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Assessing genetic diversity of tomato (*Solanum lycopersicum*) genotypes cultivated under protected condition

RAVI GAUTAM[1], PRAVEEN K SINGH[1]*, ZAKIR HUSSIAN[1], B S TOMER[1], A K SINGH[2], SHALINI GAUR RUDRA[1], SANDEEP KUMAR LAL[1] and JUGENDRA KUMAR[1]

ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India

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ABSTRACT

Present study was carried out during 2018–19 and 2019–20 at ICAR-Indian Agricultural Research Institute, New Delhi to evaluate 16 quantitative and qualitative traits of 36 genotypes of Tomato (*Solanum lycopersicum* L.) and to examine the genetic variability and character association between yield and its component traits. This investigation involved correlation and genetic divergence analyses to gain insights into the relationships among the various traits. The variance analysis revealed notable variations among genotypes, indicating a substantial level of genetic diversity among them. Among the genotypes, 178 and 115 were found promising for both yield and quality traits. Genotype no. 178 was found superior for fruit weight and yield. The principal component analysis indicated that the first 3 components i.e. component 1 (equatorial diameter, average fruit weight and fruit weight uniformity); component 2 (number of locule and equatorial/polar index); and component 3 (number of fruit and number of fruit/cluster) collectively accounted for 81.48% of the variability. The yield exhibited significant positive correlation with average fruit weight (g), pericarp thickness (cm), polar diameter of fruit (cm), equatorial diameter of fruits (cm) and average fruit weight after each harvest (kg).

Keywords: Genetic diversity, Growth, Protected cultivation, Tomato, Yield potential

Tomato (*Solanum lycopersicum* L.) (2n = 24) is an important self-pollinated and typically day neutral vegetable crop belonging to Solanaceae family. Protected cultivation of tomatoes during off-season, particularly in urban and peri-urban areas presents a viable solution to overcome seasonal and regional limitations. Today, almost every innovative farmer accepts either of the protected cultivation practices and tries to adopt them in his farm. The estimated area coverage reported under protected cultivation in India is 1,75,000 ha. This method allows for the production of fresh and high-value vegetable crops such as tomatoes to meet demand. Additionally, utilizing net houses for protected cultivation proves effective in mitigating pesticide residue issues commonly associated with open-field tomato cultivation and productivity increases. Cherry tomatoes, which are small-sized and bear in clusters are becoming popular among both growers and consumers. For breeding of tomato varieties for greenhouse cultivation, many key traits are important including indeterminate growth habit, higher number of nodes/plant, shorter internodes, early maturity with an extended harvest period, greater number of fruits/cluster, and high yield with uniform fruit size. Similarly, breeding criteria for green flesh varieties include high acidity, total soluble solids, lycopene content and less *p*H (<4.5) for processing purposes. The development of high-yielding varieties requires detailed knowledge of the genetic variability present in the germplasm of the crop, the association among yield components, input requirements and cultural practices (Dutta *et al*. 2013). The present study was carried out to evaluate 36 tomato genotypes under protected conditions and assess the genetic variability present among them to identify suitable varieties for protected cultivation.

MATERIALS AND METHODS

The present study was carried out during 2018–19 and 2019–20 at ICAR-Indian Agricultural Research Institute, New Delhi. In this study, a set of 36 genotypes (Table 1) (collected from ICAR-National Bureau of Plant Genetic Resources, New Delhi; Central Protected Cultivation Technology, ICAR-Indian Agricultural Research Institute, New Delhi and local market, New Delhi) was evaluated in a polyhouse having clay loam soil. Two rows were planted on a single bed with a spacing of 120 cm × 50 cm. The experiment was carried out using randomized complete block design (RCBD) with three replications and

[1]ICAR-Indian Agricultural Research Institute, New Delhi; [2]ICAR-Research Complex for Eastern Region, Ranchi, Jharkhand. *Corresponding author email: pksingh128@gmail.com

Table 1 List of tomato genotypes and their sources

Source	Genotypes
ICAR-NBPGR, New Delhi	EC834023, EC 705445, EC 692277, EC 705448, EC 700934, EC 700937, EC 834012, EC 834015, EC 834018, IC 419437, IC 419435, EC 904113
CPCT, ICAR-IARI, New Delhi	No. 57-1, No. 68, No. 107, No. 115, No. 123, No. 167, No. 169, No. 177, No. 178, No. 186, No. 189, No. 191, No. 197, No. 204, No. 206, No. 220, No. 264, No. 271, No. 284, No. 292, No. 296, No. 304, No. 305
Local market, New Delhi	GS. 600

10 plants/entry/replication were planted. The study involved recording observations on various parameters, including plant height (m), number of fruits/cluster, fruit shape, number of locules, pericarp thickness (cm), fruit weight (g), yield (q) and fruit quality following standard procedures. Statistical analysis of variance (ANOVA) was conducted following Panse and Sukhatme (1967) method. Additionally, Pearson correlation coefficient analysis was carried out to examine the relationships among growth, yield and biochemical traits using NTSYS-pc.Version 2.1 (Exceter, USA). The genetic associations between genotypes were calculated using Euclidian distance coefficient and the matrix was subjected to construct of dendrogram based on unweighted pair group method for arithmetic mean (UPGMA). Principal Component Analysis (PCA) was conducted using the Euclidean distance coefficient (Rohlf 2000) as the basis for the analysis.

RESULTS AND DISCUSSION

Significant variations were observed in the analysis of variance for multiple parameters especially number of fruits/plant, fruit weight, yield at each harvest, and yield (q). Performance and grand mean of different tomato genotypes for different morphological parameters related to yield are depicted in Table 2. The overall mean, range of different quantitative traits for yield revealed substantial genetic variability among the tomato genotypes for all characters.

The plant height exhibited a wide range, varying from 1.23–5.93 m. The shortest and tallest plant height was observed in T-30 (1.23 m) and 220 (5.93 m), respectively. The results were found similar to the work done by Waiba *et al*. (2021). Regarding the number of fruits/cluster, there was considerable variation, ranging from 3.66–24.67. Genotype 305 had the highest number of fruits/cluster (24.67) while genotypes T-19, T-27, T-39 and T-46 produced the least number of fruits/cluster (each having 3.66). The average fruit cluster after internode showed a range from 1.00 to 3.00. Genotypes T-36, T-39 and 68 had the highest number of fruits/cluster after internode (3.00) whereas genotype 220 had the lowest. The average fruit weight showed a diverse range, spanning from 4.12–160.41 g. Genotypes 264 and 178 exhibited the lowest fruit weight (4.12 g) and the highest fruit weight (160.41 g), respectively. The number of locules/fruit varied from 2.00–5.00. Genotype 68 had the maximum number of locules (5.00) whereas genotypes T-18, T-22, T-30, T-46, 167, 169, 191, 197, 220, 264, 271, 292, 304, 305 and 904113 recorded the minimum number of locules (2 locules each). Similar results are supported by the findings of Bayomi *et al*. (2020).

The pericarp thickness of the fruits ranged from 0.20 to 0.70 cm. The highest pericarp thickness values were observed in genotypes 271, 284, and 189 (all with 0.7 cm), while the lowest values were found in T-50, 220 and 264 (all with 0.2 cm). The mean equatorial diameter of the fruits varied from 2.10–7.30 cm. Genotypes 115 and 178 exhibited the maximum fruit equatorial diameter (both 7.3 cm) while genotype 264 had the minimum fruit polar diameter (2.1 cm). The average polar diameter of the fruit fell within the range of 1.8–6.10 cm. The maximum polar diameter was observed in genotypes 115 and 178 (both 6.1 cm) while genotype 264 had the minimum polar diameter (1.8 cm). Regarding the equatorial/polar diameter of the fruits, the values ranged from 0.780–1.375. Similar results supported the findings of Sathiyavarsha *et al*. (2023) The highest equatorial/polar diameter was found in T-42 (1.375) while the minimum was recorded in T-50 (0.780). The fruit weight uniformity within clusters varied from 4.00–166.00g. Genotype 264 exhibited the minimum fruit weight within clusters (4.00 g) while genotype 178 had the maximum (166.00 g). The fruit yield (kg/plant) at each harvest ranged from 0.42–9.14 kg with an overall mean of 3.80 kg. Genotype 178 recorded the highest average fruit weight/plant at each harvest (9.143 kg) followed by 115 (8.501 kg), while genotype 264 had the lowest average fruit weight/plant at each harvest (0.428 kg) (Fig. 1).

Significant diversity was observed among different tomato genotypes concerning the total number of fruits/plant. The number of fruits/plant ranged from 23.00–202.00. Genotype 305 had the highest number of fruits/plant (202.00) while genotypes T-29 and T-27 had the lowest number of fruits/plant (both 23.00). The high F value compared to the critical F value indicated that the variation was statistically significant. Similarly, a wide variation was noted for the yield of fruits per 1000 m^2, ranging from 7.14–152.38 q with an average value of 63.60 q. Among the genotypes, 178 had the highest fruit yield/1000 m^2 (152.38 q) while the lowest fruit yield/1000 m^2 was observed in 264 (7.14 q). The high F value compared to the critical F value indicated that the variation in yield was statistically significant.

Correlation coefficients were calculated to examine the relationships between all the studied parameters and yield, both at the genotypic and phenotypic levels. Yield serves as a crucial trait that exhibits positive or negative correlations with all other traits. In this study, the yield/1000 m^2 demonstrated a significant positive correlation with average fruit weight (g), pericarp thickness (cm) and equatorial/polar diameter.

The genetic divergence analysis revealed the categorization of tomato genotypes into 8 groups based on their quantitative traits and yield performance. In Group-1,

Table 2 Quantitative and qualitative traits, values and promising genotypes

Trait required for protected cultivation	Values	Grand mean	Promising genotypes (Min. and Max.)
Plant height (m)	Min.- 1.23 Max.-5.93	3.72	T-23
			220
Fruit cluster after internode	Min.-1	2.05	220
	Max.- 3		T-36, T-39, 68
Average fruit weight (g)	Min.-4.12	63.55	264
	Max.-160.41		178
No. of locules	Min.-2	2.77	T-18, T-22, T-30, T-46, T-50, 167, 169, 191, 197,220, 264, 271, 292, 304, 305, 904113
	Max.-5		68
Pericarp thickness (cm)	Min.-0.2	0.48	220, 264, T-50
	Max.-0.7		271, 284, 189
Fruit equatorial diameter (width) (cm)	Min.-2.1	4.77	264
	Max.-7.3		178, 11
Fruit polar diameter (length) (cm)	Min.-1.8	4.36	264
	Max.-6.1		178, 115
Equatorial/polar diameter (cm)	Min.-0.78	1.09	T-50
	Max.-1.375		T-42
Fruit weight uniformity within cluster (g)	Min.-4	65.37	264
	Max.-166		178
No. of fruits/plant	Min.-23	65.02	T-19, T-27
	Max.-202		305
No. of fruits/cluster	Min.-3.66	7.53	T-19, T-27, T-39, T-46
	Max.-24.67		305
Yield (kg/plant) at each harvest	Min.-0.428	3.80	264
	Max.-9.143		178
Yield/1000 m^2 (q)	Min.-7.14	63.60	264
	Max.- 152.38		178
Plant growth habit	Determinate	N/A	T-22, T-30, 204
	Indeterminate		Rest all are Indeterminate
Fruit colour at maturity	Yellow	N/A	68, 220, 284
	Red		Rest all are red
Fruit shape	Spherical	N/A	T-18, T-50, 220, 264, 305
	Oblong		T-22, T-46, 204, 904113
	Flattish-Round		T-30, T-36, T-39, T-42
	Round		Rest all are round

genotypes T-18, 220, 305 and 264 (Table 3 and Fig. 2) exhibited similar average fruit weight within the range of 4.12–12.35 g belonging to the cherry group and had 2.00 locules in their fruits. The highest pairwise Euclidean distance coefficient was observed between T-18 and 264 measuring 0.6, while the lowest distance was between 305 and 220 measuring 0.4. In Group-2, genotypes T-19, T-27 and T-39 shared similar equatorial/polar diameters of fruits ranging from 1.153–1.195 and had a similar number of fruits per plant, with a range of 23–27 fruits. The highest pairwise Euclidean distance coefficient was found between T-27 and T-39 measuring 0.7, while the lowest distance was between T-19 and T-27 measuring 0.3. In Group-3, genotypes T-22, T-36, 197 and 177 exhibited similar numbers of fruits per plant, ranging from 39–49 fruits. The highest pairwise Euclidean distance coefficient was observed between T-22 and 197 measuring 0.7, while the lowest distance was between T-36 and 197 measuring 0.3. In Group-4, genotypes 123, 191, 204 and 296 exhibited similarities in fruit cluster after internode, with the same number of internodes (2). The highest pairwise Euclidean distance coefficient (0.5) was observed between 123 and 204 while the lowest distance was between 123 and 191 (0.2).

In Group-5, genotypes 107, 189, 115, and 178 displayed similar average fruit weights, all exceeding 100g (>100 g). The maximum pairwise Euclidean distance coefficient (0.4)

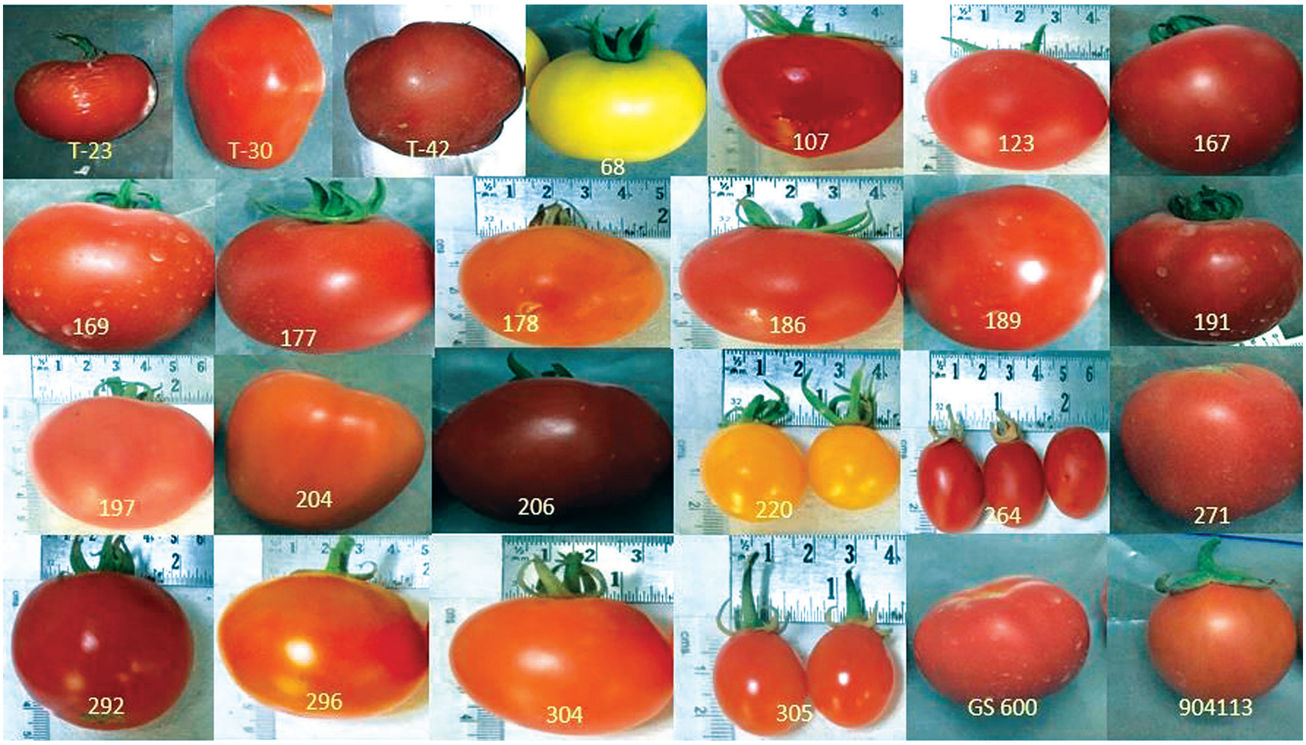

Fig. 1 Pictorial representation of genotypes.

Table 3 Cluster membership and number of genotypes in each cluster of tomato

Cluster/Group number	Genotypes	Number of genotypes
1	T-18, 220, 305, 264	4
2	T-19, T-27, T-39	3
3	T-22, T-36, 197, 177	4
4	123, 191, 204, 296	4
5	107, 189, 115, 178	4
6	57-1, 206, 68, GS-600, 169, 304	6
7	186, 271, 292	3
8	T-23, T-30, 904113	3
Total		27

was found between 107 and 115 and similarly, between 107 and 178 while the minimum distance was between 115 and 178 (0.2). In Group-6, genotypes 57-1, 206, 68, GS-600, 169 and 304 demonstrated similarities in yield per 1000 m^2., all exceeding 119.25 q (>119.25 q). The highest pairwise Euclidean distance coefficient (0.9) was observed between 169 and 206, while the minimum distance was between 68 and GS-600 (0.1). In Group-7, genotypes 186, 271 and 292 exhibited similarities in the number of fruits per cluster, ranging from 6.33–7.33 and also in average fruit weight, ranging from 54.61–57.16 g. The highest pairwise Euclidean distance coefficient (0.5) was found between 186 and 292 and similarly, between 271 and 292 while the minimum distance was between 186 and 271 (0.1). In Group-8, genotypes T-23, T-30 and 904113 shared similarities in average fruit weight, ranging from 23.45–26.27 g, fruit weight uniformity within clusters, ranging from 25.33–28.33 g, average fruit weight per harvest ranging from 1.022–1.149 kg and yield/1000 m^2, ranging from 17.04–19.15 q. The highest pairwise Euclidean distance coefficient (0.7) was observed between T-23 and T-30 while the minimum distance was between T-30 and 904113 (0.7).

The Principal Component Analysis indicated that the first three components collectively accounted for 81.48% of the variability (Table 4). Component one contributed significantly to the genetic diversity with a contribution of

Table 4 Principal component analysis-contribution of different quantitative parameters

Parameter	C1	C2	C3	C4
NFC	-0.5	0.8	0.2	-0.2
AFW	0.9	0.2	-0.1	0
NOL	0.5	-0.2	0.6	-0.3
ED	0.9	0.1	0	0
PD	0.9	-0.1	-0.4	-0.3
EPI	0.6	0	0.6	0.5
FWU	0.9	0.1	-0.1	0
AFWH	0.9	0.5	0	-0.1
NOF	-0.3	0.9	0.2	-0.2
Y1000	0.9	0.5	0	-0.1
Genetic diversity contribution	51.2139	20.3916	9.8841	-------

NFC, No. of fruits/cluster; AFW, Average fruit weight; NOL, No. of locules; D, Equatorial diameter; FPD, Fruit polar diameter; EPI, Equatorial polar diameter; FWU, Fruit weight uniformity; AFWH, Average fruit weight/harvest; NOF, No. of fruits/plant; Y1000, Fruit yield/1000 m^2.

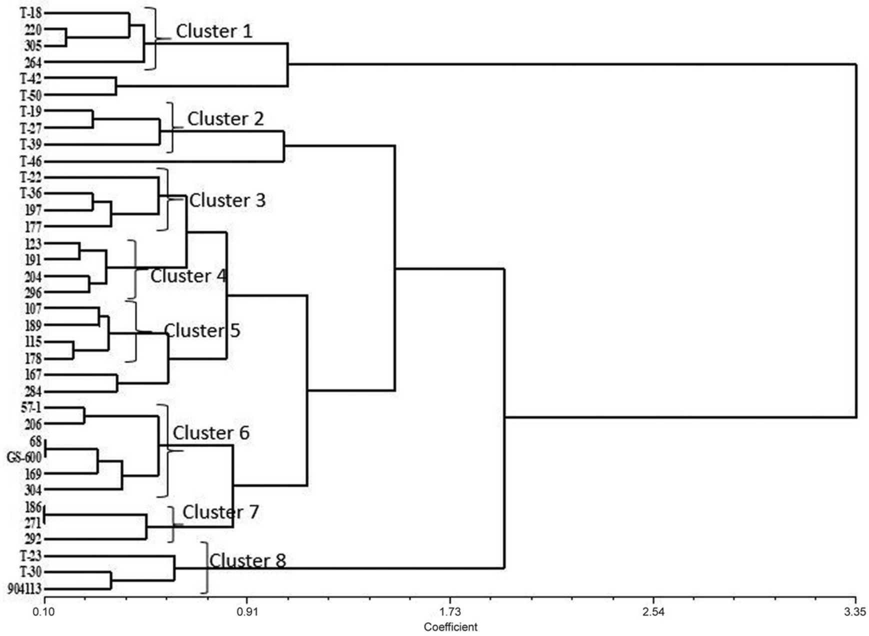

Fig. 2 Dendrogram of morphological data.

51.21%. Among the parameters analyzed (AFW, AFWH, and Y/1000), average fruit weight exhibited a significant contribution with a value of 0.9. Moreover, average fruit weight per plant at each harvest and yield/1000 m^2 also demonstrated noteworthy contributions with values of 0.9 (Table 4). Cluster 1 has fruit weight uniformity within a cluster, average fruit weight and equatorial diametre in which the contribution of component one in diversity is 0.9, 0.9, 0.9, respectively (Fig. 3).

Considerable variations were noted in various quantitative and qualitative traits examined such as plant height, number of fruits/cluster, fruit equatorial diameter, fruit polar diameter, fruit shape index, number of locules, pericarp thickness, average fruit weight, fruit cluster after number of internode, fruit weight uniformity within cluster, number of fruits/plant, average fruit weight/plant at each harvest, fruit shape, plant habit, fruit colour at maturity and yield/1000 m^2.

Significant genetic divergence analysis revealed that tomato genotypes were agro-morphological. Our results are in corroboration the findings of other researchers who worked on different sets of tomato genotypes under field as well as protected structures (Bhatt *et al*. 2004, Cheema *et al*. 2004, Dar *et al*. 2011, Dhaliwal and Jindal 2017, Jatav *et al*. 2017, Murkute *et al*. 2017, Premalakshmi *et al*. 2017, Malavika *et al*. 2018, Venkadeswaran *et al*. 2018).

The yield is controlled by multiple factors. Thus, the analysis of correlation coefficient measures the degree of proximity of the component traits. As yield is one of the main traits with which all other traits are positively or negatively correlated. In the present investigations the yield/1000 m^2 showed a significant positive correlation with average fruit weight (g), pericarp thickness (cm), polar diameter of fruit (cm), equatorial diameter of fruit (cm), fruit weight uniformity within cluster (g) and average fruit weight after each harvest (kg). This showed that these traits play an important role in the selection point of view for getting higher tomato yield. Similar results were supported by the findings of Anjum *et al*. (2009) and Khapte and Jansirani (2014) for fruit weight and no. of fruit/plant (Hannan *et al*. 2007 and Souza *et al*. 2012). On the other hand, average fruit weight showed significant positive correlation with pericarp thickness, polar diameter of fruit, equatorial diameter of fruit, equatorial/polar diameter, fruit weight uniformity within the cluster, average fruit weight after each harvest and yield/1000 m^2. The results were found similar to the work done by Prasad and Rai (1999) and Kumar *et al*. (2013).

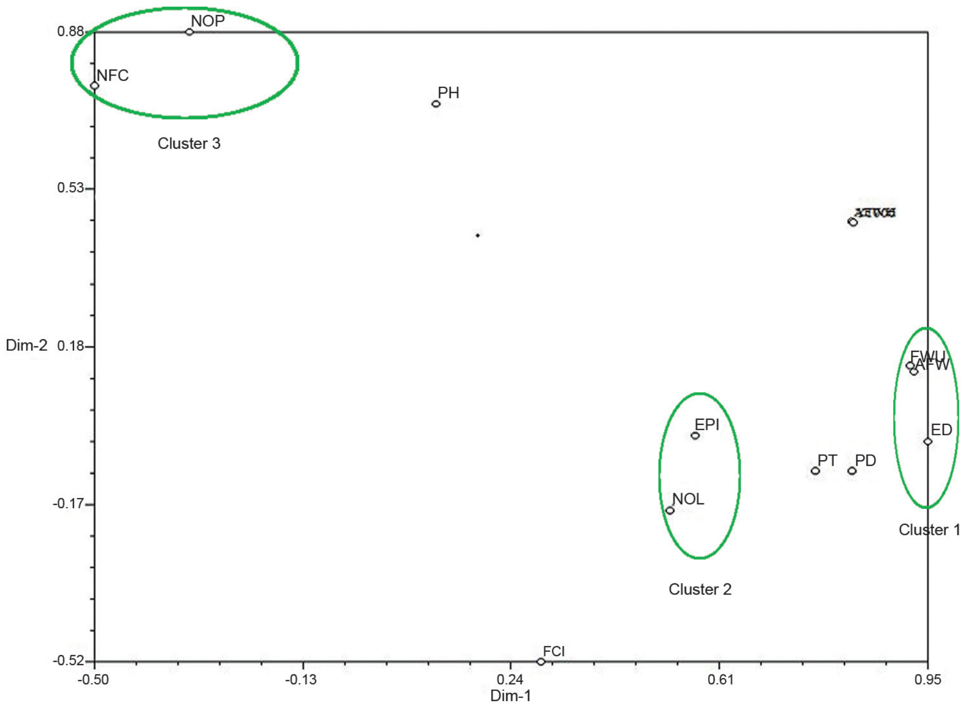

Fig. 3 Dendrogram of morphological data.

The promising genotypes like no. 305 for highest number of fruits/cluster, no.178 for fruit weight, and yield were found superior which can be further used in breeding programmes for the development of new tomato varieties suitable for green house cultivation. The present findings provide important information regarding the genetic diversity of tomato germplasm. The observation will pave the way for strengthening tomato genetic improvement of tomatoes for protected cultivation. The promising genotypes identified in the present study will serve as useful parental material for the development of future hybrids for protected cultivation.

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