomato, genetic diversity, cluster, hybridization

Introduction

Vegetables are edible parts of plants commonly used in cooking, though some are consumed raw in smaller amounts. Various plant parts serve as vegetables, including leaves (e.g., leafy greens), stems (such as knolkhol, asparagus, cauliflower), fruits (like melons, gourds, brinjal, tomato, capsicum, and okra), immature flower buds and thick stalks (e.g., broccoli), heads or buds (such as cabbage, globe artichoke, and Brussels sprouts), underground parts (like potato, sweet potato, onion, garlic, colocasia, ginger, and turmeric), fleshy leaf stalks (e.g., celery), and storage roots (including radish, carrot, turnip, and beetroot) (Arya, 2013) ^[1]. Vegetable cultivation plays a significant role in agriculture due to their richness in essential nutrients such as carbohydrates, proteins, vitamins, and minerals. Regular consumption of vegetables not only enhances taste and appetite but also contributes dietary fiber, aiding digestion and preventing constipation. Economically, vegetables are among the most affordable sources of natural food and serve as excellent dietary supplements alongside staple cereals.

Tomato (*Solanum lycopersicum* L.), a key vegetable crop, belongs to the Solanaceae family, which includes around 90 genera. This family is divided into two main subfamilies: Solanoideae and Cestroideae. The genus *Lycopersicon*, part of the Solanoideae subfamily, has a diploid chromosome number of $2n = 2x = 24$ (basic number $x = 12$). Within Solanoideae, *Lycopersicon* is categorized under the large tribe Solaneae, which includes 18 genera the largest being *Solanum*, and *Lycopersicon* being one of the smallest yet closely related (Swarup, 2014) ^[19]. Tomato (*Solanum lycopersicum* L.) is the second most produced vegetable in the world, with relevant participation in human diet (Barankevicz *et al.*, 2015) ^[3].

Cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*) is recognized as a botanical type within the broader category of cultivated tomatoes (Najeema *et al.*, 2018) [11]. It is believed to be the wild ancestor from which all domesticated tomato varieties have evolved (Ramya *et al.*, 2016) [14]. Both the cherry tomato and the modern cultivated tomato (*Solanum lycopersicum* L.) are capable of crossbreeding (Swarup, 2014) [19]. Characterized by its small, bright red, and flavorful fruits, the cherry tomato is commonly consumed fresh and is known for its resemblance to cherries in appearance (Charlo *et al.*, 2007) [6]. Cherry tomato plants are generally classified by their growth habit either determinate or indeterminate. Determinate types grow as compact bushes, producing a single harvest during the season, while indeterminate types develop long vines that continue producing fruit over an extended period (Hancock *et al.*, 1984) [7]. This tomato variety has seen rising popularity worldwide due to its desirable traits, including being rich in vitamins A and C, natural sugars, and having a low calorie content. It also performs well under high temperatures and contains beneficial antioxidants and phytochemicals such as lycopene, beta-carotene, flavonoids, and essential nutrients (Prema *et al.*, 2011; Rosales *et al.*, 2011) [13, 16]. Given the growing demand, it has become increasingly important to breed high-yielding cherry tomato cultivars that are resilient to both biotic and abiotic stresses and are well-suited for both fresh consumption and processing.

Given the rising demand and potential of cherry tomato, there is a need to improve the crop by developing high-performing varieties suited to specific agro-ecological conditions and market needs. Evaluating cultivated cherry tomato genotypes for desirable traits across different environments can reveal the extent of genetic variability, which is crucial for crop improvement. Understanding genetic parameters and character associations helps in identifying traits that significantly influence yield and adaptability. The greater the genetic diversity in the germplasm, the higher the chances of selecting superior types for breeding. Selection remains a core component of vegetable crop improvement. To select effectively, it is essential to assess the extent and nature of variation among genotypes and how environmental factors influence trait expression. Genotypes with desirable traits and high variability can serve as valuable parents in breeding programs for better yield, stress tolerance, and nutritional quality. In the West Garo Hills of Meghalaya, diverse landraces of cherry tomato are cultivated and preserved by local farmers using traditional practices. Recognizing this diversity, the present study was undertaken to assess genetic divergence among cherry tomato accessions using Mahalanobis D² statistics.

Materials and Methods

A field experiment was conducted at the Departmental Research Farm, Horticulture Department, NEHU Tura Campus, West Garo Hills, Meghalaya. The site, located at 25°31' N latitude and 90°13' E longitude, stands at 527 m above sea level. Climatic data during crop growth were recorded by the Agro-meteorological Division, Ministry of Earth Sciences, and are summarized in Table-1. The study involved 15 cherry tomato germplasm lines collected from various locations within West Garo Hills. The trial followed a randomized block design (RBD) with three replications.

Genetic divergence (D² analysis)

Genetic divergence in cherry tomato was assessed using Mahalanobis D² statistics as proposed by Rao (1952). The analysis followed these steps:

- A set of uncorrelated linear combinations (y's) was derived from the common dispersion matrix of correlated variables (x's) through pivotal condensation.
- Genotypic means for 15 traits (x₁ to x₁₅) were transformed into uncorrelated values (y₁ to y₁₅).
 - iii. D² values between the *i*th and *j*th genotypes were calculated as:

$$D_{ij}^2 = \sum (y_{ith} - y_{jth})^2, \text{ for } t = 1 \text{ to } K \text{ characters.}$$

Clustering

Genotypes were grouped into clusters based on D² values, following Rao's method. Genotypes within a cluster had smaller average D² values than those in different clusters, indicating greater similarity within than between clusters.

Results and Discussion

The experiment was conducted to evaluate 15 cherry tomato germplasm lines for genetic divergence and trait characterization, aiming to identify superior genotypes for future breeding programs. Data collected on various traits were analyzed for genetic variability using Mahalanobis D² statistics.

Table 1: Details of Germplasms collected from Garo Hills, Tura.

Accessions No.	Collection point		
	Latitude	Longitude	Altitude
T ₁	25°39'54"N	90°18'05"E	608m
T ₂	25°35'40"N	90°13'43"E	484m
T ₃	25°34'57"N	90°13'43"E	359m
T ₄	25°34'26"N	90°14'46"E	391m
T ₅	25°25'57"N	90°13'10"E	213m
T ₆	25°32'19"N	90°13'47"E	334m
T ₇	25°33'23"N	90°12'02"E	202m
T ₈	25°31'17"N	90°13'16"E	369m
T ₉	25°31'00"N	90°13'27"E	413m
T ₁₀	25°35'50"N	90°11'48"E	276m
T ₁₁	25°30'47"N	90°11'26"E	247m
T ₁₂	25°31'19"N	90°11'56"E	243m
T ₁₃	25°50'42"N	90°16'25"E	172m
T ₁₄	25°42'30"N	90°01'41"E	147m
T ₁₅	25°52'39"N	90°01'27"E	143m

Genetic divergence analysis

Genetic divergence plays a crucial role in crop improvement. Understanding the extent and nature of genetic variability helps in selecting promising lines from existing germplasm, thereby enhancing the effectiveness of breeding programs.

Grouping of genotypes into different clusters (D² analysis)

Based on genetic divergence analysis, the clustering pattern of the fifteen cherry tomato genotypes is shown in Table 2. The genotypes were divided into two distinct clusters: Cluster II contained the majority with eleven genotypes, while Cluster I included four. The grouping did not reflect any correlation between genetic and geographic origin. Similar findings were reported by Spaldon *et al.* (2017) [18]. Hence, genotype selection for hybridization should prioritize genetic variability over geographic distribution.

Table 2: Clustering pattern of 15 genotypes of Cherry Tomato.

Cluster	Number of Genotype	Genotype
I	4	T ₃ , T ₄ , T ₈ , T ₉
II	11	T ₁ , T ₂ , T ₅ , T ₆ , T ₇ , T ₁₀ , T ₁₁ , T ₁₂ , T ₁₃ , T ₁₄ , T ₁₅

Cluster means of characters

Cluster means for 22 traits are summarized in Table 3, revealing notable variation among the genotypes. Cluster II exhibited the highest stem thickness (1.0 cm), while Cluster I showed the lowest (0.9 cm). The number of primary and secondary branches per plant was also greater in Cluster II (9.75 and 23.27, respectively) compared to Cluster I (7.42 and 18.17, respectively).

Genotypes in Cluster II recorded the earliest flowering (38.24 days to 50% flowering), while Cluster I took longer (39.91 days). Conversely, Cluster I had a slightly higher number of flowers per cluster (5.55) than Cluster II (5.39). Days to first fruit set were shortest in Cluster II (45.21), followed by Cluster I (46.41).

Cluster I showed the highest average number of fruits per cluster (5.23), while Cluster II had the highest number of clusters (24.82) and fruits per plant (127.83). Cluster II also recorded the earliest fruit maturity (77.51 days), compared to 81.00 days in Cluster I. For breeding aimed at early maturity, genotypes from Cluster II may be preferred (Meena and Bahadur, 2013) [10]. Interestingly, Cluster I showed a shorter duration to first fruit harvest (86.41 days) than Cluster II (84.82 days), suggesting trait-specific selection may be needed. Genotypes in Cluster II recorded the greatest fruit length (17.62 cm), while those in Cluster I showed the shortest (1.75 cm). Similarly, maximum fruit breadth (3.69 cm) was noted in Cluster II, and the minimum (1.85 cm) in Cluster I. However, Cluster I genotypes had the highest average fruit weight (7.56 g), with Cluster II showing the lowest (3.01 g).

Peduncle length was longer in Cluster II (3.40 cm) compared to Cluster I (3.10 cm). The number of seeds per fruit was slightly higher in Cluster I (72.25) than in Cluster II (71.30). Likewise, Cluster I recorded more locules per fruit (3.33), while Cluster II had fewer (2.97). The 1000-seed weight ranged narrowly, with a minimum in Cluster II (1.60 g) and maximum also in Cluster II (1.63 g). Pericarp thickness was greater in Cluster I (2.36 mm) than in Cluster II (1.87 mm). Plant height was significantly higher in Cluster II (161.17 cm), whereas Cluster I showed shorter plants (70.60 cm). Cluster I also recorded more days to last fruit harvest (121.25) compared to Cluster II (115.30).

Importantly, fruit yield per plant was highest in Cluster I (958.43 g), while Cluster II showed the lowest yield (500.09 g). These results suggest that Cluster I genotypes have strong potential for use in breeding programs aimed at enhancing yield (Meena and Bahadur, 2015) [10].

In tomato, yield results from the combined influence of several contributing traits (Bernousi *et al.*, 2011) [4]. Key characteristics such as number of flowers per cluster, days to first fruit ripening, fruit weight, length, and breadth play a significant role and should be evaluated for genetic divergence to identify superior genotypes with desirable traits (Hussain *et al.*, 2018) [8].

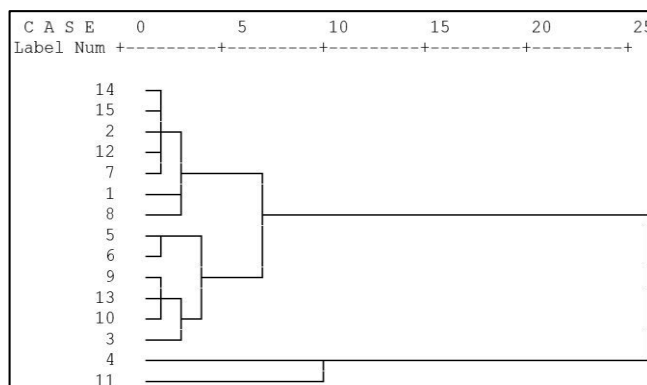
The Mahalanobis D² statistic (Mahalanobis, 1936) is a widely accepted and effective method for quantifying genetic divergence among genotypes. It helps determine the extent of variability and the relative contribution of

individual traits to overall diversity, both within and between clusters. This technique has been found highly useful for measuring genetic diversity by several researchers (Kumar *et al.*, 2010; Reddy *et al.*, 2013; Meena and Bahadur, 2013) [18, 15, 10].

Table 3: Cluster means for important yield contributing characters in 15 Cherry tomato germplasm

Character	Cluster mean		% contribution towards divergence
	I	II	
Stem thickness (cm)	0.90	1.00	2.22
Number of primary branch	7.42	9.75	0.89
Number of primary branch	18.17	23.27	0.98
Days to 50% flowering	39.91	38.24	2.34
Number of flowers per cluster	5.55	5.39	4.55
Days to first fruit set	46.41	45.21	9.89
Number of fruits per cluster	5.23	5.1	12.23
Number of clusters per plant	23.50	24.82	9.45
Number of fruits per plant	122.90	127.83	11.23
Days to first fruit maturity	81.00	77.51	7.89
Days to first fruit harvest	86.41	84.82	8.89
Fruit length(cm)	1.75	17.62	4.76
Fruit breadth(cm)	1.85	3.69	2.56
Fruit weight(g)	7.56	3.01	3.23
Peduncle length	3.10	3.40	1.23
Number of seeds per fruit	72.25	71.30	2.67
Locules number per fruit	3.33	2.97	1.45
1000 seed weight	1.60	1.63	2.12
Pericarp thickness	2.36	1.87	0.34
Plant height	70.60	84.45	1.23
Days to last fruit harvest	121.25	115.30	2.88
Fruit yield per plant	958.43	500.50	6.97

Rescaled Distance Cluster Combine

**Fig 1:** Dendrogram showing the morphogenetic relationships among 15 Genotype of Cherry tomato based on Mahalanobis D² statistics

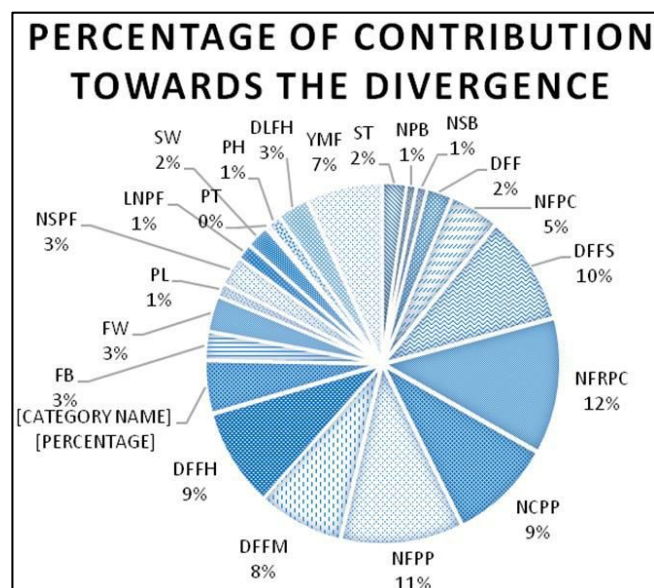
Intra and inter cluster distance

Intra-cluster distances reflect genetic variability within clusters, while inter-cluster distances represent divergence between clusters. As shown in Table 4, intra-cluster D² values among the 15 genotypes ranged from 115.11 to 119.34. Cluster II recorded the highest intra-cluster distance (119.34), suggesting greater genetic diversity among its genotypes, whereas Cluster I had the lowest (115.11). The inter-cluster D² value between Cluster I and Cluster II was also 119.34, indicating moderate genetic divergence between the two clusters.

Table 4: Average intra and inter-cluster D² values for two clusters in 15 genotypes of cherry tomato

Cluster	I	II
I	115.11	323.34
II	-	119.34

The contribution of 15 traits to genetic divergence is presented in Table 4.9. Among them, number of fruits per cluster contributed the most (12.23%), followed by number of fruits per plant (11.23%), days to first fruit set (9.89%), number of clusters per plant (9.45%), days to first fruit harvest (8.89%), days to first fruit maturity (7.89%), fruit yield per plant (6.97%), fruit length (4.76%), and number of flowers per cluster (4.55%). Similar major contributions of traits like days to 50% flowering, flowers per cluster, and fruits per plant were reported by Khanna and Misra (1977)^[9], Bhattacharya *et al.* (1979)^[5], and Prasanth (2003)^[12]. In contrast, Sekhar *et al.* (2008)^[17] and Spaldon *et al.* (2017)^[18] noted a lower contribution from traits such as days to 50% flowering and marketable yield. Traits with relatively lower contributions included fruit weight (3.23%), days to last fruit harvest (2.88%), seeds per fruit (2.67%), fruit breadth (2.56%), days to 50% flowering (2.34%), stem thickness (2.22%), 1000-seed weight (2.12%), locule number per fruit (1.45%), plant height and peduncle length (1.23% each), primary branches (0.98%), secondary branches (0.89%), and pericarp thickness (0.34%). Overall, traits such as fruits per cluster, fruits per plant, days to first fruit set, clusters per plant, and earliness-related traits accounted for 59.58% of the total divergence. These traits should be prioritized in parent selection for hybridization. Supporting this, Babu *et al.* (2018)^[2] also found that average fruit weight, number of fruits per plant, and locule number per fruit made significant contributions to genetic diversity in tomato.

**Fig 2:** Percentage of contribution of morphological characters towards divergence

Conclusions

This study revealed significant genetic diversity among 15 cherry tomato genotypes from West Garo Hills, Meghalaya, using Mahalanobis D² analysis. The genotypes were grouped into two clusters, with divergence unrelated to geographic origin, highlighting the importance of genetic

variability in breeding. Cluster I showed higher fruit yield and average fruit weight, while Cluster II exhibited greater diversity and early maturity traits. Key traits contributing most to genetic divergence included number of fruits per cluster, fruits per plant, and earliness traits. These findings support the use of genetically diverse local landraces in breeding programs to develop high-yielding, stress-tolerant cherry tomato varieties suited to regional conditions.

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Conflict of Interest

There is no conflict of interest related to the work.

References

1. Arya PS. Vegetable seed production principle. Kalyani Publisher; 2013. p. 1-2.
2. Babu MR, Reddy RK, Reddy KR, Rani AS, Saidaiah P. Genetic improvement for yield, quality and leaf curl virus resistance in tomato (*Solanum lycopersicum* L.). Journal of Pharmacognosy and Phytochemistry. 2018;1:1048-1055.
3. Barankevicz GB, Novello D, Resende JT, Schwarz K, Santos EF. Características físicas e químicas da polpa de híbridos de tomateiro, durante o armazenamento congelado. Horticultura Brasileira. 2015;33(1):7-11.
4. Bernousi I, Emami A, Tajbakhsh M, Darvishzadeh R. Studies on genetic variability and correlation among the different traits in *Solanum lycopersicum* L. Notulae Botanicae Horti Agrobotanici Cluj-Napoca. 2011;39(1):152-158.
5. Bhattacharyya MK, Nandpuri KS, Singh S. Genetic divergence in tomato. In: Symposium on Quality of Vegetables 93; 1979 Jun 11. p. 289-300.
6. Charlo HCO, Castoldi RLA, Fernandes C, Braz LT. Production of cherry tomato under protected cultivation carried out with different types of pruning and spacing. Acta Horticulturae. 2007;761:323-326.
7. Hancock RE. Alterations in outer membrane permeability. Annual Review of Microbiology. 1984;38(1):237-264.
8. Hussain I, Aslam-Khan S, Ali A, Farid A, Ali N, Ali SA, Masaud S, Hussain I, Azeem K, Raza H. Genetic diversity among tomato accessions based on agromorphological traits. Sains Malaysiana. 2018;47(11):2637-2645.
9. Khanna KR, Misra CH. Divergence and heterosis studies in tomato. SABRAO Journal. 1977;9(1):43-50.
10. Meena OP, Bahadur V. Genetic associations analysis for fruit yield and its contributing traits of indeterminate tomato (*Solanum lycopersicum* L.) germplasm under open field condition. Journal of Agricultural Science. 2015;7(3):148-155.
11. Najeema MH, Revanappa HP, Hadimani BI, Biradar IB. Evaluation of cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) genotypes for yield and quality traits. International Journal of Current Microbiology and Applied Sciences. 2018;7(6):2433-2439.

12. Prasanth SJ. Variability and divergence studies in tomato [M.Sc. thesis]. Dharwad: University of Agricultural Sciences; 2003.
13. Prema G, Indiresk KM, Santhosha HM. Evaluation of cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) genotypes for growth, yield and quality traits. Asian Journal of Horticulture. 2011;6(1):181-184.
14. Ramya R, Ananthan M, Krishnamoorthy V. Evaluation of cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme* (Dunal) A. Gray) genotypes for yield and quality traits. Asian Journal of Horticulture. 2016;11(2):329-334.
15. Reddy BR, Reddy DS, Reddaiah K, Sunil N. Studies on genetic variability, heritability and genetic advance for yield and quality traits in tomato (*Solanum lycopersicum* L.). International Journal of Current Microbiology and Applied Sciences. 2013;2(9):238-244.
16. Rosales MA, Cervilla LM, Sánchez-Rodríguez E, Rubio-Wilhelmi MD, Blasco B, Ríos JJ, Soriano T, Castilla N, Romero L, Ruiz JM. The effect of environmental conditions on nutritional quality of cherry tomato fruits: evaluation of two experimental Mediterranean greenhouses. Journal of the Science of Food and Agriculture. 2011;91(1):152-162.
17. Sekhar L, Prakash BG, Salimath PM, Sridevi O, Patil AA. Genetic diversity among some productive hybrids of tomato (*Lycopersicon esculentum* Mill). Karnataka Journal of Agricultural Sciences. 2008;21(2):264-265.
18. Spaldon S, Kumar S. Genetic divergence studies for quantitative and quality traits in tomato (*Solanum lycopersicum* L.). International Journal of Environment, Agriculture and Biotechnology. 2017;2(3):238788.
19. Swarup V. Vegetable science and technology in India. Kalyani Publishers; 2014. p. 293-295.