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Research Article

ESTIMATION OF GENETIC DIVERSITY IN SWEET PEPPER (*CAPSICUM ANNUUM* L.) THROUGH MULTIVARIATE ANALYSIS

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Abstract

Sweet pepper is an important emerging exotic vegetable crop in Bangladesh, which play an essential function in the country economy, food and nutrition but there are not enough acceptable high yielding varieties. In this regard the objectives of this investigation was to ascertain the extent of genetic variation and to mark out the diverse parents among the genotypes that was collected for the purpose of implementing a hybridization program. Twenty one genotyes were employed and the analysis of variance (ANOVA) demonstrated that the genotypes exhibited significant ($p<0.01$) differences in the majority of the studied parameters. For the purpose of choosing diverse parents, multivariate analytical system including PCA (Principal Component Analysis), PCO (Principal Co-ordinate Analysis), CVA (Canonical Variate Analysis) and Cluster analysis were performed for yield and yield attributes. Analysis using principal components showed that the first four component were accountable for 83.40% of the total variation among the fourteen yield contributing attributes. Through the use of principal coordinate analysis, the inter-genotypic distance was calculated, resulting in the SP 01 and SP 07 genotypes exhibiting the greatest distance of 2.585. The genotypes were separated into six specific cluster (I-VI), cluster I (08) had the most genotypes, the greatest distance between clusters IV and II (17.111) was observed, and the maximum cluster mean range for individual fruit weight was recorded (67.70 to 208.71 g). Considering, the different multivariate analytical results the genotypes SP 03, SP 05 and SP 08 from Cluster I, SP 14 from Cluster II, SP 01 from Cluster IV and SP 09, and SP 17 from Cluster VI were selected for the hybridization program.

Introduction

Sweet peppers (*Capsicum annuum* L.) belongs to the solanaceae family are becoming a widespread vegetable for smallholder farmers in the tropics and subtropic including Bangladesh, while hot peppers are the most traded spices in the world (Lin *et al.,* 2013). The demand for sweet pepper is steadily rising and it has the potentiality to be a profitable vegetable in Bangladesh (Ferdousi *et al.,* 2023). Sweet pepper is a wonderful source of vitamins A and C as well as abundant in antioxidant components, that are beneficial to one's health (Nadeem *et al.,* 2011). At present, the production of sweet pepper in Bangladesh is 11 MT in 2018-2019 (BBS, 2020) which is very low because of insufficient knowledge regarding the cultivation techniques and unavailability of seeds of superior quality. There has little work to develop improved varieties country wide or location specific cultivation. Two open-pollinated cultivars, BARI Mistimarich 1 and BARI Mistimarich 2 (BARI, 2019), have been generated from the cultivars assembled by the Bangladesh Agricultural Research Institute (BARI). These are not sufficient for cultivation in our country. So, it's very urgent to develop high yielding varieties through hybridization program.

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Germplasm serves as the most valuable natural reservoir to provide useful characters for developing varieties that are responsive to high yield input. For the purpose of increasing yield and achieving other desirable characteristics, plant breeders need access to genetically diverse genotypes. In the process of breeding and improving any crop, it is advisable to prioritize the selection of parents based on the trait that has the most contribution to the divergence (Alam *et al.,* 2020 and Jagadev et al., 1991). Furthermore, it is essential to estimate the genetic diversity in order to identify the origin of genes for certain characteristics within the existing genotypes (Tomooka *et al.,* 2005). When genetically diverse parents are utilized effectively, there is a significant opportunity for the production of a variety that produces high yields. Greater parental diversity within a tolerable range increases the probability that the offspring will exhibit improved economic characteristics.

There are several statistical tools available to find the best parents. As several researchers have shown, multivariate analysis is an effective method for measuring the extent of genetic variation among populations and for determining which factors contribute most to the overall variations in self-pollinated crop species (Das and Gupta, 1984; Natarajan *et al.,* 1988 and Golakia and Monke, 1992). Mohalanobis's D^2 statistic (1936) described by Rao (1952) is the level of genetic variations across populations may be effectively assessed by multivariate analysis. In view of the aforementioned information, the current study was done to evaluate the extent of genetic variations and to identify the diverse parents among the collected genotypes.

Materials and Methods

The experiment took place in the research field of Horticulture department, Bangladesh at Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur from November 2018 to April 2019. In this experiment 21 (twenty-one) sweet pepper genotypes were used and these were collected from different sources such as 8 genotypes from the World Vegetable Centre, 7 from the Bangladesh Agritultural Research Institute, 5 from the United Kingdom and 1 from the Siddike Bazar, Dhaka in Bangladesh. The entire genotypes were identified by the abbreviation SP which stands for Sweet Pepper and ranged from SP 01 to SP 21. Three replications and a Randomized Complete Block Design (RCBD) were followed to set up the experiment. The data on different parameters were recorded days required for flowering, days required for 1st harvest, harvesting term, length of fruit, diameter of fruit, firmness of pericarp, locule number, number of seed, weight of thousand seed, fruit weight**,** fruit number per plant, yield per plant, yield per plot**,** yield per hactare to test genetic diversity through multivariate analysis. Using GENSTST 5 and SPSS 16.0 software. The average data were applied to multivariate techniques of analysis for each character and these techniques included Principal Component Analysis (PCA), Principal Coordinate Analysis (PCA), Canonical Variate Analysis (CVA), and Cluster Analysis (CLSA) (Jager *et al.,* 1983, Digby *et al.,* 1989, Darlington *et al.,* 1973, Mahalanobis, 1936). The distance of inter and intra-cluster distance were calculated using the formula described by Singh and Choudhury (1977) and finally parents were selected for hybridization program based on Singh and Choudhury (1985).

Results and Discussion

The analysis of variance revealed significant variations among the genotypes for all the variables being studied, indicating a substantial level of genetic variability. These findings were further analyzed through different multivariate analysis for selection of parents in hybridization program.

Principal Component Analysis (PCA)

Based on the findings of the investigation into the primary variable, Table 1a provides the eigenvalues as well as percent of variations and cumulative percent of variations of the fourteen principal component axes. According to the data, the first principal component axis (PC1) was responsible for 44.33% of the total variability, followed by the second principal component axis (PC2), which was responsible for 17.04% of the variance. The total variation among the twenty-one sweet pepper genotypes reflecting fourteen traits was explained by the first four principal component axes (83.40%). Rahevar et al. (2021) investigated almost similar results that the PC1 had the highest variability (23.01%), followed by PC2 (18.35%), while the first four axes exhibited 66.83% cumulative variation among fourteen principal components of fifty-eight chilli genotypes.

The highest variability of PC1 in the present study is in agreed with the conclusions of Janaki *et al.,* (2015) and Singh *et al.,* (2020). A maximum variability character was determined by examining the eigen vectors of the characters through PCA, which preserved four components (Table 1b). In particular, the principal component one (PC1) days required for flowering (0.305), days required for 1st harvest (0.279), length of fruit (0.107) and fruits number per plant (0.110) had more contribution to the total diversity and the rest of the nine were negatively correlated with the PC1. In the second axis (PC 2), traits such as DRF (0.066), DH (0.057), DF (0.398), PF (0.111), LN (0.332) and FW (0.135) were positively assotiated with PC 2. Four factors such as, HT (0.259), LF (0.487), NS (0.283) and FW (0.220) were positively assotiated with PC 3. All vectors were positively associated with PC 4 except HT, PF, SN and FNPP that means most of the parameter are important for variation in the PC 4. It is evident that yield related traits (LF, FD, FW, PF and FNPP) were important or principal contributors to PC 1 to PC 2. Therefore, both PC 1 and PC 2 could be collectively referred as yield contributing axis. Singh *et al.,* (2020) found most of the important yield contributing and quality traits were present in PC 1 and PC 2 based on PCA. Rana *et al.,* (2015) also revealed that fruit length, breadth, weight and yield per plant give rise to the top positive values in PC1 and PC2 in Capsicum.

Table 1a. Calculated eigen values, percentage of variations and cumulative percentage of variations for the 14 component characters

Principal component axis	Eigen values	% variations	Cumulative % variations
PC 1	6.207	44.33	44.33
PC 2	2.385	17.04	61.37
PC 3	1.681	12.01	73.38
PC 4	1.403	10.02	83.40
PC 5	0.938	6.70	90.10
PC 6	0.708	5.06	95.16
PC 7	0.277	1.98	97.14
PC 8	0.218	1.56	98.70
PC 9	0.080	0.57	99.27
PC 10	0.064	0.46	99.73
PC 11	0.024	0.17	99.90
PC 12	0.015	0.10	100.00
PC 13	0.000	0.00	100.00
PC 14	0.000	0.00	100.00

Table 1b. Eigen vectors loading explained by the first four principle component (PC) for yield and yield attributing traits of 21 sweet pepper genotypes

Attributes	PC 1	PC 2	PC 3	PC 4
DRF	0.305	0.066	-0.132	0.126
DFH	0.279	0.057	-0.435	0.166
HT	-0.314	-0.032	0.259	-0.279
LF	0.107	-0.336	0.487	0.345
DF	-0.303	0.398	-0.024	0.075
FP	-0.328	0.111	-0.205	-0.336
LN	-0.139	0.332	-0.209	0.377
NS	0.074	-0.295	0.283	-0.082
WTS	-0.113	-0.248	-0.164	0.601
FW	-0.327	0.135	0.220	0.269
FNPP	0.110	-0.462	-0.415	-0.225
FWPP	-0.349	-0.268	-0.160	0.056
YPP	-0.348	-0.270	-0.158	0.054
YPH	-0.348	-0.270	-0.158	0.054
sd	2.459	1.539	1.294	1.181

DRF= Days Required for Flowering; DFH= days required for 1st Harvest; HT= harvesting Term; LF= Length of Fruit (mm); DF= Diameter of Fruit (mm); FP= Firmness of Pericarp (mm); LN= Locule Number; NS= Number of Seed per fruit; WTS= Weight of Thousand Seed; FW= Fruit Weight (g); FNPP= Fruit Number Per plant; FWPP= Fruit Weight Per Plant (kg); YPP= Yield Per Plot (kg); YPH= Yield Per Hectare (ton), sd= standard deviation. (Short forms of these parameters are also used in Tables 4 and 5).

A two-dimensional clustered-line (Z1Z2) was produced by employing first component score as a bar and second component score as a line (figure 1a). It was conducted in accordance with the principal component scores 1 and 2 (Appendix 1) obtained from the principal component analysis. Apparently, the genotypes in the clustered-line diagram were arranged into six distinct groups, exhibiting significant variation among them.

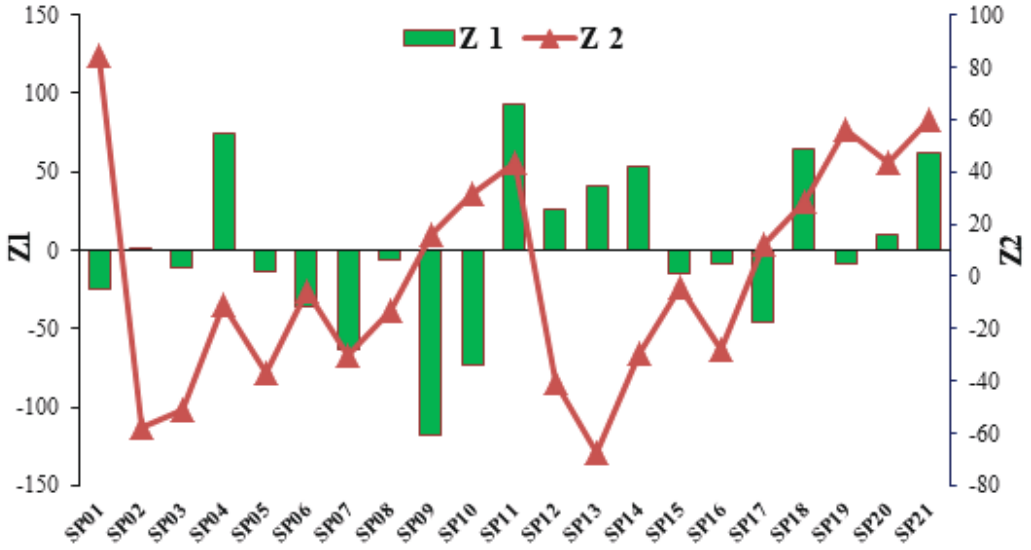

Figure 1a. Principal component scores for corresponding 14 characters.

A Scree plot, which can be shown in Figure 1b, presented an explanation of the percentage of variation that was connected with principal components and eigenvalues. According to the current study's scree plot revealed that, PC 1 exhibited the maximum variability of 44.33% with an eigenvalue of 6.20, while the remaining principal components showed a gradual reduction. Maximum variability can be explained by first four principal components are evident in figure 2. Maximum variance is accounted for first four PCs after that semi curve line ws obtained which showd the existace of little variance in remaining principal component. It was evident from the graph that the maximum amount of variation was PC 1 therefore, it could be preferable to choose lines for specific characters that fall within principal component one. A curve line that was quite similar to this one was also seen by Singh *et al.,* (2020); Memon *et al.,* (2021) and Rahevar *et al.,* (2021).

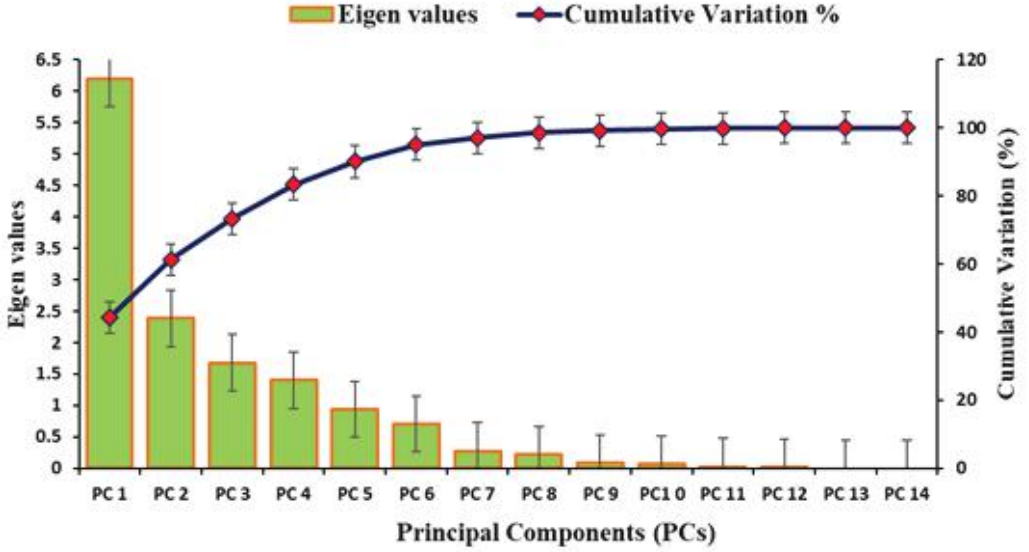

Figure 1b. Scree plot from Eigen values and cumulative percentage of variation Vs PCs.

Construction of biplots

The PCA biplots displayed both sample PC scores (number) and variables loadings (vectors). Relationships among variables and genotypes were reviewed based on bi-plot of four principal components in figure 1c.

The examined specific traits like length, diameter and weight of fruits, pericarp firmness, quantity of fruits per plant etc. helped most to explain the overall diversity in the tested genotypes. Therefore, it is essential to focus selection efforts on these specific qualities in order to achieve improved genetics in sweet pepper. The bi-plot was used to establish the location of genotypes and their grouping based on the value of principal component (Figure 1c).

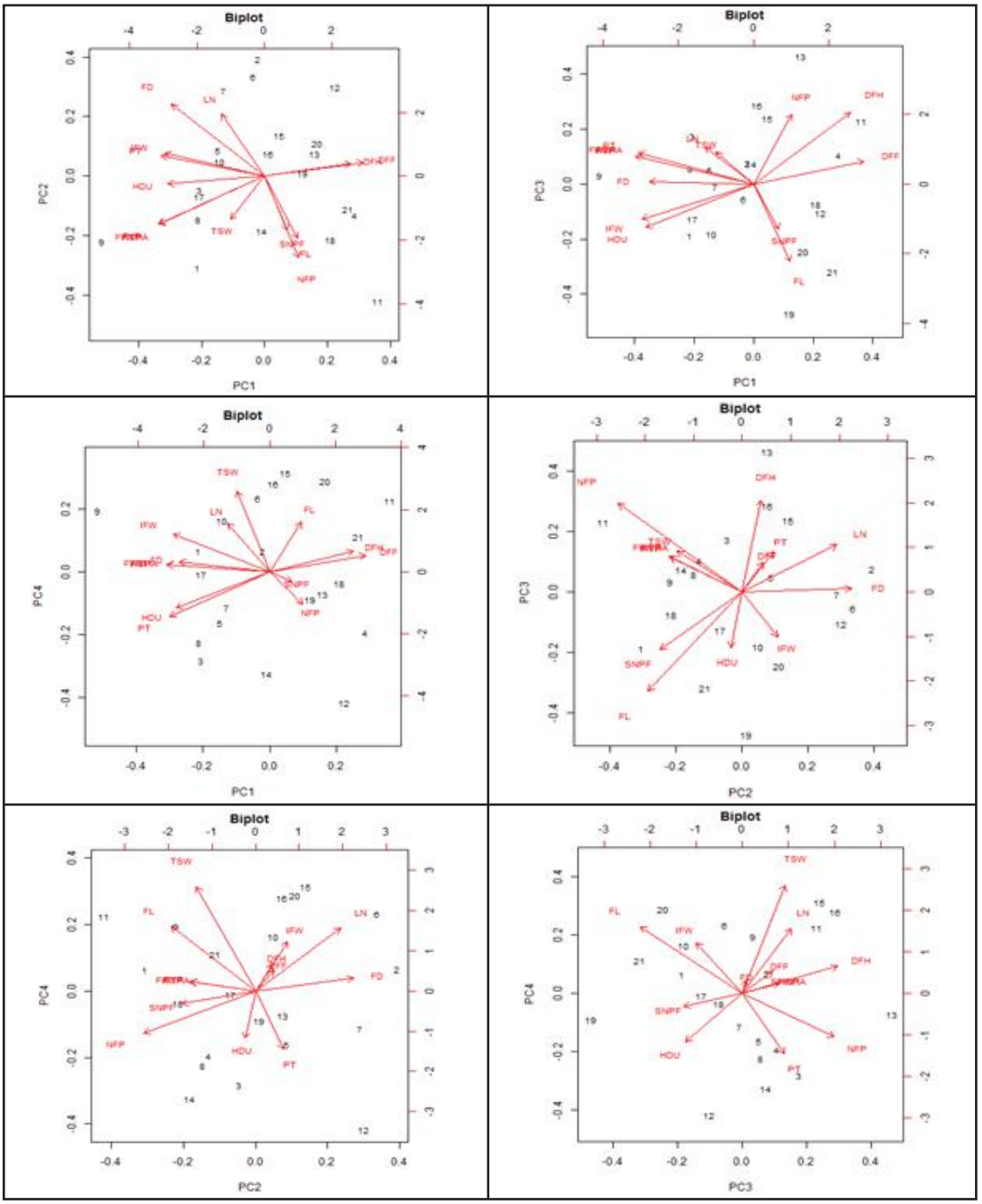

Figure 1c. Biplots of principal axis on PC 1 to PC 2, PC 1 to PC 3, PC 1 to PC 4, PC 2 to PC 3, PC 2to PC 4, PC 3 to PC 4 accordingly.

Cluster Analysis (CLA)

Utilizing Mahalanobis D^2 analysis, the calculation derived from the covariance matrix produced a non-hierarchical clustering (Figure 2a). Twenty-one genotypes were grouped into six different clusters (I-VI) in Figure 2b. Maximum genotypes fall into cluster I (08), followed by cluster IV (03), cluster V (03) and cluster VI (03). Cluster I contained the genotypes namely SP 02, SP 03, SP 05, SP 06, SP 07, SP 08, SP 15 and SP 16. Cluster IV, cluster V and cluster VI had SP 01, SP 19, SP 20; SP 11, SP 18, SP 21; SP 9; SP 10 and SP 17 genotypes respectively. Cluster II included the genotypes viz. SP 12, SP 14 and cluster III contained SP 4 and SP 13

Danojević and Medić-Pap (2018) grouped 28 sweet pepper genotypes into seven clusters based on Mahalanobis D^2 statistics. According to Sen *et al.,* (2021), a study on chilli genotypes revealed that 19 different genotypes were classified into five distinct clusters using D^2 analysis. Largest number of genotypes (12) were into the Cluster I, while clusters IV and V had the smallest number of genotypes (1 each). Yatung (2014) grouped 30 different lines of chilli into 6 clusters in accordance with D^2 analysis.

Construction of scattered diagram

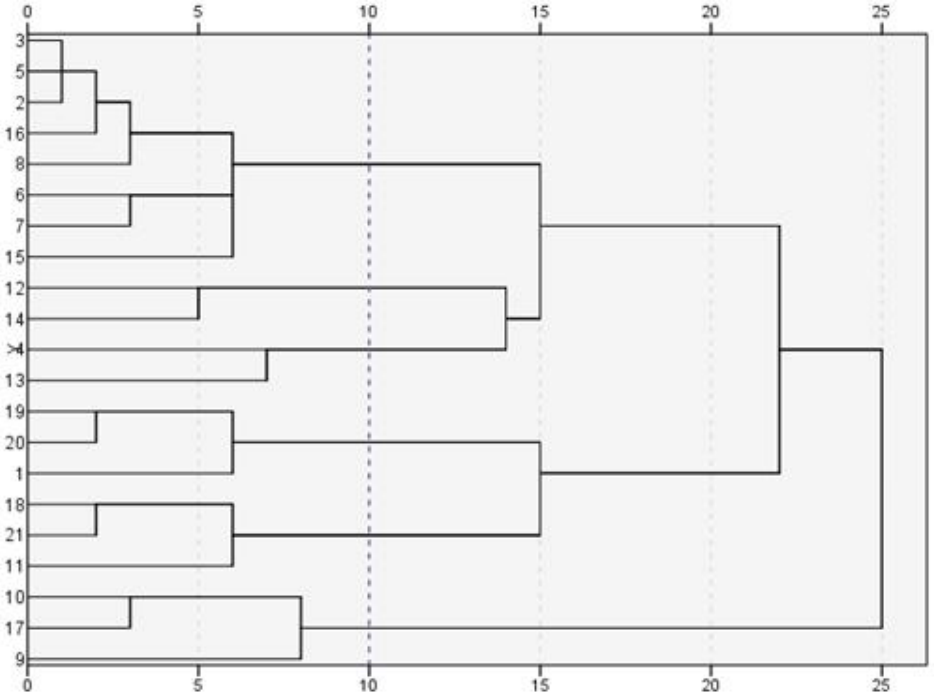

Figure 2a. A dendrogram containing twenty-one sweet pepper genotypes.

Figure 2b shows the result of a two-dimensional Z1-Z2 scattered diagram that was generated by means of PCA, using X-axis values of score1 and Y-axis values of score 2. It would appear that the genotypic position included inside the scattered diagram was divided into six distinct groups. Deepo *et al.,* (2020) confirmed that the 15 chilli lines in the scatter diagram were apparently scattered into four groups. Therefore, the groupings indicated the presence of substantial diversity amongst the genotypes.

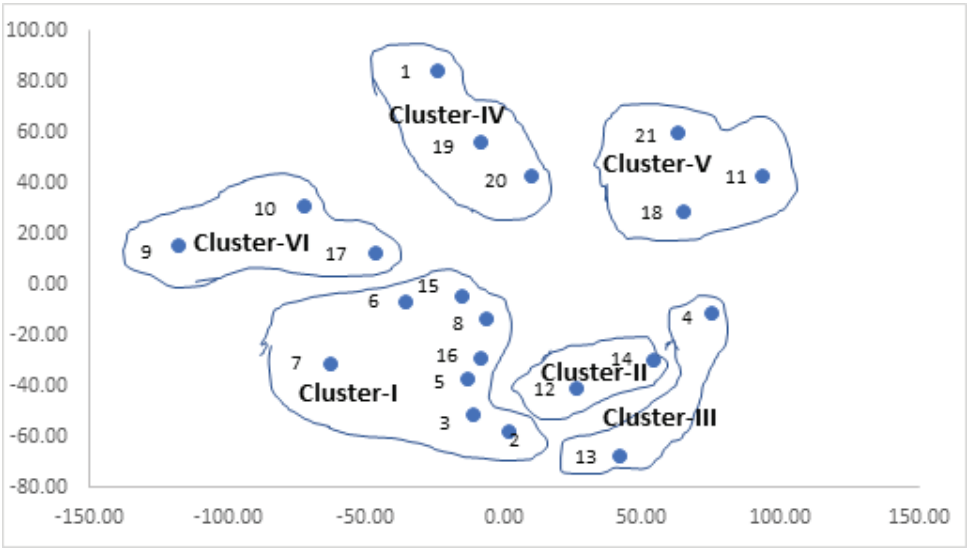

Figure 2b. Scatteredly arrangement of 21 genotypes of sweet pepper based on principal component scores.

Principal coordinate analysis (PCO)

Principal coordinate analysis (PCO), was carried out in order to determine the inter-genotype distance. There are 10 pair of both lesser and higher inter-genotype distances which are presented in Table 2. There was a distance of 2.585 between a pair of SP 01 and SP 07, which was the greatest inter-genotypical distance. However, the lowest inter-genotypical distance (0.479) between SP 17 and SP 10 was observed. There was a significant amount of variation among the twenty-one sweet pepper genotypes, as seen by the variation between the highest and the lowest inter-genotypical distance.

Table 2. Ten (10) of each maximum and minimum inter-genotypic distance between pair of genotypes

SL. No.	Genotypic Combinations	Maximum (D^2) values	Genotypic Combinations	Minimum (D^2) values
1	SP 01 and SP 07	2.585	SP 17 and SP 10	0.479
2	SP 11 and SP 09	2.555	SP 05 and SP 03	0.485
3	SP 08 and SP 04	2.351	SP 08 and SP 05	0.547
4	SP 11 and SP 03	2.228	SP 17 and SP 08	0.586
5	SP 21 and SP 05	2.219	SP 16 and SP 05	0.621
6	SP 11 and SP 17	2.215	SP 21 and SP 18	0.680
7	SP 12 and SP 09	2.162	SP 20 and SP 19	0.722
8	SP 11 and SP 06	2.147	SP 16 and SP 15	0.731
9	SP 13 and SP 09	2.116	SP 08 and SP 03	0.783
10	SP 11 and SP 10	2.091	SP 14 and SP 02	0.788

Canonical variate analysis (CVA)

The distance between clusters (Inter) was greater than the distance between clusters themselves (Intra), which indicates that there is a greater genetic variation across the genotypes of different groups. The largest distance measured in this investigation was 17.111 between clusters IV and II, followed by clusters IV and III at 14.737 and clusters IV and I at 13.921. Cluster II and I (5.380), Cluster V and I (5.474), and Cluster III and II (3.948) all showed lower inter-cluster distances, indicating a strong link between these cluster pairings (Table 3). High yields were achieved by hybrids of genotypes that clustered together with the greatest possible distance (Sen *et al.,* 2021; Kumar *et al.,* 2010) and the segregating F_2 population may have a small range of variability due to the reduced distance between clusters, which may not result in a greater heterotic value in F_1 (Belay *et al.,* 2019; Rama, 1992). However, cluster IV showed the greatest intra-cluster distance, which had three genotypes, while cluster VI, showed the smallest intra-cluster distance which also had three genotypes. It was

discovered that clusters were more distant than they were within. The explanation for this may be attributed to unique individual genotypes that were significantly different from the majority, hence playing a major role in the development of new clusters. Rahevar *et al.*, in 2021; Hasan *et al.,* in 2014 and Srinivas *et al.,* in 2015 found comparable findings for clustering and inter- and intra-cluster distance. Wei *et al.,* (1994) said that genetic diversity worked better when crossing genotypes from different groups that were genetically farther apart (D^2).

Table 3. Average value for inter and intra (bold) cluster distance (D^2) of twenty-one genotypes

Clusters	I	II	III	IV	V	VI
I	**1.001**					
II	5.380	**1.30**				
III	6.866	3.948	**1.145**			
IV	13.921	17.111	14.737	**1.149**		
V	5.474	9.759	9.007	8.588	**0.961**	
VI	9.656	9.763	6.229	9.485	7.725	**0.761**

Cluster means for fourteen characters in sweet pepper

Differences in cluster mean were found among the parameter studied (Table 4). One of the characteristics that showed the greatest amount of variation was the weight of the individual fruit, which ranged from 67.70 to 208.71g. The lowest mean (39.00 and 76.00 days) for the characters days required for flowering and days required for 1st harvest was obtained from cluster III closely followed by cluster VI and cluster I indicating earliness. Longest fruits were found in genotypes of cluster VI (157.59 mm) followed by the cluster IV (140.01 mm) and cluster III (100.80 mm). Shortest length of fruits was founding genotypes in cluster V (57.70 mm). Cluster II had the genotypes (84.18 mm) with higher diameter of fruits closely followed by cluster III (80.73) and cluster I (73.16). The genotypes under cluster III had the firmer (7.24 mm) pericarp strictly followed by the cluster I (7.21 mm) and number of fruits per plant was higher (10.86) in the same cluster. The highest yield produced by the cluster III followed by the cluster I and cluater II.

Table 4. Mean values of five distinct clusters for 14 attributes of twenty-one genotypes

Attributes	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
DRF	43.17	44.00	39.00	48.25	45.50	43.11
DFH	87.67	92.22	76.00	93.83	88.67	79.33
HT	53.11	43.11	63.22	38.58	51.67	49.56
LF	63.18	86.84	100.80	140.01	57.70	157.59
DF	73.16	84.18	80.73	40.94	63.20	63.57
FP	7.21	6.28	7.24	4.44	6.80	5.82
LN	3.51	3.83	3.41	2.91	3.26	3.02
NS	51.13	49.83	85.11	79.64	112.82	81.25
WTS	7.51	6.86	8.15	7.37	5.55	7.15
FW	118.38	163.07	208.71	67.70	88.13	148.14
FNPP	8.42	5.53	6.09	10.86	8.91	5.69
FWPP	0.98	0.90	1.28	0.72	0.74	0.86
YPP	7.86	7.16	10.24	5.73	5.88	6.89
YPH	31.45	28.63	40.96	22.93	23.53	27.55

Contribution of characters towards divergence

Accurate knowledge about the magnitude and type of genetic variation is important for breeders to select suitable parental species for hybridization program in heterosis breeding (Patel 1990; Farhad *et al.,* 2010; Khodadabi *et al.,* 2011). Canonical variate analysis was used to calculate the effects of each attribute to the entire divergence (Table 5). The vector 1 and vector 2 exhibited positive results for both days required for flowering and days required for 1st harvest. The findings showed that these two traits, out of the fourteen, contributed the most to the entire diversity.

In vector 1 (main axis) other traits like length of fruit, seed number, number of fruits and yield (ton/ha) responseded significantly to the genetic divergence while in vector 2 (second axis) diameter of fruits, weight of fruits, pericarp firmness, locule number positively contributed towards the divergence. In both vector traits including harvesting term, weight of thousand seed and yield (per plant, per plot) responded negatively indicating the smallest contribution to the entire diversity. Alam *et al.,* (2020) reported that time of 50% flowering, fruits number per cluster, fruit length, diameter and yield (t/ha) had the considerable contribution toward divergence in tomato. This information is exactly similar to the findings of the existing study.

Table 5. Comparative contribution of the fourteen attributes of 21 genotypes to the entire divergence

Attributes	Vector 1	Vector 2
DRF	0.3204	0.0754
DFH	0.2808	0.0686
HT	-0.3137	-0.0424
LF	0.1069	-0.3428
DF	-0.3016	0.3978
FP	-0.3337	0.1134
LN	-0.1402	0.3440
NS	0.0735	-0.2999
WTS	-0.1096	-0.2395
FW	-0.3228	0.1291
FNPP	0.1103	-0.4529
FWPP	-0.3437	-0.2641
YPP	-0.3426	-0.2665
YPH	0.3426	-0.2665

Selection of parents for hybridization program

Clusters IV and II exhibited the greatest distance (17.111); the following clusters were IV and III (14.737), IV and I (13.921), VI and II (9.763) and V and II (9.759). Clusters III and II (3.948) showed the lowest inter-cluster distance and the following clusters were II and I (5.380) and V and I (5.474). According to Falconar, (1960); Moll *et al.,* (1962) and Mian and Bhal, (1989) the parents who are genetically distant are capable of producing increased heterosis. The research of Endang *et al.,* (1971) that the clustering pattern may be used to pick parents for cross-breeding that would probably produce the most variation for accurately picking different economic traits. In their 1994 study, Wen Xing *et al.,* found that hybridization between the genotypes from separate groups resulting favorable impact specifically when genetical distance (D^2) larger than 12.5. There was a large amount of positive heterosis seen in parental clusters that were distinguished by medium D^2 values (Mian and Bhal, 1989). So, the genetically distant parents might produce more heterosis in the hybridization.

Therefore, we selected the genotypes SP 03, SP 05, and SP 08 from Cluster I, SP 14 from Cluster II, SP 01 from Cluster IV, and SP 09 and SP 17 from Cluster VI to hybridize, putting into focus the factors like cluster distance, divergence contribution, and cluster mean on yield and yield contributing traits.

Conclusion

From the investigation, it is evident that, both PC1 and PC 2 could be the chief or principal contributor related to yield traits. The largest inter-genotypical distance (2.585) was observed between the genotypes SP 01 and SP 07 and it was lowest in (0.479) between SP 17 and SP 10. Using Mahalanobis D^2 analysis, twenty-one genotypes were classified into six distinct clusters (I-VI). The inter-cluster distance exceeded the intra-cluster distance, indicating greater genetic diversity among the genotypes of different clusters. Taking into account the different multivariate analysis on yield and yield attributing traits, the genotypes SP 03, SP 05 and SP 08 from Cluster I, SP 14 from Cluster II, SP 01 from Cluster IV and SP 09, and SP 17 from Cluster VI may be chosen for the upcoming hybridization program, in order to provide genetic diversity for varietal development.

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Appendix 1. Factor scores for corresponding 14 characters in 21 sweet pepper genotypes

Genotypes	PC axis	
	Z_1	Z_2
SP01	-24.67	84.48
SP02	1.19	-57.68
SP03	-11.16	-51.01
SP04	74.66	-11.00
SP05	-13.28	-37.05
SP06	-36.09	-6.03
SP07	-62.86	-30.58
SP08	-6.40	-13.14
SP09	-118.45	15.93
SP10	-72.94	31.63
SP11	92.96	43.41
SP12	25.82	-40.68
SP13	41.24	-67.33
SP14	53.64	-29.55
SP15	-15.47	-4.33
SP16	-8.90	-28.30
SP17	-46.54	12.55
SP18	64.42	28.96
SP19	-9.07	56.26
SP20	9.56	43.21
SP21	62.33	60.25

Appendix 2. Mean sum square and co-efficient of variation of flowering, harvesting and fruit characters of 21 sweet pepper genotypes

Source of variation	Degrees of freedom	Mean sum square						
		DRF	DFH	HT	LF	DF	FP	LN
Replication	2	2.20	4.87	6.33	18.37	1.56	0.35	0.13
Genotypes	20	80.2**	431.6**	570.3**	4990.5**	744.7**	4.6**	0.65**
Error	40	6.88	6.10	4.95	6.12	7.00	0.13	0.01
CV (%)	-	5.98	2.85	4.48	2.49	3.93	5.81	4.08
Total	62	-	-	-	-	-	-	-

Appendix 3. Mean sum square and co-efficient of variation of yield and seed attributes of 21 sweet pepper genotypes

Source of variation	Degrees of freedom	Mean sum square						
		FW	FNPP	FWPP	YPP	YPH	NS	WTS
Replication	2	4.84	0.09	0.00	0.06	0.97	4.34	0.00
Genotypes	20	7290**	23**	0.24**	15**	254**	2243**	3.66**
Error	40	19.80	0.19	0.00	0.02	0.38	28.5	0.00
CV (%)	-	3.44	4.68	2.10	2.10	2.10	7.48	0.75
Total	62	-	-	-	-	-	-	-

DRF= Days Required for Flowering; DFH= days required for 1st Harvest; HT= harvesting Term; LF= Length of Fruit (mm); DF= Diameter of Fruit (mm); FP= Firmness of Pericarp (mm); LN= Locule Number; NS= Number of Seed per fruit; WTS= Weight of Thousand Seed; FWPP= Fruit Weight (g); FNPP= Fruit Number Per plant; FWPP= Fruit Weight Per Plant (kg); YPP= Yield Per Plot (kg); YPH= Yield Per Hectare (ton), ** indicate 1% level of significance, CV = Co-efficient of variation.