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Genetic Divergence of Sweet Pepper in Bangladesh

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ABSTRACT

The study of genetic divergence in sweet pepper is essential for enhancing crop yield, quality, and adaptability, especially in regions like Bangladesh where agriculture plays a critical role in the economy. The present investigation was carried out at the research farm of the Olericulture division, Horticulture Research Centre, Bangladesh Agricultural Research Institute, Gazipur, Bangladesh to estimate genetic divergence in 21 sweet pepper genotypes based on fourteen characters using Mahalanobis's D2 statistics during winter 2017-18 in randomized complete block design with three replications. The results revealed significant genetic variability, indicating the presence of diverse genetic resources within the cultivated 21 sweet pepper genotypes. Cluster analysis grouped the accessions into distinct clusters, reflecting their genetic relationships and divergence. The study highlights specific genotypes with desirable traits that can be utilized in

breeding programs to develop superior sweet pepper varieties. Cluster II had the maximum number (14) of genotypes and clusters I and III were composed of only two genotypes. The highest intra-cluster distance was observed in cluster II (1.286), containing fourteen genotypes and the lowest intra-cluster distance (0.056) was observed in cluster III having two genotypes. A higher inter-cluster distance was observed between clusters III and IV (14.090) and clusters I and IV (14.040) indicating the genotypes in these clusters were more diverged than those of other clusters. Cluster II exhibited maximum highest mean for fruit length at the green stage, fruit length at the mature stage and desirable minimum value for days to 50% flowering while the second highest mean values for days to last harvest, number of fruit/plant, weight of fruit/plant, average fruit weight, total number of fruit/plot, plot yield, fruit yield, while cluster IV exhibited the highest mean values for the number of fruit/plant, weight of fruit/plant, total number of fruit/plot, plot yield, fruit yield and one desirable lowest mean for days to last harvest. Therefore, more emphasis should be given to clusters II and IV for selecting genotypes as parents for crossing which may produce new recombinants with desired traits.

Keywords: Sweet pepper, Genetic divergence, Multivariate, Cluster analysis, D2 statistics

INTRODUCTION

Sweet pepper (*Capsicum annuum* L.) belongs to the family Solanaceae native to tropical South America. Brazil is thought to be the Centre of origin of sweet pepper. It was widely cultivated in Central and South America in early times and unknown in Europe before the discovery of America. The species Capsicum annuum includes eleven groups which can be divided into sweet and hot peppers. Sweet pepper holds significant nutritional and economic importance. In Bangladesh, sweet pepper is gaining popularity among farmers and consumers. However, the cultivation and productivity of sweet pepper in Bangladesh are often constrained by various biotic and abiotic factors, necessitating the exploration of genetic diversity within the species to enhance crop resilience and yield. The sweet pepper is relatively non-pungent with thick flesh. As food, sweet pepper has little energy value. But the nutritive value of sweet pepper is high as it contains 1.29 mg protein, 11 mg calcium, 870 I.U. vitamin A, 175 mg ascorbic acid, 0.06 mg thiamine, 0.03 mg riboflavin and 0.55 mg niacin per 100 g edible fruit (Joshi, 1995). One medium green bell pepper can provide up to 8 per cent of the recommended daily allowance of Vitamin A, 180 per cent of Vitamin C, 2 per cent of calcium and 2 per cent of iron. Sweet pepper contributes substantially to our diet, it is a good source of vitamins A, C (more than that obtained from tomato), E, B1, B2, and D.

Genetic divergence refers to the process through which populations of a species evolve and accumulate differences in their genetic composition over time. Understanding the genetic divergence of sweet pepper in Bangladesh is crucial for developing improved varieties that are better suited to local growing conditions, resistant to diseases, and capable of meeting market demands. By assessing the genetic variability among different sweet pepper accessions, researchers can identify potential parent lines for breeding programs, thus contributing to sustainable agriculture and food security in the region. It is particularly useful for characterizing individual accessions and cultivars and as a general guide in the selection of parents for hybridization (Furini and Wunder, 2004). Better knowledge of genetic diversity or

genetic similarity could help to sustain long-term selection gain (Chowdhury et al., 2002). Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in nature or by hybridization. The selection of parents identified based on divergence analysis would be more promising for a hybridization program. Some related results have been reported in sweet pepper (Tambe et al., 1993; Chaudhary and Pathania, 1998; Singh and Gapalakrishnan, 1999; Kumar et al., 2000).

The value of D2 statistics (Maurya, 2010) has been demonstrated in choosing parental stocks for cross-breeding (Milkova, 1996; Bhatt, 1981; Kaul and Sharma, 2008; Devi and Arumugam, 2009). However, D^2 statistics group a set of potential parents based on genetic divergence with the assumption that the best parents may be those revealing the maximum genetic diversity (Bhatt, 1981). Similarly, Sharma (1998) after statistical and biometrical studies in plant breeding indicated that genetically divergent parents used in hybridization under a transgressive breeding programme are dependent upon the categorization of breeding material based on appropriate criteria, to have a heterotic response and desirable segregates. Geleta and Labuschagne (2004) highlighted the significance of diversity among the parent population. According to Sharma and Jana (2002), the assessment of genetic variation in a species is a prerequisite for initiating an efficient breeding program, as it provides a basis for tailoring desirable genotypes. Genetically diverse parents are likely to segregate and or to produce high heterotic crosses. The more diverse the parents, the greater the chances of obtaining high heterotic F_1s and a broad spectrum of variability in segregating generations (Arunachalam, 1981). Genetic diversity study also permits to select the genetically divergent parents to obtain the desirable recombinant in the segregating generations of sweet pepper. Assessment of genetic diversity is important for selecting breeding strategies.

Generally, this type of study aims to characterize sweet pepper genotypes collected from different regions of Bangladesh and exotic sources to assess the genetic diversity within the germplasm. So, this study aims to investigate the genetic divergence of sweet pepper varieties cultivated in Bangladesh, employing advanced molecular markers and statistical tools. The findings will provide insights into the genetic relationships among different sweet pepper genotypes, aiding in the selection of superior varieties for breeding and cultivation. Through this research, we hope to contribute to the improvement of sweet pepper production in Bangladesh, ultimately benefiting both producers and consumers.

MATERIALS AND METHODS

Experimental Site

The experiment site was the farm of the Olericulture Division, Bangladesh Agricultural Research Institute (BARI) during 2017-18. The field was at 23.992º N Latitude and 90.413º E Longitudes having an elevation of 8.2 m from sea level under the agro-ecological zone (AEZ) 28 (Annon, 1995). The farm was situated in the sub-tropical climatic zone and characterized by scanty rainfall during the experimental time. The soil of the experimental field was sandy clay loam in texture having a pH range of around pH 6.20 and moisture 13%-25%. The Maximum air temperature (ºC), minimum air temperature (ºC), total rainfall (mm), sunshine (hrs.), maximum RH (%) and minimum RH (%) are mentioned in Fig 1.

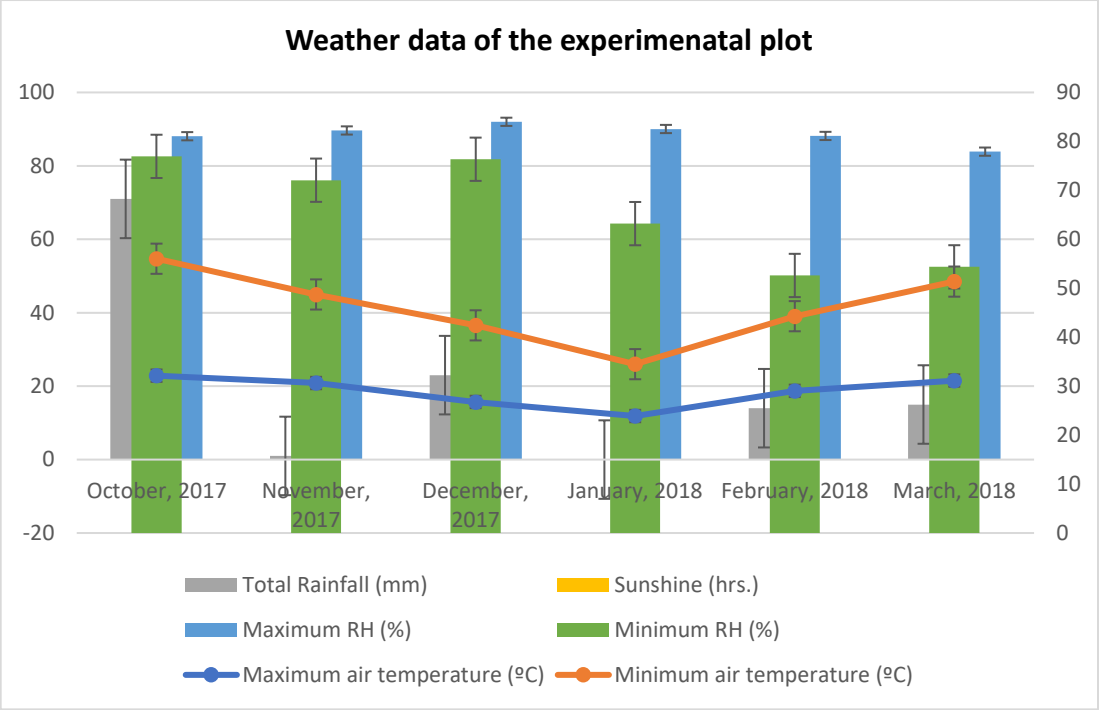

Fig 1: The Maximum air temperature (ºC), minimum air temperature (ºC), total rainfall (mm), sunshine (hrs.), maximum RH (%) and minimum RH (%).

Plant Materials

The seedlings of 21 genotypes were sown on the seedbed on 05 October 2017. Thirty days old planting materials were placed in the main field on 05 November 2017.

Experimental Design and Layout

The 21 genotypes of sweet pepper were placed in an RCBD (Randomized Complete Block Design) with three replications. Each planting material was represented by a double row of 3 m in length. Row-to-row and plant-to-plant distances were 60 cm and 50 cm, respectively with a 0.5m drain.

Land, Pit Preparation and Fertilization

The experimental land was fertilized with organic manure, N, P, K, S, B and Zn @ 3000, 80, 45, 88, 25, 1.8 and 4.5 kg/ha, respectively. The fertilization procedure was followed as half of the organic manure and all of S, Zn and B each of P and K @ 30 kg/ha was applied during final land preparation. The rest of the organic manure and P and K @ 15 kg/ha were applied as basal in the pit. The rest of N and K were applied in 4 equal instalments after 20 days of transplanting at 20 days intervals starting.

Intercultural Operation and Plant Protection

The recommended necessary agronomic practices and plant protection measures (especially fruit borer, thrips, mites, stem blight, and little leaf) were adopted for raising a good crop. Bamboo sticks were used to support the growing plants. Irrigation was applied as and when required.

Data Recorded

Green fruits were harvested when they were relatively firm and crispy (Shoemaker and Teskey, 1955). Harvesting of mature fruits was started at 60-65 DAP and continued up to 100-125 DAP. Harvesting was done manually with the help of secateurs. Data were recorded on the following parameters viz., days to 50% flowering, days to 1st harvest, days to last harvest, number of fruits/plant, weight of fruits/plants (kg), average fruit weight (g), total number of fruits/plot, plot yield (kg), fruit length at green stage (cm), fruit length at the mature stage (cm), fruit diameter at green stage (cm), fruit diameter at mature stage (cm), plant height at last harvest (cm), and fruit yield (t/ha).

Data Analysis

Genetic diversity was studied following Mahalanobis's (1936) generalized distance (D2) extended by Rao (1952). Based on the D2 values, the genotypes were grouped into clusters following the method suggested by Tocher (Rao, 1952; Jager et al., 1983; Digby et al., 1989). Intra and inter-cluster distances were calculated by the methods of Singh and Chaudhury (1985). Statistical analyses were carried out using GENSTAT 5 software.

RESULTS AND DISCUSSION

To measure the distance between two populations for several traits, genetic divergence through a clustering pattern was worked out. The clustering pattern of 21 diverse genotypes, based on genetic divergence, has been calculated. The analysis of variance showed significant differences among the twenty-one genotypes for all the 14 characters under study indicating the presence of genetic variability among the genotypes. Twenty-one genotypes were grouped into four clusters based on cluster analysis. A maximum of fourteen genotypes were grouped into Cluster II, followed by 3 in Cluster IV. Cluster I and III were composed of only two genotypes (Table 1). The immature fruit colour was highly variable, especially when the fruit was observed in the different developmental stages. For some accessions, more than four different colours were reported until reaching the final colour (mature stage). The descriptor immature fruit colour, as proposed by the IPGRI (1995), does not consider all maturation stages, but rather the phase before maturation only. A similar result was found by Indra et al. (2000), Sreelathakumary and Rajmony (2004), Farhad et al. (2010), Datta and Jana (2011), Datta and Das (2013) and Yatung et al. (2014).

Table 1: Distribution of 21 genotypes of sweet pepper in different clusters showing fruit colour

Cluster	Number of genotypes	Genotypes	Fruit colour
I	2	CA0007	Red
		BARI Mistimorich-1	Dark Red
II	14	CA0001	Dark Red
		CA0002	Red
		CA0003	Red
		CA0005	Deep red
		CA0006	Deep red
		CA0009	Greenish red
		CA0010	Deep red
		CA0011	Red

		CA0013	Yellow
		CA0016	Red
		CA0017	Yellow
		CA0019	Dark red
		CA0020	Dark red
		CA0018	Light Red
III	2	CA0008	Blackish red
		CA0004	Yellowish orange
IV	3	CA0012	Bell
		CA0014	Bell long
		CA0015	Bell

The maximum inter-cluster distances were recorded between clusters III and IV (14.090) followed by clusters I and IV (14.040) (Table 2). Genotypes from these three clusters (I, III, IV) if involved in hybridization may occur in a wide spectrum of segregating populations, as genetic variation is very distinct among the groups. Moderate distance was observed in cluster II and III, Cluster II and IV. The lowest inter-cluster distance was observed between clusters I and II (7.323) suggesting a close relationship among these clusters. The intra-cluster distance varied from 0.056 to 1.286, the maximum being from cluster II which comprised fourteen genotypes of diverse origin, while minimum distance was observed in cluster I and cluster III which comprised two genotypes.

Table 2: Mean intra (bold) and inter-cluster distances (D^2) for the 21 sweet pepper genotypes obtained based on the fourteen morphological characters

Clusters	I	II	III	IV
I	**0.828**	7.323	10.797	14.040
II		**1.286**	11.206	11.397
III			**0.056**	14.090
IV				**0.398**

Differences in cluster means existed for all the characters. Cluster I recorded the highest mean for average fruit weight (100.50g) and second highest mean for fruit length at the green stage (8.65cm), fruit diameter at the green stage (7.65cm), and plant height at 1st harvest (43.50cm). Whereas, minimum mean values for the number of fruit/plant (5.82), and fruit diameter at the mature stage (6.20cm) were recorded by cluster I. Cluster II constituted of fourteen genotypes and exhibited maximum highest mean for fruit length at green stage (8.97cm), fruit length at mature stage (7.04cm) and desirable minimum value for days to 50% flowering (66.29), while the second highest mean values for days to last harvest (143.00), number of fruit/plant (7.33), weight of fruit/plant (0.71kg), average fruit weight (96.71g), total number of fruit/plot (63.14), plot yield (6.10 kg), fruit yield (35.41t/ha) and the lowest value for fruit diameter at green stage (6.87cm). Cluster III had two genotypes and the highest mean was responsible for fruit diameter at the green stage (8.50 cm), fruit diameter at the mature stage (6.85 cm), and plant height at the last harvest (48.00). while the minimum desirable value for days to 1st harvest (87.00). Cluster IV composed of three genotypes and exhibited the highest mean values for the number of fruit/plant (8.33), weight of fruit/plant

(0.80kg), total number of fruit/plot (112.33), plot yield (10.87kg), fruit yield (40.10t/ha) and one desirable lowest mean for days to last harvest (137.00).

In the present investigation, clusters III and IV were found most divergent, but clusters II and IV contributed higher values. So, there will be more chances of getting better segregants in F_1 and subsequent generations from the crossing of genotypes between clusters II and IV. Therefore, hybridization between these groups can prove useful for further breeding programs. Number of research workers like Olufolaji and Makinde, 2004; Maurya, 2010; Savita, 2009; Maya *et al*.,2007, Zhang *et al*.,2013; Basavaraj, 2007; Farris, 1988; Maurya, 2010 have reported similar results on genetic divergence in bell pepper. Similar results were obtained for other crops with the use of morphological and agronomic data only (Olufolaji and Makinde, 2004).

Table 3: Cluster means for 14 characters in 21 genotypes of sweet pepper

Characteristics	Cluster I	Cluster II	Cluster III	Cluster IV
Days to 50% flowering	72.50	66.29	72.50	71.67
Days to 1st harvest	100.00	98.71	87.00	101.33
Days to last harvest	178.50	143.00	153.00	137.00
Number of fruits/plant	5.82	7.33	7.11	8.33
Weight of fruits/plants (kg)	0.58	0.71	0.55	0.80
Average fruit weight (g)	100.50	96.71	76.50	96.33
Total number of fruits/plot	61.00	63.14	59.50	112.33
Plot yield (kg)	6.10	6.10	4.55	10.87
Fruit length at green stage (cm)	8.65	8.97	7.70	7.40
Fruit length at the mature stage (cm)	6.10	7.04	5.70	6.60
Fruit diameter at green stage (cm)	7.65	6.87	8.50	7.60
Fruit diameter at mature stage (cm)	6.20	6.30	6.85	6.40
Plant height at last harvest (cm)	43.50	41.00	48.00	40.67
Fruit yield (t/ha)	29.35	35.41	27.10	40.10

Based on principal component axes I and II, a two-dimensional dendrogram (Z_1 and Z_2) of the genotypes is presented in Figure 1, reflecting the position of genotypes. It revealed that there were mainly four clusters. Distantly located genotypes of different clusters were cluster III (6.7) cluster IV (10,12,14) and cluster I (1,11) and IV (10,12,14). The pattern of distribution of genotypes in the dendrogram revealed that considerable variability exists in the genotypes.

The contribution of characters towards divergence of the genotype is presented in Table 4 The PCA revealed that in vector I (Z_1) the important characters responsible for genetic divergence in the major axis of differentiation were days to 1st harvest, number of fruit/plant, the weight of fruit/plant, average fruit weight, the total number of fruit/plot, plot yield, fruit length at mature stage. In vector II (Z_2) which was the second axis of differentiation, days to 1st and last harvest, average fruit weight, fruit length at the green stage, and fruit length at the mature stage were important. Several characteristics like day to 1st harvest, average fruit weight, and fruit length at the mature stage showed positive value across the two axes indicating the important components of genetic divergence in these genotypes.

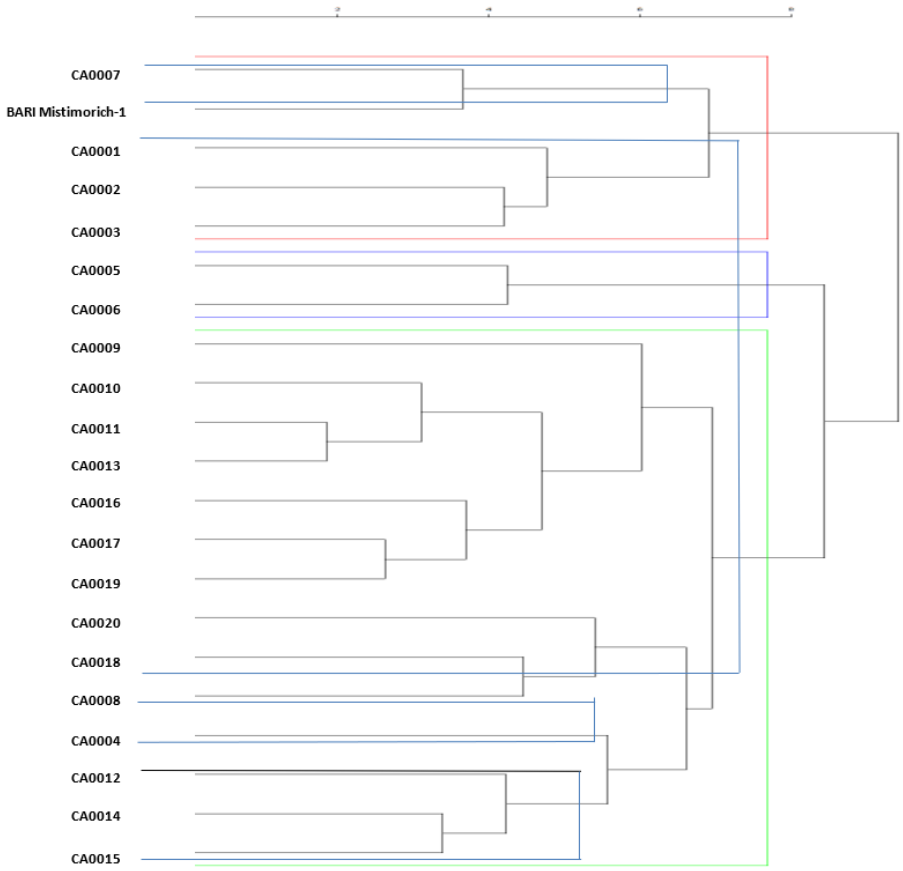

Fig 2: Dendogram showing genotypes distribution in four clusters

Table 4: Latent vectors for 14 quantitative characters of 21 genotypes of sweet pepper

Characteristics	Vector (Z_1)	Vector (Z_2)
Days to 50% flowering	-0.0625	-0.4609
Days to 1st harvest	0.3072	0.1285
Days to final harvest	-0.3086	0.0957
Number of fruits/plant	0.3395	-0.232
weight of fruits/plants (kg)	0.4138	-0.0803
Average fruit weight (g)	0.1901	0.2033
Total number of fruits/plot	0.3126	-0.1295
Plot yield (kg)	0.3312	-0.0842
Fruit length at green stage (cm)	-0.1045	0.3843
Fruit length at mature stage (cm)	0.0561	0.4698
Fruit diameter at green stage (cm)	-0.1811	-0.3931
Fruit diameter at mature stage (cm)	-0.1571	-0.1813
Plant height at 1st harvest (cm)	-0.1854	-0.2723
Fruit yield (t/ha)	-0.1025	0.3443

CONCLUSION

The investigation into the genetic divergence of sweet pepper in Bangladesh reveals a considerable level of genetic variability among the studied genotypes. This diversity is a critical asset for breeding programs aiming to develop improved sweet pepper varieties with

enhanced resistance to local biotic and abiotic stresses, better yield potential, and desirable market traits. The identification of distinct genetic clusters among the accessions provides valuable information for selecting parent lines in future breeding efforts. By harnessing the genetic diversity present in Bangladeshi sweet pepper populations, it is possible to address some of the key challenges faced by farmers, such as earliness, higher yield, and improved nutritional content. This study underscores the importance of conserving and utilizing genetic resources to ensure the sustainability of sweet pepper cultivation in Bangladesh. The findings lay a foundation for further research and breeding initiatives that could lead to the development of superior varieties, ultimately contributing to food and nutritional security and the agricultural economy of the country.

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