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Breeding Potential of Sweet Pepper Genotypes Involving Different Fruit Colours and Shapes Using Multivariate Analysis

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***Abstract*:** The study was undertaken to characterize and determine the genetic divergence of 21 sweet peppers genotypes having different fruit colours and shapes. High Shanon-Wiener diversity index with an overall mean of 70.71 % confirmed the existence of diversity among the studied genotypes. Fruits started developing colours in 19 to 68 days after anthesis depending on the genotype. High heritability coupled with high genetic advance as per cent of mean was observed for all the traits except days to first harvest, revealing additive genetic control of most traits. Number of fruits/plant and fruit weight were identified as important selection indices for yield improvement. Sweet pepper genotypes could be grouped into 5 clusters which do not represent places of origin indicating genotypes in a cluster were geographically diverse; genotypes obtained from the same region were genetically different. The principal components, β-carotene content, number of fruits/plant, lycopene content of fruit and average fruit weight, had eigen values >1 and together accounted for 100% of total variation.Based on multivariate analysis and average performance, genotypes 'C/4' (Red Group 42A, blocky), '8/4' (Orange Red Group 34A, elongate), 'Arya' (Red Group 45A, blocky), 'Baby Bell' (Red Group 42A, blocky), 'BC CAP Purple' (Purple Group N77A, blocky), 'BC CAP Yellow' (Yellow Orange Group 17A, blocky) and 'BC CAP White' (Green white Group 157 C, blocky) were identified as good donors and could be utilized in future breeding.

***Keywords*:** *Capsicum annuum* var. *grossum*, Characterization, Genetic diversity, Colour pigments

Sweet pepper (*Capsicum annuum* var. *grossum* Sendt.) is one of the highly remunerative vegetables cultivated widely throughout temperate and sub-tropical Europe, USA, Africa, India, East Asia, and China (Bose et al 2021). The crop is appreciated worldwide for their flavor, aroma, color and are a rich source of capsaicinoids, carotenoids (some of them with provitamin A activity), flavonoids, ascorbic acid (vitamin C), and tocopherols (vitamin E) (Wahyuni et al 2011). Sweet pepper fruits are available in different shapes (elongate, almost round, triangular, campanulate and blocky) and colours (red, yellow, green, white, purple and orange) which decide the market value of the produce. The choice of fruit colour varies region to region. Based on fruit shape and size, more than 20 market types of sweet peppers are known. Sweet pepper fruit undergoes a distinct phase of colour change during its development. Different genotypes carry different genes for the expression of various fruit colours. Tian et al. (2015) named four key genes phytoene synthase (*Psy*), lycopene-β-cyclase (*Lcyb*), β-carotene hydroxylase (*Crtz*), and capsanthin/capsorubin synthase (*Ccs*) in the capsanthin biosynthetic pathway of pepper cultivars with red, yellow, and orange fruits. Another gene Anthocyanin (*A*) the incompletely dominant gene for anthocyanin colour in immature pepper fruit is also suggested by Lippert et al (1965). Transfer of important genes could be possible through hybridization. Lack of study on the development of different fruit colours hinders to identify the most appropriate stage of harvesting when the fruit show maximum attractiveness. Therefore, knowledge about different colour development of sweet pepper fruit is necessary for the breeders as well as the farmers. The breeding programmes so far carried out in this economically important crop have made little use of different coloured genotypes.

In recent past sweet pepper has attained an important status of "high value vegetable crop" in India due to its high nutritional value and export potential. Cultivation of sweet pepper in the cost effective naturally ventilated polyhouses has proved to be a very remunerative venture to the greenhouse growers as they are fetching maximum returns in the markets. A few old varieties are still recommended or available for commercial cultivation under polyhouse, which becomes poor yielder and vulnerable to insect-pest and

diseases. There is a need for genetic restructuring of the sweet pepper germplasm for increasing the productivity under low cost polyhouse considering the preference of the consumers. Presence of sufficient variability in basic genetic material of any crop is a pre requisite for effective selection and improvement of superior genotypes (Jogi et al 2015). Assessment of genetic variability in the available germplasm through parameters of variability helps to identify the potential genotypes for their use either directly as varieties or as parents in future crop improvement programmes. The study on genetic variability also generates valuable information pertaining to the type of gene action involved in the manifestation of different horticultural traits. Knowledge of inter-character relationship is equally important for indirect improvement of characters that are difficult to quantify especially those which exhibit low heritability. The complexity of character relationships among themselves and with fruit yield becomes evident from the discussion alone did not provide a comprehensive picture of relative importance of direct and indirect influences of each character to fruit yield, as these traits were the resultant product of combined effects of various factors complementing or counteracting. Therefore, information about direct and indirect relationship among any characters would help more realistic interpretation regarding influence of a character on a particular trait. The basic step for crop improvement relies on characterization and identification of existing germplasm. It is generally agreed that genetically diverse parents will show the maximum heterosis and offer the maximum chance of isolating transgressive segregates. This serves the purpose of identifying probable parents for obtaining the best recombinants from the population. Assessment of genetic diversity is important for selecting breeding strategies. Quantification of genetic divergence through biometrical procedures has made it possible to assess the variability pattern of specific characters in whole germplasm and to choose genetically diverse parents for successful hybridization. The present study aimed to identify important selection indices, to assess the genetic divergence of different sweet pepper genotypes having different fruit shapes and colours based on quantitative traits for identification of parents in hybridization programme.

MATERIAL AND METHODS

Experiments of the present investigation were carried out at Bidhan Chandra Krishi Viswavidyalaya (BCKV), Kalyani, Nadia, West Bengal, India. Twenty-one advanced breeding lines of sweet pepper collected from MIDH Project, BCKV, West Bengal and ICAR-IIVR, Varanasi, constituted the plant materials for this study. The genotypes were grown under low cost polyhouse (bamboo structured covered with 250µ UV stabilized cladding material with sides open) in randomized complete block design with three replications. Seed beds were prepared in a sandy loam soil and were 15 cm tall and 1.0 m wide. Well rotten cow-dung manure at 4 kg/m^2 was mixed into the beds. Beds were drenched with chlorothalonil @ 0.2 % + carbendazim @ 0.1 % to avoid damping off disease. Seeds, treated with thiram (3.0 g/kg of seed), were sown during the 1st week of October, 2019 at a shallow depth at 5 cm apart and covered with finely sieved well rotten leaf mould which acts as soil improver and to prevent the soil drying out. After sowing, beds were covered with straw until germination which normally takes five to seven days and hand watered regularly up to last week of October, 2019. Seedlings were hardened by with holding water 4 days before transplanting. The soil under polyhouse was prepared by hand tractor thoroughly to get a fine tilth before transplanting of the seedlings. Well rotten FYM @ 15 tons/ha was applied in the soil during the final land preparation. Thirty day old seedlings were transplanted in separate beds measuring 1.0 m × 4.0 m at 50 cm × 50 cm spacing during 1st week of November, 2019 under polyhouse in the afternoon hours. A fertilizer dose of 150 kg N, 75 kg P_2O_5 and 75 kg K_2O/ha was applied to the crop. Foliar sprays of micronutrient mixtures containing Zn, B and Mo were applied time to time. All the cultural practices scheduled for its cultivation were followed in time as per Bose et al (2021).

Observations were recorded from ten randomly selected plants from each genotype and the average was worked out for statistical computation. Ten fruits per genotype per replication were taken for recording different fruit characters. The fruits were cut into two halves to record pericarp thickness (mm) and locules per fruit. Qualitative traits like growth habit (Prostrate, Indeterminate, erect), leaf shape (Deltoid, Ovate, Lanceolate), flower position (Pendent, Intermediate, Erect), corolla colour (white, light yellow, yellow, yellow green, white with purple base, white with purple margin, purple with white base, purple), male sterility (absent, present), fruit shape (elongate, almost round, triangular, campanulate, blocky), and fruit colour at marketable maturity [(Royal Horticultural Society Colour Chart (RHCC)] were taken as per the minimal descriptors of NBPGR, New Delhi. Quantitative traits like plant height (cm), days to first flowering, days to 50% flowering, days to first harvest, number of primary branches/plant, fruit length (cm), fruit diameter (cm), shape index, fruit diameter, pericarp thickness (mm) of fruit, number of locules/fruit, number of seeds per fruit, number of fruits/plants, average fruit weight (g), fruit yield/ plant (kg) were taken. The cut fruits were used to make replication-wise composite sample to estimate fruit

quality characters,TSS content of fruit (^{0} brix) determined by hand Refractometer, Vitamin-C content of fruit (mg/100 g), Lycopene content of fruit (mg/100 g) and β-carotene content of fruit (mg/100 g) as per Sadasivam and Manickam (1996).

The data were subjected to the analysis of variance for randomized block design using Windostat software (ver.8.0, Indostat Services, Hyderabad, India). Frequency distribution was calculated from a set of morphological qualitative data from all the available variations in sweet pepper descriptor showing the number of occurrences (frequency) at each value or range of values. The frequency distributions were used to calculate the Shannon-Wiener diversity index (H') for each character (Hennink and Zeven, 1991). The index is defined as:

$$H' = -\sum_{i=1}^{s} (pi \ln Pi)$$

Where H'= diversity index; S = Total number of descriptors in the i^{-th} descriptor; Pi = fraction of individuals belonging to the i^{-th} descriptor state (number of observations/descriptor state in i^{-th} descriptor divided by the total number of characterized plants).

The genotype and phenotypic co-efficient of variations were calculated as per by Burton (1952). Heritability in broad sense (H) was estimated by the formula given by Hanson et al (1956). The expected genetic advance (GA) was calculated by the formula as suggested by Johnson et al (1955) and Lush (1949). Direct and indirect effects of component traits on marketable fruit yield were calculated through path coefficient analysis as suggested by Dewey and Lu (1940). The grouping of the populations was done by using Tocher's method as described by Rao (1952). Hierarchical cluster analysis has been done with those same genotypes in order to observe the degree of association according to their characteristics that was expressed in dendrogram following Ward's (1963) method. Principal component analysis (PCA), to identify the factor dimension of the data, was used to summarize varietal information in a reduced number of factors for selection of the best performing genotypes. Statistical analyses were with Windostat (ver.8.0, Indostat Services, Hyderabad, India). Treatment means were separated using Least Significant Differences following Tukey's post hoc test.

RESULTS AND DISCUSSION

Morphological characterization of genotypes: Seven qualitative characters *viz*., plant growth habit, leaf shape, flower position, corolla colour, male sterility, fruit colour and fruit shape were recorded in 21 genotypes of sweet pepper as per the minimal descriptors of NBPGR to characterize the present diversity of sweet pepper (Table 1). In the present investigation two types of growth habit was found *viz*. erect and intermediate. All the genotypes except the Royal Wonder showed erect growth habit (95.23%). The genotype Royal Wonder exhibited intermediate (4.76 %) growth habit. Leaf shape of different sweet pepper genotypes were grouped into three categories *viz*. deltoid, ovate and lanceolate. Out of 21 genotypes, 42.85 % genotypes showed deltoid type, 47.61 % showed ovate and 9.52 % genotypes showed lanceolate type of leaf shapes. Out of 21 genotypes, 10 genotypes exhibited pendent position (47.61 %), 8 genotypes in intermediate position (38.09 %) and 3 genotypes exhibited upright flower position (14.28 %). The genotypes were grouped into 12 categories according to the Royal Horticultural Society Colour Chart (RHCC). Four genotypes each were grouped into Red Group 42A and Red Group 45A (Table 1). Under Red Group 46A, two genotypes were identified. One genotype was categorized into Orange Red Group 34A group. One genotype each was grouped into Yellow Orange Group 17A, Yellow Orange Group 21A and Yellow Orange Group 23A. Two genotypes were categorized into Green Group N137B and Green Group 141B. One genotype was categorized under Green White Group 157C group. One genotype each was grouped under Purple Group N77A and Yellow Group 10 A. Fruit shape of different sweet pepper genotypes were grouped into three categories *viz*. blocky, elongate and almost round. Out of 21 genotypes 85.71 % genotypes showed blocky type of fruit shape and 9.52 % revealed elongate type of fruit shape. Only one genotype Royal Wonder showed almost round type (4.76 %) of fruit shape. Characterization of sweet pepper genotypes has been a determinant factor to gain new insights into genes and mechanisms involved in plant morphology.

Shannon-Weaver Diversity Index of 21 sweet pepper genotypes was estimated from 5 qualitative characters and results are presented in Table 2. High Shanon-Wiener diversity index with an overall mean of 70.71 % was obtained, supporting the existence of diversity among the sweet pepper genotypes. In the present study Shannon-Wiener diversity index H' value varied from 0 to 2.318. The character fruit colour showed maximum diversity (2.318) followed by flower position (0.998), leaf shape (0.940) and fruit shape (0.707). Corolla colour and male sterility did not show any diversity among the genotypes.

Frequency distribution of different traits showed a considerable variation present in the population. Leaf shape, flower position, fruit colour and fruit shape showed higher variation than other characters. Selection could be useful for the trait fruit colour and fruit shape to develop attractive sweet pepper variety. Roy et al (2019) also reported such type of fruit colour and fruit shape.

Table 1. Qualitative parameters of 21 sweet pepper genotypes

Genotype	Plant growth habit	Leaf shape	Flower position	Fruit colour*	Fruit shape
C/4	Erect	Ovate	Intermediate	Red Group 42A	Blocky
8/4	Erect	Deltoid	Pendent	Orange Red Group 34A	Elongate
Arya	Erect	Deltoid	Intermediate	Red Group 45A	Blocky
Baby Bell	Erect	Deltoid	Intermediate	Red Group 42A	Blocky
BC CAP Purple	Erect	Ovate	Pendent	Purple Group N77A	Blocky
Royal Wonder	Intermediate	Deltoid	Intermediate	Green Group N137B	Almost round
BC CAP White	Erect	Deltoid	Pendent	Green White Group 157C	Blocky
BC CAP Green	Erect	Lanceolate	Pendent	Green Group 141B	Blocky
BC CAP Red	Erect	Lanceolate	Pendent	Red Group 45A	Blocky
Fiza (DG)	Erect	Ovate	Pendent	Red Group 46A	Blocky
Fiza (LG)	Erect	Ovate	Pendent	Red Group 45A	Blocky
Ayesha	Erect	Deltoid	Intermediate	Red Group 45A	Blocky
BC CAP Yellow	Erect	Deltoid	Pendent	Yellow Orange Group 17A	Blocky
Arka Mohini	Erect	Deltoid	Pendent	Green Group 141B	Blocky
Arka Basant	Erect	Ovate	Upright	Yellow Group 10 A	Blocky
Arka Gaurav	Erect	Ovate	Upright	Yellow Orange Group 21A	Blocky
BC CAP Orange	Erect	Deltoid	Pendent	Yellow Orange Group 23A	Blocky
2018/CAP 2	Erect	Ovate	Intermediate	Red Group 42A	Blocky
2018/CAP 3	Erect	Ovate	Intermediate	Yellow Orange Group 23A	Blocky
2018/CAP 4	Erect	Ovate	Upright	Red Group 42A	Elongate
2018/CAP 5	Erect	Ovate	Intermediate	Red Group 46A	Blocky

*Royal Horticulture Society (RHS) Colour Chart

Table 2. Frequency distribution for different qualitative characters in sweet pepper genotypes

Character	Specification	No. of genotypes	Percentage of genotypes (%)	H'-index
Plant growth habit	Erect	20	95.23	0.191
	Intermediate	1	4.76	
Leaf shape	Deltoid	9	42.85	0.940
	Ovate	10	47.61	
	Lanceolate	2	9.52	
Flower position	Pendent	10	47.61	0.998
	Intermediate	8	38.09	
	Upright	3	14.28	
Fruit colour	Red Group 42A	4	19.04	2.318
	Red Group 45A	4	19.04	
	Red Group 46A	2	9.52	
	Orange Red Group 34A	1	4.76	
	Green Group N137B	1	4.76	
	Green Group 141B	2	9.52	
	Yellow Orange Group 17A	1	4.76	
	Yellow Orange Group 21A	1	4.76	
	Yellow Orange Group 23A	2	9.52	
	Yellow Group 10 A	1	4.76	
	Green White Group 157C	1	4.76	
	Purple Group N77A	1	4.76	
Fruit shape	Blocky	18	85.71	0.501
	Elongate	2	9.52	
	Almost round	1	4.76	
Overall mean of H'				0.707

Biodiversity in crops can be summarized with two of its components, allelic evenness and allelic richness. The descriptor and descriptor states are parallel to the locus and alleles, respectively in morphological evaluation. The allelic evenness in this study was measured using the Shannon-Wiener Diversity Index, whereas the allelic richness was measured by counting the descriptor states for each descriptor without considering their individual frequencies. The richness indicates the number of genotype present in a designated area whereas evenness stands for the relative abundance of each genotype. The value of Shannon-Wiener diversity index (H') for all characters varied from 0 to 2.318. High Shanon-Wiener diversity index with an overall mean of 70% was obtained, confirming the existence of diversity among the genotypes. The predominant traits that showed wider variations among the genotypes were fruit colour, followed by flower position, leaf shape and fruit shape. The Shannon-Wiener index values can range from 0 to ~ 4.6. A value near 0 indicated that every genotype in the sample is the same and a value near 4.6 indicated the numbers of individual are evenly distributed between the sweet pepper genotypes. A low H' indicates unbalance frequency class and lack of diversity for the traits for corolla colour and male sterility mechanism. A higher H' value indicates presence of variability or diversity for the trait (Hennink and Zeven 1991). Values below overall mean indicate unbalance frequency class and lack of diversity for the traits. Belay and Tsehaye (2020) also studied the Shanon-Wiener diversity index and they observed highly divergent qualitative traits of 63 hot pepper Ethiopian landraces.

Mean performance of genotypes: The character plant height was influenced significantly by the genotypes under study (Table 3). The genotype BC CAP Orange showed maximum plant height followed by Ayesha and BC CAP Yellow. The minimum plant height was observed in Arka Gaurav (83.16 cm) and 2018/CAP 5 (83.16 cm). Early

Table 3. Mean performance of twenty one sweet pepper genotypes

Genotype	Plant height (cm)	Days to first flowering	Days to 50% flowering	Days to first harvest	Number of primary branches/plants	Fruit length (cm)	Fruit diameter (cm)	Shape index	Pericarp thickness (mm)
C/4	109.38	42.67	48.33	128.00	2.33	8.75	7.18	1.22	5.22
8/4	86.02	44.67	52.67	108.67	2.50	11.93	5.46	2.19	5.17
Arya	120.70	33.33	41.67	130.33	2.50	10.44	6.15	1.69	5.92
Baby Bell	126.14	46.00	48.00	124.33	2.50	7.98	7.27	1.10	5.04
BC CAP Purple	120.00	53.00	70.67	126.33	2.00	8.69	6.45	1.35	4.50
Royal Wonder	95.69	40.33	46.00	130.00	3.50	9.14	8.32	1.11	5.96
BC CAP White	89.05	40.00	42.33	105.00	2.50	7.36	5.47	1.39	6.96
BC CAP Green	99.66	36.00	54.67	135.67	2.50	9.40	7.05	1.34	5.81
BC CAP Red	104.83	43.33	55.67	138.00	2.17	9.32	6.79	1.37	5.90
Fiza (DG)	103.11	43.00	65.67	126.33	2.33	10.03	5.51	1.83	3.96
Fiza (LG)	123.44	45.00	60.67	122.00	2.33	6.91	4.68	1.48	5.28
Ayesha	141.77	37.33	48.67	136.67	2.00	11.12	4.76	2.34	5.73
BC CAP Yellow	132.50	34.00	50.67	122.33	2.33	8.22	6.60	1.26	5.18
Arka Mohini	85.83	40.67	48.33	136.00	3.00	10.44	7.28	1.44	6.57
Arka Basant	86.16	52.00	74.67	136.33	2.83	7.48	5.28	1.43	5.70
Arka Gaurav	83.16	46.00	48.67	134.33	3.00	10.31	6.68	1.55	5.46
BC CAP Orange	146.77	43.00	54.67	134.67	2.83	8.86	6.70	1.32	5.78
2018/CAP 2	105.00	47.33	75.33	137.67	2.17	6.73	5.03	1.36	3.26
2018/CAP 3	83.66	50.00	78.00	138.33	2.17	6.48	5.29	1.22	3.23
2018/CAP 4	90.61	48.00	74.33	140.00	2.00	9.66	3.99	2.43	5.30
2018/CAP 5	83.16	54.67	80.67	133.67	2.17	8.46	5.40	1.57	3.54
Mean	105.56	43.83	58.11	129.75	2.46	8.94	6.06	1.52	5.21
								0.11	0.33
C.D. at 5%	16.73	5.19	4.98	8.04	0.40	1.27	0.87	0.31	0.94
C.V. (%)	9.61	7.17	5.19	3.75	9.77	8.61	8.73	12.28	10.95

flowering leads to early and higher production of fruit which can fetch higher market price.Days to first flowering and days to 50% flowering are the main traits to judge earliness of the genotypes. In the present investigation, the genotype Arya takes minimum days (33.33 days) to open first flower followed by BC CAP Yellow and BC CAP Green . The maximum days taken to first flowering was in 2018/CAP 5 (54.67 days) followed by BC CAP Purple. The minimum days to produce 50% flowering was taken by the genotype Arya (41.67 days) followed by BC CAP White, Royal Wonder. The genotype BC CAP White taken minimum days to first harvest (105.00 days) followed by 8/4. The maximum days taken to first harvesting was in 2018/CAP 4 (140 days) followed by 2018/CAP 3. The highest number of primary branches/plants was noticed in the genotype Royal Wonder (3.50) followed by Arka Mohini and Arka Gaurav. The genotype showed maximum fruit length was 8/4 (11.93 cm) followed by Ayesha. The genotype Royal Wonder revealed maximum fruit diameter (8.32 cm) followed by Arka Mohini and Baby Bell. The genotype 2018/CAP 4 produced highest shape index (2.43) followed by Ayesha and 8/4 . The thickest pericarp was documented in BC CAP White (6.96 mm) followed by Arka Mohini and Royal Wonder (Table 3). The minimum number of locule/fruit was in 2018/CAP 2 (2.00) followed by 2018/CAP 5 (Table 4). The maximum number of seeds/fruits was recorded by BC CAP Green (277.67) followed by Fiza (LG) and BC CAP Red. The genotype 8/4 recorded the highest TSS content of fruit (8.91^{0}brix) followed by C/4 . The highest vitamin C content was in C/4 (180.88 mg/100 g) followed by Arka Gaurav. The genotype BC CAP Red recorded the maximum Lycopene content of fruit (3.04 mg/100 g) followed by Baby Bell .The genotype Arya recorded the highest β-carotene (2.74 mg/100 g) followed by Baby Bell . The maximum number of fruits was produced by BC CAP Orange (15.02) followed by Arka Basant. The heaviest fruit was documented in Arka Gaurav (137.68 g) followed by Arka

Table 4. Mean performance of twenty one sweet pepper genotypes

Genotype	Number of locule/ fruit	Number of seeds/ fruits	TSS content of fruit (^{0} brix)	Vitamin C content of fruit (mg/100 g)	Lycopene content of fruit (mg/100 g)	β- carotene content of fruit (mg/100 g)	Number of fruits/ plants	Average fruit weight (g)	Fruit yield/ plant (kg)
C/4	3.70	154.04	8.44	180.88	1.07	2.39	9.34	112.01	1.05
8/4	3.13	104.56	8.91	138.85	1.62	2.12	9.00	87.01	0.79
Arya	3.43	77.03	6.90	146.34	2.00	2.74	8.34	108.02	0.90
Baby Bell	3.33	105.14	6.74	175.19	2.25	2.59	7.34	90.04	0.65
BC CAP Purple	3.67	152.50	7.11	126.98	0.16	0.21	6.33	73.02	0.46
Royal Wonder	3.40	160.96	5.61	123.09	0.21	0.16	6.67	120.03	0.80
BC CAP White	3.64	77.26	6.64	178.87	0.06	0.09	6.00	78.09	0.47
BC CAP Green	3.67	277.67	4.30	119.28	0.31	0.31	6.50	115.43	0.75
BC CAP Red	4.01	218.78	7.93	171.38	3.04	1.43	7.50	98.03	0.73
Fiza (DG)	3.00	48.72	7.30	148.24	1.08	0.92	10.50	53.59	0.56
Fiza (LG)	2.67	263.48	6.40	155.72	1.78	1.56	11.62	50.32	0.58
Ayesha	3.00	91.22	7.60	159.64	1.31	1.01	10.50	107.14	1.13
BC CAP Yellow	3.00	101.74	8.00	178.87	0.14	0.66	9.00	94.47	0.85
Arka Mohini	3.67	144.71	8.20	173.10	0.11	1.14	8.01	131.33	1.05
Arka Basant	2.67	115.72	6.73	138.52	0.30	0.42	13.76	54.48	0.75
Arka Gaurav	3.67	52.35	8.20	180.82	0.23	0.61	6.01	137.68	0.83
BC CAP Orange	3.34	160.71	7.53	172.39	1.02	0.76	15.02	80.75	1.21
2018/CAP 2	2.00	83.43	7.13	55.84	0.20	0.27	10.02	41.08	0.41
2018/CAP 3	2.67	197.34	7.20	53.85	0.17	0.39	7.00	55.00	0.39
2018/CAP 4	3.00	123.70	7.30	78.87	0.25	0.40	11.00	46.26	0.51
2018/CAP 5	2.33	85.50	6.57	92.36	0.24	0.29	11.00	47.51	0.52
Mean	3.19	133.17	7.18	140.43	0.84	0.97	9.07	84.82	0.73
								2.01	0.04
C.D. at 5%	0.17	30.52	1.01	9.31	0.07	0.05	1.22	5.76	0.12
C.V. (%)	3.18	13.89	8.55	4.02	5.20	3.39	8.13	4.11	9.59

Mohini. The maximum fruit yield/plant was recorded in BC CAP Orange (1.21 kg) closely followed by Ayesha (Table 4).

Genetic variability and heritability: The result on analysis of variances using randomized block design revealed that the genotypes exhibited highly significant differences for all the characters studied even at 1% level of significance (Table 5) which clearly endorsed the justification of studying genetic variability of different characters employing these genotypes. The estimates of mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance as per cent over mean (GAM) were worked out for 18 characters of 21 sweet pepper genotypes (Table 6).

The knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is much helpful in predicting the amount of variation present in a given assemblage of genotypes. The estimates of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) in the present investigation for all characters under study were very close but PCV was higher than GCV (Table 6). The value of GCV ranged from 6.91% (days to first harvest) to 103.72% (lycopene content of fruit). On the other hand PCV ranged from 7.86 % (days to first harvest) to 103.85 % (lycopene content of fruit). High GCV values (>20.00 %) were documented for the traits days to 50 % flowering, shape index, number of seeds/fruits, vitamin-C content of fruit, lycopene content of fruit, β-carotene, number of fruits/plants, average fruit weight, fruit yield/plant. Moderate GCV values (10-20 %) were recorded for the traits plant height, days to first flowering, number of primary branches/plant, fruit length, fruit diameter, pericarp thickness, number of locule/fruit and TSS content of fruit. Likewise, high PCV values (>20.00 %) were recorded for plant height, days to 50% flowering, shape index, pericarp thickness, number of seeds/fruit, Vitamin-C content of fruit, lycopene content of fruit, β-carotene, number of fruit/plant, average fruit weight and fruit yield/plant, whereas days to first flowering, number of primary branches/plant, fruit length, fruit diameter, number of locule/fruit, and TSS content of fruit showed moderate PCV (10-20 %). The proportion of GCV to PCV noticed in this investigation ranged from 83.25% in number of primary branches/plant to 99.85% in β-carotene content. GCV alone do not estimate the variations that are heritable for this reason, estimation of heritability becomes essential. High broad sense heritability (60 % and above) was recorded for most characters under study. High magnitude (>20.00 %) of genetic advance as per cent of mean was observed for most traits under study except days

Table 5. Analysis of variance (mean square) for 18 characters of sweet pepper genotypes

Source of variation	Mean sum of square		
	Replication	Treatments	Error
Degrees of freedom	2	20	40
Plant height (cm)	1.4848	1229.4362**	102.8202
Days to first flowering	3.3492	104.6540**	9.8825
Days to 50% flowering	3.9206	481.8111**	9.1040
Days to first harvest	3.4444	264.5302**	23.7111
Number of primary branches/plants	0.1243	0.4492**	0.0578
Fruit length (cm)	1.5203	6.5358**	0.5919
Fruit diameter (cm)	0.5398	3.5402**	0.2801
Shape index	0.0044	0.4262**	0.0350
Pericarp thickness (mm)	0.1244	3.0543**	0.3257
Number of locule/fruit	0.0134	0.7938**	0.0103
Number of seeds/fruits	1.1092	12182.0462**	341.9874
TSS content of fruit (^{0} brix)	0.3755	3.1096**	0.3764
Vitamin-C content of fruit (mg/100 g)	7.0351	4929.8251**	31.7973
Lycopene content of fruit (mg/100 g)	0.0006	2.2553**	0.0019
β- carotene content of fruit (mg/100 g)	0.0001	2.1462**	0.0011
Number of fruits/plants	0.8325	18.9603**	0.5431
Average fruit weight (g)	34.4900	2726.8796**	12.1734
Fruit yield/plant (kg)	0.0007	0.1741**	0.0049

** Significant at 0.01 level of probability

to first harvest which showed moderate magnitude of GA (Table 6).

The difference between phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for most characters under study was very close suggesting less influence of environment for the expression of characters. High magnitude of GCV and PCV was observed in days to 50% flowering, shape index, number of seeds/fruits, vitamin-C content of fruit, lycopene content of fruit, β-carotene content of fruit, number of fruits per plant, average fruit weight and fruit yield/plant indicating ample scope for the improvement of such traits through simple selection. Similar findings were reported by Rana et al (2015), Anuradha and Sood (2019) and Thakur et al (2019). In this investigation, the proportion of GCV to PCV illustrate that genetic contribution to the overall phenotypic expression of most traits was high. Therefore, their use as important discriminatory variables for sweet pepper classification study seems relatively dependable.

High broad sense heritability was recorded for all the characters indicated that selection based on phenotypic expression could be dependable as there was major role of genetic constitution in the expression of these characters. High magnitude (>60.00 %) of heritability estimates had also been reported earlier by Rana et al (2015), Anuradha and Sood (2019) and Thakur et al (2019) in sweet pepper. In the present study, high heritability coupled with high genetic advance as per cent of mean was observed for all the traits under study except days to first harvest. These characters can be regarded as most reliable for selection because these characters are controlled by additive gene action and selection of these traits would be rewarding for the improvement of these traits. Such observations find support for plant height, days to 50% flowering, number of primary branches/plant, TSS content of fruit (Thakur et al 2019); fruit length (Anuradha and Sood 2019); fruit diameter (Pandey et al 2013); Vitamin-C content of fruit (Anuradha and Sood 2019, Thakur et al 2019); number of fruits/plant (Rana et al 2015); average fruit weight (Pandey et al 2013, Sharma et al 2017); fruit yield/plant (Rana et al 2015, Sharma et al 2017, Thakur et al 2019).

Correlation analysis: Association analysis of different morphological characters with fruit yield of sweet pepper genotypes and their inter-relationships were investigated

Table 6. Genetic parameters of sweet pepper genotypes and genotypic and phenotypic correlations and direct effects of 17 characters on fruit yield /plant

Character	GCV* (%)	PCV* (%)	GCV:PCV	h^2 in broad sense (%)	Genetic advance as % of mean	rg with fruit yield/plant	rp with fruit yield/plant	Direct effect of characters on fruit yield/plant at phenotypic level
Plant height (cm)	18.36	20.72	88.60	78.51	33.51	0.477*	0.377	0.071
Days to first flowering	12.82	14.69	87.28	76.17	23.06	-0.576**	-0.486*	-0.028
Days to 50% flowering	21.60	22.22	97.23	94.54	43.27	-0.638**	-0.587**	-0.118
Days to first harvest	6.91	7.86	87.86	77.20	12.50	0.136	0.143	-0.070
Number of primary branches/plants	14.68	17.64	83.25	69.30	25.18	0.443*	0.357	-0.100
Fruit length (cm)	15.75	17.95	87.75	77.00	28.47	0.586**	0.473*	0.073
Fruit diameter (cm)	17.19	19.28	89.17	79.50	31.57	0.460*	0.381	-0.045
Shape index	23.71	26.70	88.80	78.86	43.38	0.069	0.054	-0.129
Pericarp thickness (mm)	18.30	21.33	85.81	73.63	32.35	0.591**	0.497*	-0.020
Number of locule/fruit	16.02	16.33	98.09	96.22	32.37	0.413	0.404	0.090
Number of seeds/fruits	47.18	49.18	95.93	92.03	93.23	0.003	0.005	0.008
TSS content of fruit (^{0} brix)	13.30	15.81	84.12	70.77	23.04	0.329	0.286	0.091
Vitamin-C content of fruit (mg/100 g)	28.77	29.05	99.04	98.09	58.70	0.634**	0.601**	-0.168
Lycopene content of fruit (mg/100 g)	103.72	103.85	99.87	99.75	213.40	0.230	0.217	-0.020
β- carotene content of fruit (mg/100 g)	86.79	86.86	99.92	99.85	178.65	0.389	0.368	-0.001
Number of fruits/plants	27.32	28.50	95.85	91.87	53.94	0.248	0.301	0.885
Average fruit weight (g)	35.46	35.70	99.33	98.67	72.57	0.687**	0.665**	1.038
Fruit yield/plant (kg)	32.38	33.77	95.88	91.93	63.95	-	-	-

*GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation,h^2 = Heritability estimatein broad sense, rp = Phenotypic correlation coefficient; rg = Genotypic correlation coefficient *, ** Significant with $P \leq 0.05$ and 0.01, respectively
Residual effect= 0.021

through the study of both phenotypic and genotypic correlation co-efficient (Table 6). The genotypic and phenotypic correlation co-efficient agreed very closely for most traits under study. In general, the genotypic correlations were higher than the phenotypic ones. The characters plant height, number of primary branches/plants, fruit length, fruit diameter, pericarp thickness, vitamin-C content of fruit, and average fruit weight showed positive significant genotypic correlations with fruit yield/plant. Shape index, number of locules/fruit, number of seeds/fruits, number of fruits/plants, TSS content of fruit, lycopene content of fruit, and β-carotene content of fruit showed positive but non-significant correlations with fruit yield/plant. The negative significant genotypic correlation was found by two characters namely, days to first flowering and days to 50% flowering. Besides, genotypic correlation, the traits fruit length, pericarp thickness, vitamin-C content of fruit, and average fruit weight expressed positive significant phenotypic correlations with fruit yield/plant. Plant height, number of primary branches/plant, fruit diameter, shape index, number of locules/fruit, number of seeds/fruits, number of fruits/plants, TSS content of fruit, lycopene content of fruit and β-carotene content of fruit showed positive but non-significant phenotypic correlations with fruit yield/plant. Besides, days to first flowering and days to 50% flowering exhibited negative significant phenotypic correlation coefficients with fruit yield/plant.

Close values of genotypic and phenotypic correlation co-efficient demonstrating little control of environment on the correlated response on most of the pair of fruit and fruit quality characters. From the result of genotypic and phenotypic correlation co-efficient suggested that fruit yield/plant can be increased through increase in important component traits like fruit length, pericarp thickness, vitamin-C content of fruit and average fruit weight. An inverse correlation was also found between days to first flowering and days to 50% flowering with yield indicating early flowering genotype gives more yield than the late one. Therefore, selection for the earliness traits would automatically improve the yield. Afroza et al (2013) reported positive significant correlation of fruit length with fruit yield/plant. Positive significant correlation of average fruit weight (Afroza et al 2013, Sharma et al 2017, Thakur et al 2019) with fruit yield/plant also supported the present findings. Inverse correlation of the traits days to first flowering (Afroza et al 2013) with fruit yield/plant had also been reported.

Path co-efficient analysis: The result showed that, among the yield component traits, number of fruits/plant (0.885) and average fruit weight (1.038) showed high positive direct effects on fruit yield/plant (Table 6). The direct effects of other traits as well as their indirect effects *via* other characters were negligible. Some other characters like plant height,fruit length, number of locules/fruit, number of seeds/fruit and TSS content of fruit also showed direct positive effects on fruit yield but their magnitude was very low. Rest of the characters showed negative direct effects on fruit yield/plant. Residual effect of the path analysis was very low (0.021). Number of fruits/plant and average fruit weight exhibited high positive direct effects on fruit yield/plant. This was the main cause of their positive association with fruit yield/plant. These results are in conformity with the observations of Sharma et al (2010) and Thakur et al (2019). Hence, direct selection through number of fruits/plant and average fruit weight could be beneficial for yield improvement of sweet pepper. Residual effect of the path analysis was very low suggesting the inclusion of maximum fruit yield determining characters in the present study. From the study of character association ships, combining both correlation and path co-efficient, two characters namely, number of fruits/plant and average fruit weight should be considered as important selection indices for yield improvement of sweet pepper as they showed positive correlation and high direct effects on fruit yield per/plant.These observations find support from Afroza et al (2013), Roy et al (2019) and Thakur et al (2019).

Genetic diversity through multivariate analysis: The present study aimed at analyzing the genetic divergence of 21 sweet pepper genotypes employing 18 important quantitative characters. Based on the degree of divergence (D^2 values) between any two genotypes a logical grouping of the genotypes with low D^2 value could be arrived at by Tocher's method as described by Rao (1952). Based on determination of divergence, all the 21 genotypes were grouped into 5 clusters by treating estimated D^2 values as the square of the generalized distance (Table 7). Cluster III was the largest having 9 genotypes (BC CAP Purple, BC CAP White, Royal Wonder, BC CAP Green, 2018/CAP-2, 2018/CAP-3, 2018/CAP-4, 2018/CAP-5, Arka Basant) followed by cluster I with 4 genotypes (C/4, 8/4, Arya, Baby Bell). Cluster IV (Fiza (DG), BC CAP Orange, Ayesha) and cluster V (BC CAP Yellow, Arka Gaurav, Arka Mohini) were having 3 genotypes each. Cluster II contained 2 genotypes (BC CAP Red, Fiza (LG)). In further study of Ward's (1963) dendrogram method (Fig. 1) by using squared Euclidean distance, it became clearly evident that there was high genetic diversity among the sweet pepper genotypes along with strong relationships among the genotypes. The intra- and inter-cluster distances among 21 sweet pepper genotypes are presented in Table 7. Among the 5 clusters, cluster II had the maximum intra-cluster value (1402.254)

followed by cluster I (1032.162). Cluster IV showed the minimum intra-cluster value. At inter-cluster level, the maximum inter-cluster value was observed between Cluster I and III (15686.9) followed by between Cluster I and V (10997.850). The minimum inter-cluster value was observed between Cluster III and V (1926.627).

The maximum cluster mean was in cluster V for number of primary branches/plant (2.78), fruit diameter (6.85 cm), pericarp thickness (5.73 mm), number of locule/fruit (3.44), TSS content of fruit (8.13 ^{0}brix), Vitamin-C content of fruit (177.60 mg/100 g) and average fruit weight (121.16 g) (Table 8). The highest cluster mean in cluster IV was for plant height (130.56 cm), fruit length (10.00 cm), shape index (1.83), number of fruits/plant (12.01) and fruit yield/plant (0.97 kg). Highest mean value for the traits number of locule/fruit (3.34) and lycopene content of fruit (2.41 mg/100 g) was shown by cluster II. Cluster I showed maximum mean value for the trait β-carotene content of fruit (2.46 mg/100 g). However, the minimum days taken to first flowering (40.22) revealed by the cluster V whereas, minimum number of days to 50 % flowering (47.67) and first fruit harvest (122.83) showed by the cluster I.The relative contribution of individual characters towards genetic divergence was estimated in terms of number of times it ranked first and is presented in Table 8. Among 18 characters, β-carotene content of fruit (37.62 %) expressed the maximum contribution towards the diversity followed by number of fruits/plant (21.9 %), lycopene content of fruit (13.81 %), average fruit weight (10.95 %), Vitamin C content (9.52 %) and fruit yield/plant (3.33 %).

The PCA was performed to obtain a simplified view of the relationship between the characters β-carotene content, number of fruits/plants, lycopene content of fruit and average fruit weight which explained almost 100% contribution towards divergence and variable loadings for components PC_1 (β-carotene content of fruit), PC_2 (number of fruits/plant), PC_3 (lycopene content of fruit) and PC_4 (fruit weight) were estimated (Table 9). These components were chosen because their eigenvalues were more than 1.0 and explained almost 100.00 % of total variance. The first component (PC1) explained 81.65 % of total accounted for variance in which an increase of β-carotene content of fruit content leads to increase in lycopene content of fruit and fruit weight, and decrease in amount of fruits/plant. The second component (PC2) explained an additional 18.13 % of the variance in which a decrease in number of fruits/plants leads to decrease in β-carotene content of fruit and lycopene content of fruit, and increase in fruit weight. The third component (PC3) explained an additional 0.16 % of the variance in which an increase in lycopene content of fruit leads to increase in β-carotene content, number of fruits/plant and average fruit weight (Table 9). Genotypes in close proximity are perceived as being similar in PCA; Genotypes that are further apart are more diverse. The differences observed in the data, and summarized in the PCA (Fig. 2), indicated genotypes Royal Wonder, BC CAP Green, Arya, 2018/CAP-3, Arka Mohini, Arka Gaurav, Fiza (LG), Fiza (DG), Arka Basant, BC CAP White, BC CAP Orange and Baby Bell were quantitatively dissimilar from others. The remainder of genotypes had similar features forming a separate cluster.

In the present study, 21 sweet pepper genotypes employing 18 important quantitative characters were grouped into 5 clusters based on the degree of divergence (D^2 values) between any two genotypes a logical grouping of the genotypes with low D^2 value could be arrived at by

Table 7. Cluster classification and inter-and intra-cluster distances of 21 sweet pepper genotypes

Clusters with the number of genotypes in parentheses	Name of the genotype with source of collection	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I (4)*	C/4 (BCKV, W.B.), 8/4 (BCKV, W.B.), Arya (BCKV, W.B.), Baby Bell (BCKV, W.B.)	**1032.162****	4155.689	15686.900	7044.672	10997.850
Cluster II (2)	BC CAP Red (BCKV, W.B.), Fiza (LG) (BCKV, W.B.)		**1402.254**	8298.652	2433.589	6629.095
Cluster III (9)	BC CAP Purple (BCKV, W.B.), BC CAP White (BCKV, W.B.), Royal Wonder (BCKV, W.B.), BC CAP Green (BCKV, W.B.), 2018/CAP-2 (IIVR, Varanasi), 2018/CAP-3 (IIVR, Varanasi), 2018/CAP-4 (IIVR, Varanasi), 2018/CAP-5 (IIVR, Varanasi), Arka Basant (IIHR, Bangalore)			**954.417**	2984.470	1926.627
Cluster IV (3)	Fiza (DG) (BCKV, W.B.), BC CAP Orange (BCKV, W.B.), Ayesha (BCKV, W.B.)				**647.289**	1973.834
Cluster V (3)	BC CAP Yellow (BCKV, W.B.), Arka Gaurav (IIHR, Bangalore), Arka Mohini (IIHR, Bangalore)					**897.165**

*Figures in parentheses indicate number of genotypes.**Bold values indicate intra-cluster distance between genotypes

Tocher's method as described by Rao (1952). The grouping pattern of genotypes was observed to be random, indicating no direct relationship was noticed between geographical distribution and genetic distance. Hence, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. Several earlier studies also reported that different set of sweet pepper genotypes were grouped under 4-6 clusters (Rana et al 2015, Dabral et al 2016, Devi et al 2017, Sharma et al 2017). Cluster II being maximum intra-cluster value followed by cluster I indicating existence of wide genetic divergence among the component genotypes in it as compared to other clusters. Based on inter-cluster distance, maximum inter-cluster value between Cluster I and III followed by between Cluster I and V indicated that the genotypes in these clusters can be used as parents in hybridization programme to develop higher heterotic hybrids and segregating population will expect to give transgressive segregates in the advanced generation. Genetic divergence of sweet pepper using multivariate analysis was earlier studied by Rana et al (2015),

Table 8. Cluster means and per cent contribution towards divergence of 18 characters of sweet pepper genotypes

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	% contribution towards divergence
Plant height (cm)	110.56	114.14	94.78	130.56	100.50	0.00
Days to first flowering	41.67	44.17	46.82	41.11	40.22	0.00
Days to 50% flowering	47.67	58.17	66.30	56.33	49.22	0.00
Days to first harvest	122.83	130.00	131.44	132.56	130.89	0.00
Number of primary branches/plants	2.46	2.25	2.43	2.39	2.78	0.00
Fruit length (cm)	9.78	8.11	8.16	10.00	9.66	0.00
Fruit diameter (cm)	6.51	5.74	5.81	5.66	6.85	0.00
Shape index	1.55	1.42	1.47	1.83	1.42	0.00
Pericarp thickness (mm)	5.34	5.59	4.92	5.15	5.73	0.00
Number of locule/fruit	3.40	3.34	3.01	3.11	3.44	2.38
Number of seeds/fruits	110.19	241.13	141.56	100.22	99.60	0.48
TSS content of fruit (^{0} brix)	7.75	7.17	6.51	7.48	8.13	0.00
Vitamin-C content of fruit (mg/100 g)	160.32	163.55	107.52	160.09	177.60	9.52
Lycopene content of fruit (mg/100 g)	1.73	2.41	0.21	1.14	0.16	13.81
β- carotene content of fruit (mg/100 g)	2.46	1.50	0.28	0.90	0.80	37.62
Number of fruits/plants	8.50	9.56	8.70	12.01	7.67	21.90
Average fruit weight (g)	99.27	74.17	70.10	80.49	121.16	10.95
Fruit yield/plant (kg)	0.85	0.66	0.56	0.97	0.91	3.33

Table 9. Results of principal component analysis (PCA) for characters contributing to divergence in sweet pepper and contribution of diverse traits in the principal components of sweet pepper

Principal components	Eigenvalue %	% Variance	% Cumulative variance	
Eigenvalues and variance accounted for (%) by PCA based on correlation matrix				
PC_1	2090.54865	81.65	81.65	
PC_2	464.19798	18.13	99.79	
PC_3	4.19595	0.16	99.95	
PC_4	1.04796	0.04	99.99	
Variables	PC_1	PC_2	PC_3	PC_4
Factor loadings due to PCs with eigenvalues greater than 1				
β- carotene content of fruit (mg/100 g)	0.007941	-0.003849	0.032368	0.686042
Number of fruits/plants	-0.011586	-0.064189	0.991897	-0.028470
Lycopene content of fruits (mg/100 g)	0.006106	-0.010310	0.008407	0.726529
Average fruit weight (g)	0.523937	0.849507	0.060787	0.001495

Dabral et al (2016), Devi et al (2017) and Sharma et al (2017).

β-carotene content of fruit, number of fruits/plants, lycopene content of fruit, average fruit weight, vitamin C content and fruit yield/plant are the maximum contributing traits towards the diversity indicating the possibility for selection of these characters for the improvement of these traits. In sweet pepper biochemical trait was as important as some morphological traits for measurement of genetic diversity. Similar type of results was also documented previously by Devi et al (2017). Cluster V being the higher yielder and Cluster I early flowering and harvesting type a high yielding early type with better fruit quality could be breed by utilizing genotypes from these two clusters as parents which is based on cluster mean analysis. Based on principal component analysis (PCA), four components (β-carotene content, number of fruits/plants, lycopene content of fruit and average fruit weight) explained almost 100% of total genetic variation in this study. These characters are highly genetic variable and genotype having these characters in different cluster could be used in breeding programme to develop high yielding better quality cultivars in sweet pepper. These variations may suggest the existence of genetic diversity in sweet pepper that can be harnessed to improve the crop. Based on D^2 statistics, principal component analysis and average performance for fruit yield and fruit colour traits, genotypes Arya, Royal Wonder, Baby Bell, BC CAP White, C/4, 8/4, and BC CAP Purple are good candidates for utilization in breeding programme.

Colour development in selected sweet peppers genotypes: In the present study, distinct fruit colour development of 9 selected genotypes has been studied in details (Table 10). All the genotypes were green in different intensities (whitish green, light green, green, and dark green) at the immature stage. Distinct colour in fruits started developing after 19 to 68 days after anthesis depending on the genotype. In genotype C/4, red colour development started from 56 days after anthesis and 8/4 developed orange red (brick colour) colour 50 days after anthesis. In Arya, red colour in fruit started developing 68 days after anthesis, while it was 60 days after anthesis to develop red colour in Baby Bell. The genotype Royal Wonder remained green colour till harvest but if it is allow ripening this genotype develop faded red colour. The inbreed BC CAP Purple developed purple colour 19 days after anthesis which was quite early as compared to other genotypes. The genotype BC CAP White having whitish green colour at immature stage and developed creamy white colour at maturity. BC CAP Yellow and BC CAP Orange developed yellowish orange and orange colour at 64 and 68 days after anthesis, respectively.

Colour development of the whole fruit from the incitation of colour development (breaker stage) of selected genotypes has also been studied. The genotype Baby Bell took minimum days (9 days) to develop colour of the whole fruit followed by 8/4. BC CAP Purple took maximum days (17 days) to develop colour of the whole fruit followed by C/4. The genotype Arya and BC CAP Orange took 13 days to complete colour development from the breaker stage. BC CAP Yellow took 12 days from the breaker stage to complete colour development. Coloured sweet peppers are recognized for their visual appeal, sweet flavor, antioxidant activities, nutritive carotenoids and anti-inflammatory compounds (Park et al 2012). Capsicum species produce fruits that synthesize and accumulate carotenoid pigments, which are responsible for the fruits' yellow, orange and red colours. Chilli peppers have been used as an experimental model for studying the biochemical and molecular aspects of carotenoids biosynthesis. Both chilli and sweet pepper fruits undergo profound morphological, physiological, and metabolic transformations in terms of pigment composition and content during ripening. These changes in fruit

Table 10. Colour development and pigment contents in 9 sweet pepper genotypes

Genotypes	Immature colour	Colour after physiological maturity	Days taken from anthesis to breaker stage	Days taken from breaker stage to full colour development
C/4	Dark green	Red (Red Group 42A)	56c	16a
8/4	Light green	Orange Red (Orange Red Group 34A)	50d	11bc
Arya	Dark green	Red (Red Group 45A)	68aa	13b
Baby Bell	Dark green	Red (Red Group 42A)	60bc	9c
BC CAP Purple	Dark green	Purple (Purple Group N77A)	19e	17a
Royal Wonder	Green	Green (Green Group N137B)	0.000f	0.000d
BC CAP White	Whitish green	White (Green White Group 157C)	0.000f	0.000d
BC CAP Yellow	Dark green	Yellowish orange (Yellow Orange Group 17A)	64ba	12b
BC CAP Orange	Dark green	Orange (Yellow Orange Group 23A)	68aa	13b

[a]Values in columns followed by the same letter are not significantly different, $p< 0.05$, Tukey's post hoc test

composition are affected by the genotype, maturity and growth conditions (Marin et al 2004). According to the most accepted theory, the synthesis of carotenoids in chilli peppers is controlled by three loci: c1, c2 and y. Carotenoids are responsible for a variety of colours in fully mature pepper fruits, ranging from yellow to red, and they are stored in chromoplasts (Deli et al 2001). The carotenoid synthesis pathway begins with the synthesis of phytoene by phytoene synthase during development and ripening pepper fruits (Hirschberg 2001). Several enzymes participating in carotenoids biosynthesis in chilli and sweet pepper fruits have been isolated and characterized, and the corresponding gene sequences have been reported. However, there is currently limited information on the molecular mechanisms that regulate this biosynthetic pathway. In the present investigation, 9 genotypes of different fruit colour were taken for the study of the colour development. All the genotypes except BC CAP White showed different shades of green colour during immature stage. The point of colour change in capsicum (often termed 'breaker') is usually marked by the appearance of small coloured patches or streaks (initially 5-10% of the fruit surface) (O'Donoghue et al 2017). Fruit harvested with 80% colour coverage can continue to develop full, even colour. Colour development is affected by light and temperature. Degradation of chlorophyll and development of carotenoids pigments (breaker stage) started to develop 50 to 68 days after flowering. However, in the case of BC CAP Purple, anthocyanin pigment development started quite early 19 days after flowering. Red colour development in fruits takes 9-16 days to complete colour development depending upon genotypes, whereas, purple colour development require more days (17 days) compare to red coloured genotypes. Yellow and orange colour development was quite similar to red colour development. β-carotene and lycopene content of fruit decides the different fruit colour of sweet pepper fruit. Here, out of 9 genotypes C/4, 8/4, Arya and Baby Bell having red colour and their β-carotene content was comparatively more than the lycopene content suggested that the red colour of fruit is due to the presence of more β-carotene in the fruit. A single gene *B* (high beta carotene content complementary with another gene *t*) is responsible for the development of red colour in pepper (Lippert et al 1965). The fruit BC CAP White possessed very low amount of β-carotene and lycopene due to the fact that this genotype produces white colour fruit. However, BC CAP Purple showed high amount of anthocyanin pigment in their fruit which resulted deep purple colour fruit. In case of BC CAP Yellow genotype, β-carotene and lycopene content of fruit is comparably lower than other red colour fruit which revealed that the yellow colour development of fruit is due to the pigments other than β-carotene and lycopene. In this case, gene *y* (Lippert et al 1965) is responsible for the development of yellow colour. In BC CAP Orange, lycopene content of fruit is higher than the β-carotene content which suggested that more lycopene is necessary for the development of orange colour fruit. β-carotene is the precursor for the predominant orange and red pigments in sweet pepper and genotypes with high concentrations of β-carotene proved to be richest in total carotenoid content. Therefore, β-carotene may be a

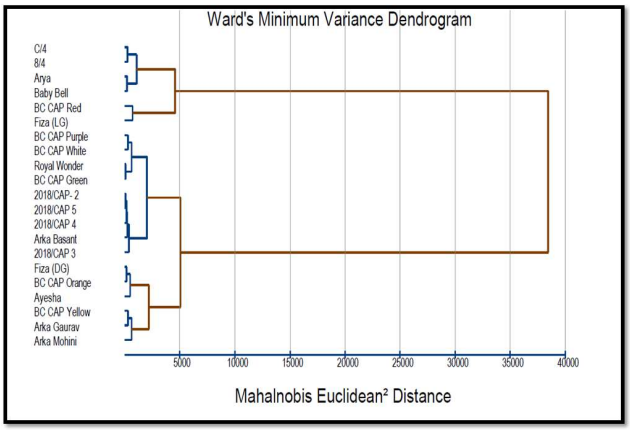

Fig. 1. Dendrogram of 21 genotypes of Sweet pepper following Ward's method

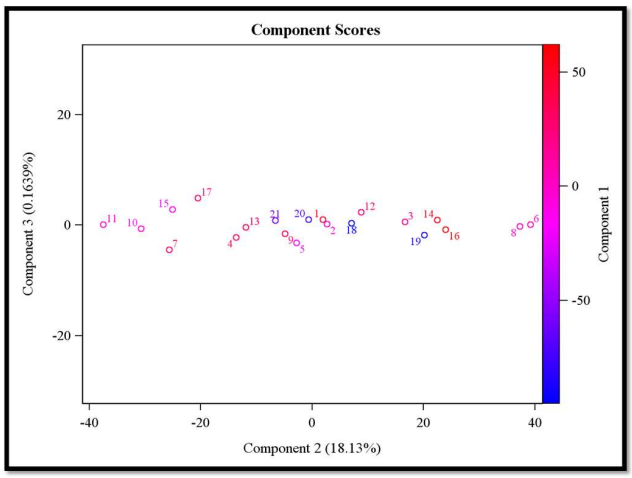

Fig. 2. Scatter diagram of regression factor scores for the first, second and third components as determined by principal component analysis. Points in diagram closest to the intersection of 0 on the X- and Y-axes indicate similarity. Outliers on the X-axis, that is, 6 = Royal Wonder, 8 = BC CAP Green, 3 = Arya, 19 = 2018/ CAP-3, 14 = Arka Mohini, 16 = Arka Gaurav, 11 = Fiza (LG), 10 = Fiza (DG), 15 = Arka Basant, 7 = BC CAP White, 17 = BC CAP Orange, 4 = Baby Bell, indicate diversity. Numbers correspond to the name of the genotype (Fig. 1)

selection criterion for developing highly coloured sweet pepper. The genotype Royal Wonder retained its green colour for longer time. It may be due to the expression of the chlorophyll retainer (*cl*) capsicum is mutated in the STAY-GREEN gene and ripening-related chlorophyll breakdown is prevented (Borovsky and Paran 2008).

CONCLUSIONS

The present study illustrated significant variation among sweet pepper genotypes for growth, yield components and quality traits. High Shanon-Wiener diversity index also suggest the existence of diversity among the sweet pepper genotypes for the morphological traits. Characters such as number of fruits/plant and average fruit weight should be considered the most important indicators of choice to enhance fruit yield. Based on multivariate analysis and average values the sweet pepper genotypes , 'C/4' (Red Group 42A, blocky), '8/4' (Orange Red Group 34A, elongate), 'Arya' (Red Group 45A, blocky), 'Baby Bell' (Red Group 42A, blocky), 'BC CAP Purple' (Purple Group N77A, blocky), 'BC CAP Yellow' (Yellow Orange Group 17A, blocky) and 'BC CAP White' (Green white Group 157 C, blocky) could be utilized as donor parents for developing hybrids, or to isolate promising lines with superior horticultural traits, suitable for growing under protected structure.

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