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Assessment of genetic diversity in tomato (*Solanum lycopersicon* L.) genotypes using cluster and principal component analysis

Bhavesh Verma, Dhananjay Sharma and Jhanendra Kumar Patel

Abstract
Selection of diverse and superior parents is the most important task to be performed before quality improvement program. Tomato is one of the most important vegetable crops, which provides several important dietary components and high nutritional value. The present investigation aimed to assess genetic diversity using cluster and principal component analysis. For this purpose, fifteen tomato genotypes were evaluated in the field of AICRP on vegetable crops, Horticultural Research cum Instructional Farm, Department of Vegetable Sciences, Indira Gandhi Krishi Vishwavidyalaya, Raipur during 2019-20 in randomized complete block design with three-replication. There is considerable diversity among genotypes for morphological and quality traits. In cluster analysis, the genotypes were a grouped into five distinct clusters. The highest number of genotypes appeared in cluster V which possessed 5 genotypes and the lowest genotype was found in cluster II and IV comprised of only one genotype; 2019/TODVAR-8 and 2019/TODVAR-9. The maximum intra-cluster distance was obtained for cluster I followed by cluster III. The minimum intra-cluster D^2 values were observed by cluster II, IV, V, and the highest inter cluster D^2 values were observed between cluster III and IV followed by cluster I and IV, and cluster I and II and the lowest inter-cluster D^2 value was found between cluster I and III followed by cluster III and V. PCA showed the contribution of each character to the classification of the tomato genotypes. The first five principal components explained about 84.50% of the total variation among the fifteen characters. On the basis of PC score it is cleared that 2019/TODVAR-9 is the best genotype for both quality and yield traits followed by 2019/TODVAR-8.

Keywords: Diversity, PCA, cluster analysis, genotypes

Introduction
Tomato (*Solanum lycopersicum* L.) is one of the most important vegetables (Zhou *et al.* 2015) with chromosome number 2n=24 belong to the nightshade family Solanaceae. It is a herbaceous, annual to perennial, sexually propagated and typically day-neutral plant. Due to its high nutritional value and various uses, tomato is the second most consumed vegetable crop after potato in the world. The optimal temperature for tomato growth and fruit set ranges from 25-30 °C to 22-25 °C. It has determinate or indeterminate growth habits. Scientific evidence suggests that the cultivated tomato originated in the Peru-Ecuador-Bolivia area of the Andes (South American). Among many tomato varieties, only two species (*Lycopersicon esculantum* and *L. pimpinellifolium*) are commonly edible. Even if the origin of the tomato is South America, it is produced in a wide area of the world. Especially, China, India, Türkiye and the USA are globally shining out for tomato production (FAO, 2021) [3]. A loss of genetic diversity, particularly among commercial cultivars, has resulted from numerous genetic bottlenecks caused by self-pollination or artificial selection throughout the domestication phase of the cultivated tomato.

Tomato pulp and juice are digestible moderate aperients and gastric secretion promoters and blood purifiers. The red color of the tomato is due to the presence of a pigment called "Lycopene" varying from 30 to 50 mg/100 g of the edible part. Due to the relatively high content of key antioxidant components, the regular consumption of tomatoes lowers the danger of developing different diseases, including various forms of cancers and heart diseases. The yellow and orange color of tomato fruit is due to the presence of carotene and prolycopene (tangerine) pigments; both are anti-oxidants, respectively.

Phenotypic evaluation in tomatoes has traditionally been based on seed and fruit characteristics. Although the tomatoes are self-pollinated crops, there is a genetic diversity was found not only in morphological features but also in quality attributes (Abushita *et al.*, 2000) [1].

In India, the yield of tomatoes (*Solanum lycopersicon* L.) is lower than the global average. So the development of superior varieties/hybrids is needed to boost productivity. Because yield is a complex character, its direct improvement is difficult. Therefore, the evaluation of tomato germplasm is of great importance for crop agronomic and genetic enhancement in the current and future time (Ramzan *et al.*, 2014) [7]. Tomato yield is a multigenic trait and is greatly affected by environmental factors (Wang *et al.*, 2021) [9]. The breeders used potential hybridization techniques to obtain tomatoes with high-yield potential. Crop genetic diversity should be considered a sustainable approach for a climate-resilient and self-dependent production system. The higher the genetic diversity in farming land, the more chance of receiving multiple benefits in the agriculture system. Selection of diverse and superior parents is the most important task to be performed before any hybridization or quality improvement program. Genetic diversity is an effective way to determine the genetic variation among the genotypes. Diversity not only induces variations but also provides new combinations of genes. Therefore, information on the nature and degree of genetic divergence generally helps in the selection of appropriate parents for the breeding program.

Materials and Methods

The experimental materials consisted of fifteen determinate-type tomato genotypes that were spread out in a three-replication randomized block design (RBD). Crops are shown in plot size 3.6 x 3.0 m. Firstly, prepared the nursery beds to get the seedlings of tomato crops and then transplanted them in the main plot. For transplanting different treatments, a plot size of 3.6 × 3m was prepared. Healthy seedlings were selected from the nursery and were transplanted on 20/11/2020 with a spacing of 60×40 cm, respectively. Newly planted tomatoes were irrigated lightly to keep the soil moist. During the early growing period, watering was done daily in the early morning. During severe temperatures, the plants were watered daily twice.

All the 15 determinate types of genotypes are from entries of AICRP on Vegetable Crops, IGKV, Raipur, Chhattisgarh.

Table 1: List of tomato (*Solanum lycopersicon* L.) genotypes and their sources

S. No.	Treatments	Source
1.	2018/TODVAR-1	AICRP on Vegetable Crops, Raipur, Chhattisgarh
2.	2018/TODVAR-2	AICRP on Vegetable Crops, Raipur, Chhattisgarh
3.	2018/TODVAR-3	AICRP on Vegetable Crops, Raipur, Chhattisgarh
4.	2018/TODVAR-5	AICRP on Vegetable Crops, Raipur, Chhattisgarh
5.	2018/TODVAR-6	AICRP on Vegetable Crops, Raipur, Chhattisgarh
6.	2019/TODVAR-1	AICRP on Vegetable Crops, Raipur, Chhattisgarh
7.	2019/TODVAR-2	AICRP on Vegetable Crops, Raipur, Chhattisgarh
8.	2019/TODVAR-3	AICRP on Vegetable Crops, Raipur, Chhattisgarh
9.	2019/TODVAR-4	AICRP on Vegetable Crops, Raipur, Chhattisgarh
10.	2019/TODVAR-5	AICRP on Vegetable Crops, Raipur, Chhattisgarh
11.	2019/TODVAR-6	AICRP on Vegetable Crops, Raipur, Chhattisgarh
12.	2019/TODVAR-7	AICRP on Vegetable Crops, Raipur, Chhattisgarh
13.	2019/TODVAR-8	AICRP on Vegetable Crops, Raipur, Chhattisgarh
14.	2019/TODVAR-9	AICRP on Vegetable Crops, Raipur, Chhattisgarh
15.	PANT Tomato-3	AICRP on Vegetable Crops, Raipur, Chhattisgarh

A field experiment was conducted at AICRP on vegetable crops, Horticultural Research cum Instructional Farm, Department of Vegetable Sciences, Indira Gandhi Krishi Vishwavidyalaya, Raipur, during 2019-20. Raipur is located between 22˚33' N to 21˚14' N latitude and 82˚6' E to 81˚38' E longitude in the Middle Eastern part of Chhattisgarh state. As per the observations recorded at Agro-meteorological Observatory, IGKV, Raipur, the Maximum temperature varied between 21.3 °C to 39.0 °C as against the normal of 29.63 °C. Similarly, the minimum temperature varied between 10.8 °C to 23.0 °C as against the normal of 16.70 °C. Around 1080.8 mm of rainfall was recorded during session 2019-20.

The fertilizer application depends on the soil requirement. Full doses of P_2O_5 and K_2O are applied and half of the N fertilizer was applied as a basal dose and the rest of the N fertilizer was applied 30 and 60 days after transplanting as a top dressing. The intercultural operations *viz*., hoeing, earthing up, irrigation, fertigation, weeding, cutting, training, pruning, and staking were carried out following recommended package of practices to ensure a healthy crop development.

Observations were recorded on a single-plant basis from five randomly tagged competitive plants of each genotype for all the traits separately. The fruit picking was done during the coolest period on each genotype and the number of pickings counted and cumulative yield was taken.

For statistical analysis, average values of each genotype in each replication were used for every trait of interest. The Statistical analyses windostat 9.2 are used for diversity analysis using cluster and principal component analysis.

Results and Discussion

Genetic divergence analysis through cluster analysis

The existence of genetic divergence among the 15 genotypes of tomato was examined by employing Mahalanobis D^2-statistics. The clustering pattern of 15 genotypes on the basis of the D^2-statistics analysis has been presented in Table 2. The genotypes were a grouped into five distinct clusters. The highest number of genotypes appeared in cluster V which possessed 5 genotypes namely, 2019/TODVAR-4, 2019/TODVAR-5, 2019/TODVAR-6, 2019/TODVAR-7 and Pant Tomato 3. The second highest number of genotypes was found in cluster I and III which was comprised of 4 genotypes namely, 2018/TODVAR-1, 2018/TODVAR-2, 2019/TODVAR-1, 2019/TODVAR-2 and 2018/TODVAR-3, 2018/TODVAR-5, 2018/TODVAR-6, 2019/TODVAR-3, respectively. The lowest genotype was found in cluster II and IV comprised of only one genotype; 2019/TODVAR-8 and 2019/TODVAR-9.

Intra and inter clusters distance

The estimate of intra and inter cluster distance represent by D^2 values have been given in Table 3. The maximum intra-cluster distance was obtained for cluster I (19.22) followed by cluster III (17.58). The minimum intra-cluster D^2 values were shown by cluster II (0.00), IV (0.00), V (0.00), they all have only one genotype. The highest inter cluster D^2 values were observed between cluster III and IV (31.15) followed by cluster I and IV (28.99), and cluster I and II (24.67). The lowest inter-cluster D^2 value was found between cluster I and III (8.68) followed by cluster III and V (14.55).

Inter cluster mean

Cluster II (74.31) showed the highest cluster mean for plant height followed by cluster III (58.39) and cluster IV (58.10). The lowest cluster mean was showed by cluster V (56.05). Cluster II (8.67) showed the highest cluster mean for number of primary branches followed by cluster IV (8.33) and cluster V (8.07). The lowest cluster mean was showed by cluster I (5.17). Cluster IV (15.00) showed the highest cluster mean for number of secondary branches followed by cluster V (14.07) and cluster II (12.67). The lowest cluster mean was showed by cluster I (8.92). Cluster III (36.92) showed the highest cluster mean for days to 50% flowering followed by cluster II (34.33) and cluster I (33.58). The lowest cluster mean was showed by cluster IV (32.33). Cluster II (34.67) showed the highest cluster mean for days to fruit maturity followed by cluster V (33.00) and cluster II (32.33). The lowest cluster mean was showed by cluster IV (31.33). Cluster III (67.17) showed the highest cluster mean for fruit weight followed by cluster II (64.33) and cluster I (63.83). The lowest cluster mean was showed by cluster IV (62.33). Cluster IV (89.61) showed the highest cluster mean for polar diameter followed by cluster II (75.44) and cluster V (71.75). The lowest cluster mean was showed by cluster III (61.53). Cluster II (5.25) showed the highest cluster mean for equitorial diameter followed by cluster IV (5.06) and cluster V (4.72). The lowest cluster mean was showed by cluster III (4.33). Cluster IV (6.35) showed the highest cluster mean for number of fruits per cluster followed by cluster II (5.41) and cluster V (4.93). The lowest cluster mean was showed by cluster I (4.20). Cluster IV (4.47) showed the highest cluster mean for pericarp thickness followed by cluster V (4.01) and cluster II (4.00). The lowest cluster mean was showed by cluster III (3.10). Cluster IV (4.64) showed the highest cluster mean for total soluble solids followed by cluster I (4.58) and cluster II & III (4.56). The lowest cluster mean was showed by cluster V (4.43). Cluster III (0.78) showed the highest cluster mean for acidity followed by cluster I (0.71) and cluster II (0.68). The lowest cluster mean was showed by cluster V (0.66). Cluster II (0.84) showed the highest cluster mean for pulp juice ratio followed by cluster III (0.83) and cluster III (0.80). The lowest cluster mean was showed by cluster V (0.75). Cluster IV (1.93) showed the highest cluster mean for fruit yield per plant followed by cluster II (1.90) and cluster V (1.75). The lowest cluster mean was showed by cluster I (1.14). Cluster IV (35.64) showed the highest cluster mean for fruit yield per hectare followed by cluster II (35.21) and cluster V (32.64). The lowest cluster mean was showed by cluster I (21.00). Similar result found by Reddy *et al.* 2013 [8] and Meena and Bahadur, 2017 [5].

Table 2: Genotypes included in different clusters based on D^2 analysis in tomato

Clusters No.	No. of genotypes	Name of the genotypes
I	4	2018/TODVAR-1, 2018/TODVAR-2, 2019/TODVAR-1, 2019/TODVAR-2
II	1	2019/TODVAR-8
III	4	2018/TODVAR-3, 2018/TODVAR-5, 2018/TODVAR-6, 2019/TODVAR-3
IV	1	2019/TODVAR-9
V	5	2019/TODVAR-4, 2019/TODVAR-5, 2019/TODVAR-6, 2019/TODVAR-7, Pant Tomato 3

Table 3: Average intra and inter cluster distance

Cluster No	I	II	III	IV	V
I	19.22	24.67	8.68	28.99	14.55
II		0.00	23.83	21.90	19.01
III			17.58	31.15	14.53
IV				0.00	18.41
V					0

Table 4: Cluster means for yield and its components in 15 tomato genotypes

Class	I	II	III	IV	V
Plant height (cm)	57.50	74.31	58.39	58.10	56.05
Number of Primary branches	5.17	8.67	6.17	8.33	8.07
Number of Secondary branches	8.92	12.67	10.50	15.00	14.07
Days 50% flowering	33.58	34.33	36.92	32.33	32.87
Days to fruit maturity	32.08	32.33	34.67	31.33	33.00
Fruit weight	63.83	64.33	67.17	62.33	62.87
Polar diameter	65.78	75.44	61.53	89.61	71.75
Equatorial diameter	4.46	5.25	4.33	5.06	4.72
No. of fruits per cluster	4.20	5.41	4.54	6.35	4.93
Pericarp thickness	3.57	4.00	3.10	4.47	4.01
T.S.S.	4.58	4.56	4.56	4.64	4.43
Acidity	0.71	0.68	0.78	0.67	0.66
Pulp juice ratio	0.77	0.84	0.80	0.83	0.75
Fruit yield per plant	1.14	1.90	1.40	1.93	1.75
Fruit yield per hectare	21.00	35.21	25.87	35.64	32.64

Principal component analysis

Principal component analysis (PCA) is a powerful tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets. With minimal effort, PCA provides a roadmap for how to reduce a complex data set to a lower dimension to reveal sometimes hidden, simplified structures that often underlie it. It reduces the dimensionality of the data while retaining most of the variation in the data set. PCA accomplishes this reduction by identifying directions, called Principal Components (PCs), along which the variation in the data is maximal. By using a few components, each sample can be represented by relatively few numbers instead of by values for thousands of variables. Thus, the primary benefit of PCA arise from quantifying the importance of each dimension for describing the variability of a data set in more interpretable and more visualized dimensions through linear combinations of variables that accounts for most of the variation present in the original set of variables. Therefore, principal component analysis is a variable reduction procedure.

In the present investigation, PCA was performed for fifteen fruit yield and quality contributing traits in 15 genotypes of tomato presented in Table 5. As per the criteria set by Brejda *et al.* (2000) [2], the PC with Eigen value >1 in the data were considered in the present study. The PC with higher Eigen values and variables which had high factor loading was considered as best representative of system attributes. Out of 15, only five principal components (PCs) exhibited more than 1 Eigen value, and showed about 84.50% cumulative variability among the traits studied. So, these 5 PCs were given due importance for further explanation. The PC^{-1} showed 42.50% while, PC-2, PC-3, PC-4 and PC-5 exhibited 16.30%, 10.00%, 8.30% and 7.40% variability, respectively among the genotypes for the traits under study. The first PC accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible.

Table 5: Eigen values of 15 yield and quality traits of 15 tomato genotypes

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14	PC15
Eigenvalues	**6.38**	**2.44**	**1.50**	**1.25**	**1.11**	**0.90**	**0.71**	0.38	0.15	0.10	0.07	0.01	0.01	0.00	0.00
Variability %	42.50	16.30	10.00	8.30	7.40	6.00	4.70	2.50	1.00	0.70	0.50	0.10	0.00	0.00	0.00
Cumulative %	42.50	58.80	68.80	77.10	84.50	90.50	95.20	97.80	98.70	99.40	99.90	100.00	100.00	100.00	100.00

Table 6: Factor loading (Eigen vectors) of 15 tomato genotypes for yield and quality traits

Traits	Components				
	PC1	**PC2**	**PC3**	**PC4**	**PC5**
Plant height (cm)	0.04	0.11	0.37	0.04	0.71
Number of Primary branches	0.34	0.23	0.13	0.18	-0.06
Number of Secondary branches	0.34	0.24	-0.01	0.16	-0.21
Days 50% flowering	-0.16	0.52	0.26	-0.14	-0.04
Days to fruit maturity	-0.08	-0.20	0.37	0.54	-0.29
Fruit weight	-0.18	0.51	0.24	-0.14	-0.04
Polar diameter	0.33	0.06	-0.24	-0.26	0.07
Equatorial diameter	0.27	-0.13	0.02	-0.42	-0.04
No. of fruits per cluster	0.32	0.25	-0.07	-0.11	0.02
Pericarp thickness	0.33	-0.23	0.02	-0.18	0.06
T.S.S.	-0.06	0.22	-0.44	0.35	0.45
Acidity	-0.19	0.22	-0.02	-0.27	-0.33
Pulp juice ratio	0.02	-0.26	0.53	-0.25	0.19
Fruit yield per plant	0.37	0.11	0.14	0.19	-0.07
Fruit yield per hectare	0.37	0.08	0.15	0.21	-0.07

Values in bold represent highly weighted factors in respective PC

Scree plot explained the percentage of variation associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. First 5 components explains the 84.50% variation and eign value >1. The PC^{-1} showed 42.50% variability with eigen value 6.38 which then declined gradually. From the graph, it is clear that the maximum variation was observed in PC^{-1}. Similarly, Meena and Bahadur, 2017 [5] also observed that more than 70% variation is present in first four principal component and Merk *et al.* 18 reported that the first three PCs explained 57.1% of the total variation for 143 promising tomato genotypes evaluated in North America.

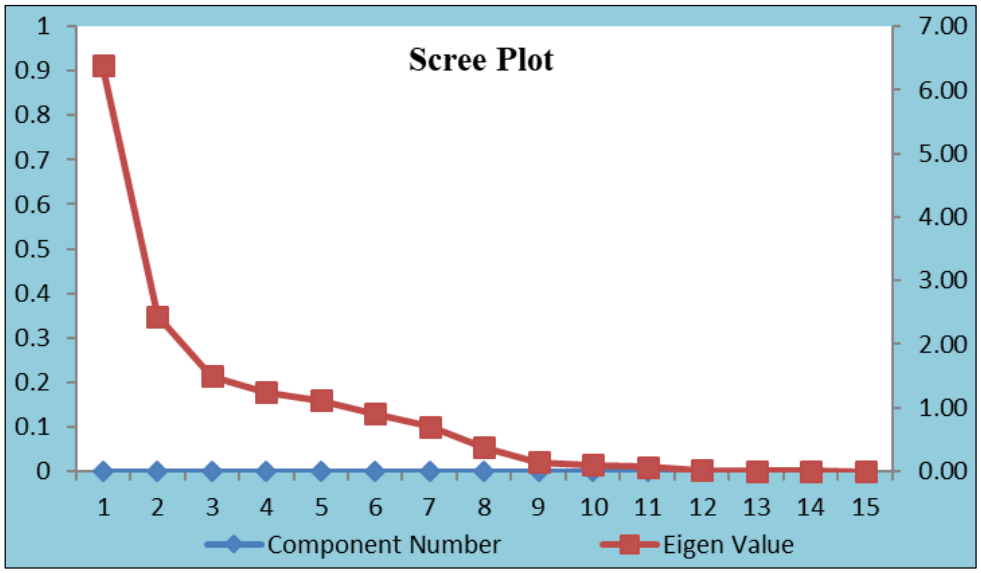

Fig 1: The different of component number and Eigen value

The results of the PCA explained the genetic diversity of the tomato genotypes. Proper values measure the importance and contribution of each component to total variance, whereas each co-efficient of proper factors indicates the degree of contribution of every original variable with which each principal component is associated. The higher the coefficients, regardless of the direction (positive or negative), the more effective they will be in discriminating between accessions.

Within each PC, only highly loaded factors or traits were retained for further explanation. Component matrix revealed that the PC^{-1} which accounted for the highest variability (42.50%) was mostly related with traits such as fruit yield per plant (0.37) and fruit yield per hectare (0.37) followed by number of primary branches (0.34), number of secondary branches (0.34), polar diameter (0.33), pericarp thickness (0.33), number of fruits per cluster (0.32) and equatorial diameter (0.27) (Table 6). As a result, the first component differentiated those genotypes that have high fruit yield per plant, fruit yield per hectare, number of primary branches, number of secondary branches, polar diameter, pericarp thickness, number of fruits per cluster and equatorial diameter. The second principal component accounted for 16.30% of total variance. Variables highly and positively correlated were days to 50% flowering, fruit weight and acidity. The third principal component accounted for 10.00% of the variability and was highly loaded with pulp juice ratio. The PC-4 was positively and more related with days to fruit maturity and the PC-5 was positively related with plant height (0.71) and total soluble solid (0.45). Thus, the prominent characters coming together in different principal components and contributing towards explaining the variability have the tendency to remain together which may be kept into consideration during utilization of these characters in breeding program.

Top 05 principal component scores (PC scores) for all the genotypes were estimated in five principal components and presented in Table 7. These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of the principal component. High PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype. Perusal of results revealed that the 2019/TODVAR-9 had highest PC score followed by 2019/TODVAR-6, 2019/TODVAR-8, PANT Tomato-3 and 2019/TODVAR-7 in PC^{-1} indicated that they had high quality and yield characters. In PC-2, 2019/TODVAR-7 had the highest score followed by 2018/TODVAR-5, 2018/TODVAR-6, 2019/TODVAR-8 and 2019/TODVAR-9 for the highly loaded component traits. The highest PC score of PC-3 recorded by 2018/TODVAR-3 followed by 2019/TODVAR-8, 2019/TODVAR-3, 2019/TODVAR-5 and PANT Tomato-3 it indicates that they had high yielding characters. In PC-4 2019/TODVAR-3 had highest score followed by 2018/TODVAR-6, 2019/TODVAR-4, 2019/TODVAR-1 and PANT Tomato-3 for yield related trait. In PC-5 2019/TODVAR-8 had highest score followed by 2019/TODVAR-1, 2019/TODVAR-3, 2019/TODVAR-9 and 2019/TODVAR-2. On the basis of top 5 PC scores in each principal component, genotypes are selected and presented in summarized form in Table 8.

Thus, it is cleared that the principal component analysis highlights the characters with maximum variability. So, intensive selection procedures can be designed to bring about rapid improvement of yield and quality traits. PCA also help in ranking of genotypes on the basis of PC scores in corresponding component.

Table 7: Principal component score of different genotypes

Genotypes	PC1	PC2	PC3	PC4	PC5
2018/TODVAR-1	-1.01	-0.48	-0.54	-1.75	0.33
2018/TODVAR-2	-1.10	-0.06	-0.82	-0.71	0.55
2018/TODVAR-3	-1.00	-0.10	2.62	-1.31	-0.68
2018/TODVAR-5	-1.05	1.66	-0.59	0.00	-0.96
2018/TODVAR-6	-0.90	0.63	-0.14	1.29	-0.63
2019/TODVAR-1	-0.73	-0.97	0.06	0.60	0.83
2019/TODVAR-2	-0.53	-0.61	-1.71	-0.13	0.56
2019/TODVAR-3	-0.35	-0.14	0.71	1.89	0.68
2019/TODVAR-4	0.33	-0.68	-0.10	1.10	0.42
2019/TODVAR-5	0.37	-1.05	0.26	0.25	-0.61
2019/TODVAR-6	1.24	-0.56	-0.34	-0.78	-1.54
2019/TODVAR-7	0.71	2.47	0.02	0.23	-0.25
2019/TODVAR-8	1.15	0.49	1.22	-0.43	2.17
2019/TODVAR-9	1.77	0.36	-0.82	-0.81	0.63
PANT Tomato-3	1.09	-0.97	0.18	0.57	-1.49

Table 8: List of selected genotype in each principal component on the basis of top 05 PC score

PC1	PC2	PC3	PC4	PC5
2019/TODVAR-9	2019/TODVAR-7	2018/TODVAR-3	2019/TODVAR-3	2019/TODVAR-8
2019/TODVAR-6	2018/TODVAR-5	2019/TODVAR-8	2018/TODVAR-6	2019/TODVAR-1
2019/TODVAR-8	2018/TODVAR-6	2019/TODVAR-3	2019/TODVAR-4	2019/TODVAR-3
PANT Tomato-3	2019/TODVAR-8	2019/TODVAR-5	2019/TODVAR-1	2019/TODVAR-9
2019/TODVAR-7	2019/TODVAR-9	PANT Tomato-3	PANT Tomato-3	2019/TODVAR-2

Conclusions

Genetic diversity is an effective way to determine the genetic variation among the genotypes. Diversity not only induces variations but also provides new combinations of genes. Therefore, information on the nature and degree of genetic divergence generally helps in the selection of appropriate parents for the breeding program. Appreciable diversity within and between the clusters was observed among the genotypes. The above findings indicated that the smallest inter-cluster distance was observed between cluster I and III followed by cluster III and V. The lines belonging to these clusters were relatively closer to each other, in comparison to lines grouped in other clusters. PCA provides a roadmap for how to reduce a complex data set to a lower dimension to reveal sometimes hidden, simplified structures that often underlie it. PCA accomplishes this reduction by identifying directions, called Principal Components (PCs), along which the variation in the data is maximal. Thus, it is cleared that the principal component analysis highlights the characters with maximum variability. So, intensive selection procedures can be designed to bring about rapid improvement of yield and quality traits. PCA also help in ranking of genotypes on the basis of PC scores in corresponding component. From the above investigation, it is cleared that 2019/TODVAR-9 is the best genotype for both quality and yield traits followed by 2019/TODVAR-8. It can be used in the further improvement programmes.

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