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Genotypes Performance, Characterization and Genetic Variability Studies of Sweet Pepper Accessions for Different Traits

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ABSTRACT

The study was conducted during two consecutive years 2018–2019 and 2019–2020 at IARI, Regional Station, Pune, Maharashtra, India to evaluate for genetic variability, heritability and genetic advance of nineteen genotypes. Our objective was to select the promising genotypes under open condition with better horticultural attributes under Western Maharashtra plain zone. Based on average of two years data, total yield ranged from 1.79-4.22 t ha^{-1} and maximum observed in Orobelle Yellow. TSS ranged from 6.35–9.66˚Brix, maximum in KTC-153 while Vitamin C content varied between 129.99–175.57 mg 100 g^{-1} FW maximum in ATS-89. Phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all traits. However, GCV values were near to PCV values for most of the characters indicating high contribution of genotypic effect for phenotypic expression. High heritability coupled with high genetic advance (Mean %) was obtained for plant height, number of fruits plant^{-1}, yield plant^{-1}, yield ha^{-1}, fruit length, fruit diameter, fruit cavity, fruit weight, number of seeds per fruit, and hundred seed weight, reflecting the presence of additive gene effects for the expression of these traits. Genotypes NS-281, KTP-141, SH-SP-4-1, SH-SPH-603, ATS-89, ATS-86, KTC-153, ATS-86 were found promising in one or the other characters like number of fruits plant^{-1}, yield plant^{-1}, yield (t ha^{-1}), Vitamin C content, TSS. These lines can be used as pre-breeding material for hybridization programme.

KEYWORDS: Bell pepper, genetic advance, heritability, quantitative characters, variability

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1. INTRODUCTION

Sweet pepper commonly known as bell pepper and is one of the sensitive solanaceous crops grown for its pleasant flavoured and bright coloured variant fruits. It is an economically important horticultural crops widely cultivated in tropical as well as subtropical parts of the world (Tsegay et al., 2013). Being a warm-season crop it performs better in frost-free season. It is an important source of antioxidants such as carotenoids, flavonoids, ascorbic acid (vitamin C), tocopherol (vitamin E) with specific component such as capsaicinoids responsible for pungency (Bogusz et al., 2018). Due to its delicacy, low pungency, pleasant flavour and coupled with rich content of ascorbic acid, other vitamins and minerals, it has occupied a place of pride among vegetables in Indian cuisine (Nalwa et al., 2017). It is considered as a low volume and high value vegetable crop as it is mostly grown under protected condition with limited production. Low productivity, weak supply chain and heavy demand had made high market price of bell pepper. To overcome the problem of market demand and high market price, we need to develop prominent hybrids/varieties to have year-round production. Commercial cultivation is limited to only few varieties which rule the market, indicating limited improvement work due to narrow genetic base. For this, there is pre-requisite of germplasm, diversity study and creation of gene bank (Santos-Pessoa et al., 2018; Karim et al., 2022). Heritability criteria determine the extent to which it is transmissible from parents to offspring and is mostly preferred when used in association with other parameters. The goals of horticultural plant breeding programs should be focused on agronomic performance and to meet the new requirements specifically linked to consumer preferences and product differentiation (Kaushik et al., 2015). The evaluation of genetic diversity among the accessions of a germplasm collection results in information about promising materials suitable for breeding programs (Leonel et al., 2020).

Germplasm collection, maintenance and its evaluation for economically important traits is a pre-requisite for starting any breeding programme for the genetic improvement of the crop (Shilpa et al., 2018). Therefore, creating variability in germplasm is first and foremost step for identification of potential genotypes for their use either directly as varieties or as parents in breeding program. Phenotypic variability of plant character mainly controlled by the genetic makeup of the plant and environment, in which it is grown and the interaction between the genotypes and environment while the genetic variability plays an important role in crop breeding for selecting the elite genotypes for making rapid improvement in yield and other desirable characters as well as is selecting the potential parent for hybridization programmes (Singh et al., 2017). The study of genetic diversity and phenotypic variability generates information on genetic variability, genotypic coefficient of variation, heritability, and genetic advance of the sweet pepper which is essential for crop improvement. The knowledge on the estimates of variability in respect of yield and its heritable components in the genetic material with which the breeder is working is essential for straightening selection strategies. It is also necessary to partition the total variability into heritable and non-heritable components viz., phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) and further to compute heritability and genetic gain for various traits of interest to the breeder. Heritability estimates provides information on heritable traits. It is an index for calculating the relative influence of environment on expression of genotypes. Genetic advance shows the degree of gain in trait from each cycle of selection. High genetic advance coupled with high heritability offers suitable criteria for selection. Successful crop improvement program depends on the amount of genetic variation present in crop and on magnitude to which trait is heritable from the parent to the progeny (Bello et al., 2012). In view of these, nineteen sweet pepper genotypes were characterized for their use in breeding programme.

2. MATERIALS AND METHODS

2.1. *Description of the experimental site*

Capsicum genotypes collected from CITH, Srinagar, NBPGR, New Delhi and Indian Agricultural Research Institute, Regional Station, Katrain, Himachal Pradesh, India. The study was conducted during two consecutive years (2018–2019 and 2019–2020) at IARI, Regional Station, Pune, Maharashtra, India. Healthy seedlings were raised in plug trays kept under net house. Six weeks old seedlings transplanted in the field and observations were recorded time to time.

2.2. *Morphological, phenological and biochemical studies*

Plant height was recorded after sixty days after transplanting. Yield and morphological parameters were recorded by selecting randomly five plants from each accession and from each replication. The average of five plants was used for statistical analysis. Fruit length, fruit diameter; fruit cavity was measured by scale. The Total Soluble Solids (TSS) of fruits was measured using digital refractometer. Fresh fruits washed, wiped with tissue paper and crushed to extract the juice for TSS measurement. The ascorbic acid content in fruits was estimated by the method described by Ranganna (1986).

2.3. *Variability and heritability studies*

Variability in population was estimated by mean, phenotypic and genotypic variance and coefficient of variation. The phenotypic and genotypic variance, genotypic and phenotypic coefficients of variation were estimated based on formula as follow:

Genotypic variance (σ^2G): $\sigma^2G=[(MSG) - (MSE)]/r$

Phenotypic variance (σ^2P):$\sigma^2P=[\sigma^2G+(\sigma^2E/r)]$ where σ^2E=Environmental variance; MSG=mean square of genotypes; MSE=error mean square; r=number of replications.

Genotypic coefficient of variation (GCV)=$[(\sigma^2G)^{1/2} / GM]\times100$

Phenotypic coefficient of variation (PCV)=$[(\sigma^2P)^{1/2}/GM]\times100$ where σ^2G=Genotypic variance; σ^2P= Phenotypic variance; and GM is grand mean. Estimation of broad senseheritabilityh^2 (bs)=$[(\sigma^2G)/(\sigma^2P)]\times100$, where h^2 (bs)=heritability in broad sense; σ^2G=Genotypic variance; σ^2P=Phenotypic variance. Estimation of genetic advance (GA)=K (σP) h^2, where K=the selection differential (K=2.06 at 5% selection intensity); σP=the phenotypic standard deviation of the character; h^2=broad sense heritability. Genetic advance as percentage of the mean GAM (%)=(GA/GM)×100, where GAM=genetic advance as percentage of the mean, GA=genetic advance and GM=grand mean. Observation on growth and yield parameter was recorded from five randomly chosen plants/replication and mean was calculated.

3. RESULTS AND DISCUSSION

3.1. *Evaluation of genotypes for different traits*

Data on eighteen different traits was recorded for all the genotypes for two seasons and pooled mean was calculated as shown in Table 1. Based on pooled mean maximum plant height (Table 1) was observed in Orobelle Yellow (55.80 cm) followed by SH-SP-3 (52.18cm) while minimum plant height observed in KTCH-11(29.34 cm). The vegetative growth amongst genotypes differs due to differences in genetic constituents. Days to first harvest significantly varied among the genotypes. Minimum days for first harvest were

Table 1: Pooled Mean performance of growth, yield and fruit characters in sweet pepper genotypes

Genotypes	PH (cm)	DFP (days)	Fruits plant^{-1}	Yield plant^{-1} (g)	Yield (t ha^{-1})	FL (cm)	FD (cm)	FC (cm)	FW (g)	Seeds fruit^{-1}	100 Seed weight (g)	TSS	Vitamin C
KTC-131	32.48	63.17	2.69	55.09	2.02	3.95	4.26	3.31	28.49	51.4	0.53	6.51	156.76
Sweet banana	35.71	58.25	4.28	59.66	2.38	10.74	2.17	1.71	22.12	56.9	0.53	7.83	171.66
Seln-1	30.05	61.42	2.76	62.71	2.45	4.57	4.27	3.69	32.97	49.9	0.52	6.72	143.16
KTCH-11	29.34	65.50	2.72	67.89	2.75	5.22	4.00	3.86	43.81	39.5	0.59	8.48	150.89
KTP-149	50.60	68.00	3.72	67.75	2.76	5.52	4.66	3.97	28.03	91.4	0.60	7.12	143.94
NS-281	51.58	62.42	3.90	93.92	3.87	5.54	4.52	4.02	57.51	83.7	0.49	7.29	160.17
Solan Bharpoor	47.34	62.01	4.46	49.25	1.79	4.51	3.85	3.18	22.76	113.6	0.43	7.89	159.10
SH-SP-603-1	45.86	63.97	3.69	67.37	2.74	5.66	4.46	3.79	32.13	67.6	0.41	6.90	154.97
KTP-141	48.57	62.28	6.01	68.34	2.76	7.36	3.86	2.22	28.70	73.9	0.30	8.12	141.92
SH-SP-4-1	48.31	67.21	4.83	83.14	3.58	4.40	4.14	3.65	32.41	46.6	0.31	9.45	140.84
Yolo wonder	45.04	60.72	5.64	86.76	3.69	5.54	5.18	4.17	50.79	78.8	0.50	6.35	152.41
ATS-89	49.01	68.74	4.76	93.58	3.80	7.09	2.90	2.66	57.17	122.2	0.41	7.58	175.57
California Wonder	49.59	66.26	4.38	61.34	2.46	5.66	5.72	3.38	30.70	156.5	0.30	8.81	158.06
Bomby red	50.87	64.32	5.35	89.18	3.67	6.48	7.39	4.92	69.24	151.4	0.69	7.61	137.03
KTC-153	44.27	61.20	4.00	63.08	2.48	4.25	4.35	3.79	26.13	62.7	0.28	9.66	137.27
SH-SP-3	52.18	65.40	3.91	74.12	3.04	6.32	4.38	2.49	28.99	84.7	0.60	7.13	141.75
Orobelle yellow	55.80	60.09	5.47	101.59	4.22	6.27	6.70	5.52	55.72	43.0	0.69	8.07	129.99
ATS-86	46.25	63.70	3.64	70.91	2.85	6.56	3.76	2.75	50.02	65.3	0.54	8.28	172.80
SH-SPH-603	42.06	66.37	4.67	59.09	2.23	6.21	4.87	4.01	30.35	99.4	0.65	8.08	145.74

PH: Plant height; DFP: Days to first picking; FL: Fruit length; FD: Fruit diameter; FW: Fruit weight; FC: Fruit cavity; TSS: Total soluble solids (°Brix); Vitamin C (mg /100 g FW) in Sweet Banana (58.25 days) and the maximum in ATS-89 (68.74 days) followed by KTP-149 (68 days).

Significant variations among genotypes were observed for number of fruits, yield per plant and total yield per plant in Table 1. Pooled mean reveals that maximum number of fruits harvested in KTP-141 (6.01) and minimum in KTC-131(2.69). Yield is an ultimate goal and is a complex character. It is necessary to judge the genetic variability of characters concerning different characters which helps in planning a successful breeding program to develop hybrids/varieties and hence the basic requirement is to utilize or create genetic variability (Waiba et al., 2021).

Munshi et al. (2000) reported variation of fruits number/plant in chilli, usually influenced by both genotypic and environmental conditions. Highest yield plant^{-1} recorded in Orobelle Yellow (101.59 g) followed by NS 281(93.92 g) and ATS-89 (93.58g). Higher accumulation of photosynthates in fruits might be responsible for higher fruit weight. The overall yield was maximum in Orobelle Yellow (4.22 t ha^{-1}).

NS-281 and ATS-89 were the next best lines with 3.87 and 3.80 t ha^{-1}. Higher yield might be due to combined effect of higher number of flowers plant^{-1}, lesser flower drop, better percent fruit set plant^{-1}, higher mean fruit weight and fruit volume. Similar findings were reported in capsicum by Kurubetta and Patil (2008).

Fruit length varied significantly ranging from 3.95 to 10.74 cm. Maximum lengths observed in Sweet Banana and minimum in KTC-131. Variation in fruit length may be due to varietal character of genotypes or influenced by agronomic and environmental conditions. Maximum fruit diameter observed in Bomby Red (7.39 cm), Orobelle Yellow (6.70cm), California Wonder (5.72 cm) and Yolo Wonder (5.18 cm). Similar results were observed by Karak et al., (2015). Significant variations observed for fruit cavity being maximum in Orobelle Yellow (5.52 cm) followed by Bomby Red (4.92 cm) and lowest in Sweet Banana (1.71 cm). Variations in fruit internal structure are probably due to length and size of fruits. Fruit weight ranged from 22–69 g being maximum in Bomby Red (69.24 g) followed by NS-281 (57.51 g) and ATS-89 (57.17 g).

Significant differences were observed in number of seeds per fruit being maximum in California Wonder (156.50) followed by Bomby Red (151.40) and minimum in KTCH-11 (39.50). Similar results were reported by Amit et al. (2014). Significant variation observed for 100 seed weight among genotypes. Orobelle Yellow and Bomby Red recorded maximum seed weight due to bold and bigger size of seeds. SH-SPH-603 and SH-SP-3 and KTP-149 were also at par in respect to seed weight. High TSS improves its flavour and palatability and also preferred for salad making. Pooled mean reveals that maximum TSS observed in KTC-153 (9.66°Brix) followed by SH-SP-4-1 (9.45°Brix). Yolo Wonder recorded the minimum TSS (6.35 °Brix). ATS-89 recorded highest vitamin C content (175.57 mg 100 g^{-1} FW) followed by ATS-86 (172.80 mg 100 g^{-1} FW) and minimum in Orobelle Yellow (129.99 mg 100 g^{-1} FW). Sood et al. (2007) observed that higher ascorbic acid content would increase the nutritive value, retention of colour and flavour in capsicum.

3.2. Estimation of genetic parameters

3.2.1. Phenotypic and genotypic coefficients of variation

The estimates of phenotypic variances (σ^2P), genotypic variances (σ^2G), Phenotypic Coefficients of Variation (PCV) and Genotypic Coefficients of Variation (GCV) are given in Table 2. Genetic (1220.35) and phenotypic variance (1313.17) was maximum for number of seeds per fruit in the year 2019–2020. Higher values of genetic and phenotypic variance were for the traits yield plant^{-1}, fruit weight and vitamin C content for both the years.

PCV values ranged from 4.97 % for days to first picking to 48.55 % for fruit weight. Similarly, the GCV values ranged from 4.01% for days to first picking to 43.36% for fruit weight. PCV and GCV values greater than 20% regarded as high and values between 10% and 20% to be medium, whereas values less than 10% are considered to be low. GCV and PCV values greater than 20% was observed for fruit length, fruit diameter, fruit cavity, fruit weight, number of seeds/fruit and 100 seed weight for both years respectively. The results suggest the existence of wide range of genetic variability in the germplasm for the trait and thus the scope for improvement of these characters through simple selection would be better. High phenotypic and genotypic coefficients of variation (PCV & GCV) indicates that the population had sufficient variability and effective selection could be made using these traits for the improvement of the characters (Singh et al., 2022)

Traits with PCV and GCV values greater than 20% indicate the existence of wide range of heritable genetic variability. This indicates that traits are under the control of additive gene effects ensuring scope for further improvement of these traits through selection. Similar findings are in congruence with results of Krishnamurthy et al. (2013) in chilli.

The difference between GCV and PCV were found narrow for most of the characters, suggesting that traits are least affected by environment. Selection for these traits on phenotype basis would be beneficial. Characters where the estimates of PCV greater than GCV indicates that variation for these traits has combined effect of both genotypes and environmental factors. Selection based on phenotype for these traits may not be rewarding. Similar observations were reported in chilli by Thakur et al., 2017 and Ain, 2018.

Table 2: Estimates of variance components of sweet pepper genotype

Characters	Year	Range	$\bar{x}$(mean) ±SE	σ^2G	σ^2P	GCV (%)	PCV (%)	h^2(bs) (%)	GA	GAM
Plant height	2018–19	29.72–77.56	54.88±1.36	190.69	193.48	25.15	25.34	98.55	28.24	51.45
	2019–20	28.45–47.50	35.10±2.98	24.23	33.14	14.02	16.40	73.12	8.67	24.70
DFP	2018–19	59.0–69.47	63.44±1.45	8.00	9.96	4.45	4.97	80.27	5.22	8.22
	2019–20	57.50–69.0	64.02±2.09	6.61	11.02	4.01	5.18	60.03	4.10	6.41
No. of fruits plant^{-1}	2018–19	3.33–8.50	5.91±0.91	2.42	3.67	26.33	32.39	66.06	2.60	44.08
	2019–20	1.86–3.85	2.59±0.53	0.18	0.61	16.46	30.32	29.45	0.47	18.04
Yield plant^{-1}	2018–19	60.99–110.02	80.44±3.17	158.75	173.88	15.66	16.39	91.30	24.80	30.83
	2019–20	37.5–97.65	64.26±11.77	237.25	375.85	23.96	30.16	63.12	25.21	39.22
Yield (t ha^{-1})	2018–19	2.26–4.07	2.98±0.16	0.21	0.23	15.45	7.95	89.45	0.89	30.11
	2019–20	1.33–4.40	2.86±0.36	0.80	0.93	31.21	32.43	86.14	1.71	59.66
Fruit length	2018–19	4.03–11.37	6.32±0.22	3.20	3.28	28.29	28.63	97.62	3.64	57.59
	2019–20	3.85–10.10	5.44±0.74	1.85	2.40	25.01	28.50	77.04	2.46	45.23
Fruit diameter	2018–19	2.14–3.16	4.84±0.21	2.23	2.30	30.90	31.36	97.09	3.03	62.72
	2019–20	2.19–6.09	4.14±0.36	1.07	1.20	24.99	26.46	89.20	2.01	48.63
Fruit cavity	2018–19	1.78–5.50	3.55±0.05	0.816	0.821	25.41	25.49	99.39	1.85	52.19
	2019–20	1.64–5.53	3.50±0.31	0.79	0.94	25.45	27.71	84.33	1.68	48.14
Fruit weight	2018–19	23.03–84.77	40.68±1.55	308.62	312.26	43.17	43.43	98.83	35.97	88.42
	2019–20	14.19–70.80	35.95±7.85	243.04	304.69	43.36	48.55	79.76	28.68	79.78
No. of seeds fruit^{-1}	2018–19	44.33–157.22	80.71±3.85	1138.05	1160.29	41.80	42.20	98.08	68.83	85.27
	2019–20	34.62–155.84	81.25±9.63	1220.35	1313.17	42.99	44.59	92.93	69.37	85.37
100 Seed weight	2018–19	0.28–0.70	0.49±0.025	0.018	0.019	27.84	28.58	94.91	0.27	55.88
	2019–20	0.28–0.67	0.49±0.03	0.01	0.01	25.85	26.62	94.28	0.25	51.71
TSS	2018–19	6.29–9.51	7.71±0.12	0.819	0.842	11.73	11.89	97.26	1.83	23.83
	2019–20	6.40–9.80	7.84±0.84	0.50	1.21	9.04	14.06	41.37	0.94	11.98
Vitamin C	2018–19	111.78–175.63	145.69±1.73	381.26	385.79	13.40	13.48	98.82	39.98	27.44
	2019–20	114.60–178.50	156.82±9.55	246.64	337.96	10.01	11.72	72.97	27.63	17.62

3.2.2. Estimation of heritability and genetic advance

The components of genetic variability like h^2 and genetic advance (GA) are essential biometric tools for assessing dissimilarity in population for making a selection (Akhter et al., 2021) and evaluating germplasm for improvement through breeding techniques. Heritability estimates the proportion of phenotypic variation due to genetic variation, thus giving an idea of heritable portion of variability and enabling the plant breeder in isolating the elite genotype in the crop (Saisupriya et al., 2022). Heritability (broad sense) estimates ranged from 29.45 to 99.39%. High value of heritable estimates for characters like plant height, days to first picking, yield/plant, yield (t ha^{-1}), fruit length, fruit diameter, fruit cavity, fruit weight, number of seeds per fruit, 100 seed weight, and vitamin C. This is in accordance with the findings of Sarkar et al. (2009) for plant height, length of fruit and fruit yield, Ain (2018) for fruit length, fruit diameter, fruit weight, number of fruits plant and fruit yield. Sran and Jindal (2019) also reported high heritability fruit weight, fruit length and width.

High heritability indicates variation observed mainly under genetic control, less influenced by environmental effects and effectively transmitted to the progeny while low heritable characters controlled by many genes. Genetic constitution plays major role in expression of character and thus selection based on phenotypic expression could be relied upon. Character with very low heritability coupled with low genetic advance which can be improved through hybridization.

High heritability coupled with high genetic advances preferred for improvement through selection for a particular quantitative character. This was observed for characters *viz.*, yield per plant, fruit weight and number of seeds per fruit and they can be improved through selection. Traits like plant height, days to first harvest, number of fruits per plant, total yield (t ha^{-1}), fruit length, fruit diameter, fruit cavity, 100 seed weight, TSS and Vitamin C content showed high heritability with low genetic advances revealing the predominance of non-additive gene action. High heritability with high genetic advance as per mean is usually more helpful in predicting gain under selection than heritability alone. In the present study, very high heritability coupled with very high genetic advance as per cent of mean was observed for traits yield (t ha^{-1}), fruit weight, number of seeds fruit^{-1} and 100 seed weight indicating the predominance of additive gene action making simple selection more effective as reported in chilli. These results are in conformity with Thakur et al. (2017) for number of fruits plant^{-1}, fruit weight, fruit length and fruit yield per plant. High heritability coupled with moderate GAM observed for TSS and Vitamin C suggesting can be improved through selection indicating greater role of non-additive gene action in their inheritance. Low heritability with low GAM indicates non-additive gene action and improvement could be achieved through heterosis breeding.

4. CONCLUSION

Selection strategy for yield improvement should rely on fruit characters during selection process as they contribute directly towards the yield (Bhojaraja et al., 2010). Genotypes NS-281, KTP-141, SH-SP-4-1, SH-SPH-603, ATS-89, ATS-86, KTC-153, ATS-86 were found promising in one or the other characters like number of fruits plant^{-1}, yield plant^{-1}, yield (t ha^{-1}), Vitamin C content, TSS. These lines can be used as pre-breeding material for hybridization programme.

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