RESEARCH ARTICLE

Assessment of Genetic Divergence for Yield and Yield Related Traits in Chilli (*Capsicum annuum* L.) Germplasm

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Evaluation of 35 Chilli genotypes in two seasons during *Kharif*, 2019 and *Rabi*, 2019-20 was taken up with an objective to estimate the genetic divergence for yield and yield attributing traits. In respect of per plant fruit yield , Only one genotype IC-347044 (0.82 kg) recorded significantly higher value than the best check LCA-625 (0.65 kg). The genetic divergence of genotypes was estimated using Mahalanobis's D^2 statistics. The genotypes were grouped into six different clusters, among which cluster I was the largest comprising of 16 genotypes. Results revealed that the character capsanthin content contributed maximum (48.91%) towards diversity followed by ascorbic acid (47.23%), capsaicin content (1.85 %), number of fruits per plant (1.18%), fruit weight (0.67%) and chlorophyll content (0.17%). The inter cluster D^2 values revealed that the highest inter cluster generalized distance (4626.16) was between cluster IV and cluster V and the lowest (619.86) was between cluster I and cluster III. The genotypes belonging to the cluster IV (IC-526448, EC-378632, IC-561622) and V (IC-394819, IC-570408, EC-378688, IC-528442) should be crossed to develop superior chilli hybrids with yield and its component traits through heterosis breeding.

Key Words: Chilli, *Capsicum annuum*, Clusters, Genotypes, Divergence

Introduction

Chilli (*Capsicum annuum* L.) also known as hot pepper is an important Solanaceous vegetable widely cultivated throughout the world. Chilli is considered as one of the most important commercial spice crops and is widely used as universal spice. Indian chilli occupied an area of 7.33 lakh hectares (18.11 lakh acres) with a production of 17.64 lakh tonnes and productivity of 2400 Kg per hectare (971 Kg per acre) (FAO, 2019-20). In 2018-19, around 4-5 lakh tonnes of chilli was exported to countries like China, Sri Lanka, Bangladesh, U.A.E, Malaysia, Vietnam and Thailand.

Different varieties are cultivated for varied uses like pickles, vegetable, spice and oleoresin. The green chilli fruits are rich source of ascorbic acid, phytonutrients, carotenoids and rutin which are of immense importance in pharmaceutical needs (Purseglove, 1977). It is mainly used for its pungency and pleasant flavour (Saisupriya *et al.,* 2020). The pungency in chilli is due to the presence of group of alkaloids called capsaicinoids. Due to its anti-bacterial, anti-carcinogenic, analgesic and anti-diabetic properties, capsaicin is in high demand in pharmaceutical industry (Pallerla *et al.,* 2021).

Chilli belongs to the genus *Capsicum* which possesses enormous wealth of genetic diversity. Extent of genetic diversity determines the success level of crop improvement programme. Maximum diversity can be noticed among different cultivars available in India and outside with respect to shape, size, yield, quality and other traits. Germplasm collection, evaluation and maintenance of the genetic diversity in capsicum are important to avoid genetic erosion.

Genetic divergence is important as the germplasm are of wide varied origins and are highly variable regarding their production potential. Divergence analysis generates valuable information on the nature and degree of genetic diversity. Therefore, a clear characterization of germplasms is the first step to facilitate successful

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breeding efforts. It is essential for the breeder to choose the right type of parents for purposeful hybridization in heterosis breeding (Farhad *et al.*, 2010; Khodadabi *et al.*, 2011; Yatung*et al.*, 2014). The degree of genetic divergence can be quantified using Mahalanobis's D^2 statistic of multivariate analysis which is recognized as a powerful tool for assessing the relative contribution of different characters to the total divergence (Das and Gupta 1984; Natarajan *et al.* 1988; Shidhu*et al.* 1989; Golakia and Makne 1992; Kalyani*et al.* 2017). In this regard, D² statistics was used in the present study to assess the genetic divergence of 35 chilli genotypes.

Materials and Methods

An investigation was undertaken with chilli accessions as treatments at College of Horticulture, Rajendranagar, Sri Konda Laxman Telangana State Horticultural University, Hyderabad during *Kharif*, 2019 and at National Bureau of Plant Genetic Resources Regional Station, Rajendranagar, Hyderabad during *Rabi*, 2019-20 to study genetic divergence. The accession numbers of the respective genotypes with source are presented in Table 1. Thirty five genotypes were grown in randomized block design and each treatment was replicated thrice. Nursery of 35 chilli genotypes was raised in pro trays with 50 cells. Six weeks old healthy seedlings were transplanted in the main field after allotting entries randomly in each replication. Each germplasm line was

grown in a plot of 1.8 m × 4.2 m. All the recommended package of practicesprovided by university was adopted for raising a healthy crop.

Observations were recorded on 5 randomly tagged plants of each genotype in each replication for the traits *viz.,* plant height (cm), plant spread (cm²), number of primary branches plant⁻¹, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest, fruit length(cm), fruit diameter(cm), number of fruits plant⁻¹, fruit weight (g), fruit yield plant⁻¹ (kg/plant), fruit yield plot⁻¹(kg), ascorbic acid content (mg/100g of fruit), chlorophyll content of green chilli, capsaicin content (%) and capsanthin content (ASTA units). The capsaicin content (%) was estimated by procedure proposed by Palacio (1977). Capsanthin was estimated as per the procedure given by Ranganna (1986).

Pooled data from the two seasons (*Kharif*, 2019 and *Rabi*, 2019-20) was obtained and the genetic divergence between genotypes was estimated using Mahalanobis's D^2 statistics (1936). Since all the seventeen variables were correlated, they were transformed into uncorrelated linear combinations through pivotal condensation method. Procedure suggested by Tocher (Rao, 1952) has been used to group 35 genotypes into clusters by treating estimated D^2 values as the square of the generalized distance. The intra and inter-cluster distance were computed.

Table 1. List of chilli genotypes used for evaluation along with their sources

Tr. No	Genotype	Source	Tr. No	Genotype	Source
T_1	IC-347044	NBPGR Regional Station, Hyderabad	T_{19}	IC-528442	NBPGR Regional Station, Hyderabad
T_2	IC-363918	NBPGR Regional Station, Hyderabad	T_{20}	EC-399535	NBPGR Regional Station, Hyderabad
T_3	IC-363993	NBPGR Regional Station, Hyderabad	T_{21}	EC-378632	NBPGR Regional Station, Hyderabad
T_4	IC-561676	NBPGR Regional Station, Hyderabad	T_{22}	IC-215012	NBPGR Regional Station, Hyderabad
T_5	IC-561622	NBPGR Regional Station, Hyderabad	T_{23}	EC-378688	NBPGR Regional Station, Hyderabad
T_6	IC-610381	NBPGR Regional Station, Hyderabad	T_{24}	IC-214966	NBPGR Regional Station, Hyderabad
T_7	IC-505237	NBPGR Regional Station, Hyderabad	T_{25}	IC-319335	NBPGR Regional Station, Hyderabad
T_8	IC-447018	NBPGR Regional Station, Hyderabad	T_{26}	IC-394819	NBPGR Regional Station, Hyderabad
T_9	IC-572459	NBPGR Regional Station, Hyderabad	T_{27}	IC-572498	NBPGR Regional Station, Hyderabad
T_{10}	IC-610383	NBPGR Regional Station, Hyderabad	T_{28}	EC-399581	NBPGR Regional Station, Hyderabad
T_{11}	IC-214965	NBPGR Regional Station, Hyderabad	T_{29}	IC-526737	NBPGR Regional Station, Hyderabad
T_{12}	EC-402113	NBPGR Regional Station, Hyderabad	T_{30}	IC-570408	NBPGR Regional Station, Hyderabad
T_{13}	IC-410423	NBPGR Regional Station, Hyderabad	T_{31}	IC-561648	NBPGR Regional Station, Hyderabad
T_{14}	IC-526448	NBPGR Regional Station, Hyderabad	T_{32}	IC-334383	NBPGR Regional Station, Hyderabad
T_{15}	EC-399567	NBPGR Regional Station, Hyderabad	T_{33}	SINDHUR[c]	RARS , Lam , Guntur, AP
T_{16}	IC-561655	NBPGR Regional Station, Hyderabad	T_{34}	LCA-625[c]	RARS , Lam , Guntur, AP
T_{17}	EC-390030	NBPGR Regional Station, Hyderabad	T_{35}	PUSA JWALA[c]	IARI, New Delhi
T_{18}	IC-528433	NBPGR Regional Station, Hyderabad			

Results and Discussions

The mean performance of 35 genotypes of chilli in respect to 17 yield and yield contributing characters were studied. The mean performance of fruit yield per plant, capsanthin and capsaicin are only presented. Fruit yield per plant ranged from 0.11 kg to 0.82 kg with a total mean of 0.28 kg (Table 1). Among the genotypes, IC-347044 showed maximum fruit yield per plant (0.82 kg), while the minimum fruit yield per plant (0.11 kg) was observed in EC-390030 and IC-572498. Only one genotype IC-347044 (0.82 kg) recorded significantly higher value for fruit yield per plant than the best check LCA-625 (0.65 kg). The mean values for the quality trait capsaicin content ranged from 0.21 % to 0.83 % with a total mean of 0.44 %. Among the genotypes, maximum capsaicin content (0.83 %) was observed in IC-363993 followed by IC-570408 (0.80 %) which was at par, while EC-399567 showed minimum capsaicin content (0.21 %). Eleven genotypes *viz.,* IC-363993 (0.83 %), IC-570408 (0.80 %), IC-363918 (0.74 %), IC-526448 (0.71 %), IC-319335 (0.70 %), IC-410423 (0.67 %), EC-399535 (0.59 %), IC-561622 (0.58 %), IC-505237 (0.51 %), EC-390030 (0.51 %) and IC-561648 (0.50 %) recorded significantly higher values for capsaicin content

than the check LCA-625 (0.42%). Capsanthin content ranged from 137.55 ASTA units to 373.52 ASTA units with a grand mean of 240.08 ASTA units. Among the genotypes, IC-561622 showed maximum capsanthin content (373.52 ASTA units), while the minimum capsanthin content (137.55 ASTA units) was observed in IC-610381. Eight genotypes serially IC-561622 (373.52 ASTA units), IC-526448 (322.18 ASTA units), EC-390030 (319.60 ASTA units), EC-378632 (311.15 ASTA units), IC-610383 (286.18 ASTA units), IC-215012 (283.67 ASTA units), IC-363918 (285.33 ASTA units) and IC-410423 (279.05 ASTA units) recorded significantly higher values for capsanthin content than the check LCA-625 (275.77 ASTA units).

The pattern of distribution of 35 genotypes into various clusters is indicated in Supplementary Table 1. All the genotypes evaluated were grouped into six clusters. Cluster I was the largest group comprising of 16 genotypes, followed by cluster III with 7 genotypes, cluster II and cluster V with 4 genotypes each, cluster IV with 3 genotypes, whereas cluster VI was monotypic or solitary with only one genotype suggesting diverse origin of this genotype. Pandit and Adhikary (2014)

Table 2. Mean values of fruit yield per plant (Kg), Capsaicin (%) and Capsanthin (ASTA units) in 35 chilli genotypes

Sl. No.	Genotype	Fruit yield per plant (Kg)	Capsaicin (%)	Capsanthin (ASTA units)	Sl. No.	Genotype	Fruit yield per plant (Kg)	Capsaicin (%)	Capsanthin (ASTA units)
1.	IC-347044	0.82	0.38	218.37	20.	EC-399535	0.15	0.59	212.66
2.	IC-363918	0.42	0.74	283.53	21.	EC-378632	0.28	0.40	311.15
3.	IC-363993	0.13	0.83	212.48	22.	IC-215012	0.27	0.32	283.67
4.	IC-561676	0.14	0.35	255.80	23.	EC-378688	0.13	0.31	199.42
5.	IC-561622	0.40	0.58	373.52	24.	IC-214966	0.18	0.46	191.92
6.	IC-610381	0.32	0.24	137.55	25.	IC-319335	0.18	0.70	203.17
7.	IC-505237	0.39	0.51	274.80	26.	IC-394819	0.14	0.31	165.33
8.	IC-447018	0.30	0.32	252.91	27.	IC-572498	0.11	0.24	253.41
9.	IC-572459	0.19	0.44	207.03	28.	EC-399581	0.20	0.42	227.98
10.	IC-610383	0.23	0.37	286.18	29.	IC-526737	0.13	0.26	186.36
11.	IC-214965	0.47	0.27	225.21	30.	IC-570408	0.56	0.80	175.06
12.	EC-402113	0.30	0.32	266.82	31.	IC-561648	0.17	0.50	222.41
13.	IC-410423	0.28	0.67	279.05	32.	IC-334383	0.13	0.38	247.00
14.	IC-526448	0.20	0.71	322.18	33.	Sindhur	0.46	0.35	240.95
15.	EC-399567	0.27	0.21	232.80	34.	LCA-625	0.65	0.42	275.77
16.	IC-561655	0.14	0.39	243.93	35.	Pusa Jwala	0.31	0.41	243.82
17.	EC-390030	0.11	0.51	319.60	–	Mean	0.28	0.44	240.08
18.	IC-528433	0.17	0.38	230.05	–	C.D. (5%)	0.06	0.04	2.63
19.	IC-528442	0.39	0.31	140.88	–	S.E. (m)	0.02	0.01	0.94

and Janaki *et al.* (2015) suggested that monogenotypic clusters were more divergent from others.

In order to get benefit of transgressive segregation, the knowledge of genetic distance between parents is necessary (Khodadabi *et al.,* 2011). In this regard, the mean intra and inter cluster D^2 values among the various clusters were estimated and were presented in the Supplementary Table 2. Similar studies were conducted by Varalakshmi and Haribabu (1991); Dutonde *et al.* (2008); Priyanka *et al.* (2018) and Manoj *et al.* (2019). Statistical distance represents the extent of genetic diversity among clusters. The intra cluster distance varied from 0.00 (Cluster VI) to 462.07 (Cluster V). Cluster II displayed least intra cluster distance denoting the similarity of genotypes. While maximum intra cluster distance was recorded in cluster V indicating the presence of sufficient amount of diversity with genotypes of the cluster. Thus, there is scope for selection among the genotypes within the clusters. Similar results were also obtained by Farhad *et al.* (2008), Datta *et al.* (2013); Yatung *et al.* (2014); Pujar *et al.* (2017)

The inter cluster distance was minimum between cluster I and III indicating narrow genetic diversity, whereas maximum recorded between clusters IV and V indicating wider genetic diversity in these groups. Similarly Indira (1994), Roy and Sorma (1996), Mishra *et al.* (2004), Yatung *et al.* (2014), Hasan *et al.* (2015), Sharma *et al.* (2017) also reported the presence of a high genetic divergence among chilli genotypes in their respective experiments.

The nearest and distant clusters from each of the cluster based on D^2 values are presented in Supplementary Table 3. Selection of parents from these diverse clusters for hybridization would help in achieving novel recombinants. The more diverse the parents within its limits of fitness, the greater are the chances of heterotic effects and broad spectrum of variability in segregating generations (Arunachalum *et al.* 1981). Therefore, it is logical to attempt crosses between genotypes falling in different clusters based on inter-cluster distance. This is simply to maximize overall genetic diversity and potential for genetic gain in the progeny (Nielson *et al.,* 2014).

The cluster means for each of the 17 traits are presented in Supplementary Table 4. From the data it can be seen that considerable differences exist for all the traits studied and they could be utilized as indicators for

Table 3. Percent contribution of different characters towards genetic divergence in thirty five chilli genotypes

S No.	Character	Rank	Contribution
1	Plant height (cm)	0	0%
2	Plant spread (cm^2)	0	0%
3	No. of primary branches per plant	0	0%
4	Days to first flowering	0	0%
5	Days to 50 % flowering	0	0%
6	Days to first harvest	0	0%
7	Days to last harvest	0	0%
8	Fruit length (cm)	0	0%
9	Fruit diameter (cm)	0	0%
10	No. of fruits/plant	7	1.18%
11	Fruit weight (g)	4	0.67%
12	Fruit yield per plant (Kg)	0	0%
13	Fruit yield per plot (Kg)	0	0%
14	Ascorbic acid (mg/100g)	281	47.23%
15	Chlorophyll content (%)	1	0.17%
16	Capsaicin content (%)	11	1.85%
17	Capsanthin content (ASTA unis)	291	48.91%

selecting diverse parents for specific trait in hybridization program (Farhad *et al.,* 2008; Smitha and Basavaraja, 2013, Sharma *et al.* 2017). Cluster VI recorded highest mean plant height (84.83 cm) followed by cluster IV (68.59 cm). While, cluster I registered lowest mean plant height (55.15 cm). Plant spread was highest in cluster VI (6712.00 cm^2) followed by cluster II (5051.79 cm^2). While cluster III (3073.12 cm^2) recorded lowest plant spread. The character numbers of primary branches per plant were highest in cluster VI (5.13) followed by cluster IV (3.46), whereas less number of primary branches was observed in cluster III (3.11).

Cluster V recorded maximum number of days to first flowering (62.09) followed by cluster IV (61.88). While the cluster III recorded least number of days to first flowering (52.89). Days to fifty per cent flowering recorded minimum value in the cluster III (60.57 days). While the cluster IV (66.33 days) exhibited maximum mean value followed by cluster VI (65.33 days). The number of days for first harvest was observed to be minimum (83.76) among the genotypes of the cluster III, while the maximum number of days (98.00) has been observed among the genotypes of the cluster VI. The genotypes grouped into cluster I recorded lower number of days (147.73) to last harvest, while the genotypes of the cluster VI showed highest number of days (162.33) for last harvest. Cluster V (9.82 cm)

recorded highest fruit length followed by the cluster II (9.22 cm). Whereas, the cluster VI (2.77 cm) recorded lowest fruit length. Highest fruit diameter was recorded in the cluster VI (2.06 cm) followed by the cluster III (1.33 cm) whereas, lowest fruit diameter was recorded in the cluster IV (1.01 cm).

The mean values for maximum number of fruits per plant were recorded by the cluster IV (94.33) followed by cluster II (81.33), while minimum number of fruits per plant was recorded by the cluster VI (55.33). Maximum fruit weight was observed in the cluster VI (6.08 g) followed by the cluster V (5.85 g). While the cluster IV (3.52 g) recorded minimum fruit weight. The character fruit yield per plant was recorded maximum in the cluster II (0.35 kg) followed by the cluster V (0.34 kg). While the cluster I (0.27 kg) recorded minimum fruit yield per plant. The character fruit yield per plot was recorded maximum in the cluster II (4.95 kg) followed by the cluster V (4.80 kg). While the cluster I (3.80 kg) recorded minimum fruit yield per plot.

Ascorbic acid content of the fruits was found to be highest (182.54) in cluster II followed by cluster V (127.27), while the lowest ascorbic acid content (46.24) was noted among the genotypes of the cluster VI. Chlorophyll content of the green fruits was found to be highest (2.08) in cluster VI followed by cluster I (1.95), while the least chlorophyll content (1.79) was observed among the genotypes of the cluster V. The genotypes of the cluster IV showed highest capsaicin content (0.59) followed by (0.48) among the genotypes of the cluster I, while the genotypes of the cluster VI recorded lowest capsaicin (0.25). Capsanthin content was observed to be highest (336.25) in cluster IV followed by (269.80) among the genotypes of the cluster III, while the lowest capsanthin content (138.40) was recorded among the genotypes of the cluster VI.

Genetic divergence among thirty five genotypes revealed that the genotypes *viz*., IC-363918, IC-610381, EC-378632, IC-363993 and Pusa Jwala were identified as promising genotypes for plant height. Hence, these genotypes can be utilized in crop improvement programme as donor parents for improving plant height. The genotypes *viz.,* IC-215012, IC-610381, IC-570408 and Pusa Jwala are promising genotypes for improving plant spread. The genotypes IC-215012, IC-610381, IC-528433 and Pusa Jwala are promising for improving number of primary branches per plant. The genotypes IC-561655, IC-610383, IC-528433, IC-363993, IC-

347044, Pusa Jwala, LCA-625 and IC-363918 were found to be promising lines for less number of days to first flowering and 50% flowering. Five genotypes *viz.,* IC-561655, IC-610383, LCA-625, Pusa Jwala and Sindhur for days to first harvest and another two genotypes, IC-447018 and IC-610383 for days to last harvest were found to be promising. The other promising genotypes include IC-347044, LCA-625, IC-570408, Pusa Jwala, EC-378688, IC-214965, IC-572459, EC-390030 and Sindhur for fruit length, IC-610381 and Sindhur for fruit diameter, IC-363918, IC-347044, LCA-625, Pusa Jwala and IC-410423 for number of fruits per plant, Sindhur, EC-378688, IC-561655, IC-214965, IC-570408, IC-572459 and IC-347044 for fruit weight. IC-347044, LCA-625 and IC-570408 can be potentially used for improving the yield.

Six genotypes *i.e.,* IC-215012, Pusa Jwala, IC-214965, EC-399581 and IC-528442 for ascorbic acid, EC-402113, EC-399535, IC-610383, IC-561655 and IC-215012 for chlorophyll content, IC-363993, IC-570408, IC-363918, IC-526448 and IC-319335 for capsaicin content, IC-561622, IC-526448, EC-378632 and EC-390030 for capsanthin content can be potentially used for improving the respective characters.

The percent contribution of different characters towards genetic divergence was presented in Table 3. The relative contribution of capsanthin content was maximum (48.91 %) towards diversity by taking 291 times ranking first followed by ascorbic acid (47.23 %) by 281 times, capsaicin content (1.85 %) by 11 times, no. of fruits per plant (1.18 %) by 7 times, fruit weight (0.67 %) by 4 times and chlorophyll content (0.17 %) by 1 time. Similar results were reported by Srinivas *et al.* (2021). In contrast, plant height, plant spread, number of primary branches per plant, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest, fruit length, fruit diameter, fruit yield per plant and fruit yield per plot did not contribute towards total diversity.

Conclusion

The present study revealed that considerable genetic diversity exists among and within the six clusters. Selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants. Hence, apart from selecting genotypes from the clusters which have high inter-cluster distance for hybridization, one can also think of selecting parents

based on extent of genetic divergence in respect to a particular character of interest. This means, if breeder's intention is to improve fruit yield, he can select parents which are highly divergent with respect to that character. Emphasis should be laid on characters contributing maximum D^2 values for choosing the cluster for the purpose of further selection and choice of parents for hybridization. The novel genotypes identified in this study could be utilized in further genetic studies.

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Conflict of Interest

No conflcts of interest exist among the authors.

*Supplementary Table or Figure mentioned in the article are available in the online version.

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Supplementary Table 1. Clustering pattern of thirty five chilli genotypes (Tocher's method)

Clusters	Genotypes
I	IC-528433, IC-561648, EC-399535, IC-363993, IC-319335, IC-214966, IC-526737, IC-347044, IC-334383, IC-447018, IC-561676, EC-402113, IC-410423, IC-572498, IC-572459, LCA-625
II	IC-214965, EC-399581, PUSA JWALA, IC-215012
III	IC-505237, IC-610383, EC-390030, IC-561655, SINDHUR, EC-399567, IC-363918
IV	IC-526448, EC-378632, IC-561622
V	IC-394819, IC-570408, EC-378688, IC-528442
VI	IC-610381

Supplementary Table 2. Average intra (bold) and inter-cluster D^2 values for six clusters in thirty five genotypes of chilli

Cluster	I	II	III	IV	V	VI
I	**316.38**	2289.29	619.86	1420.32	1519.31	946.28
II		**206.24**	1277.10	4387.88	1067.69	3282.76
III			**325.24**	1383.09	1493.98	1930.75
IV				**269.66**	4626.16	3776.11
V					**462.07**	1192.37
VI						0.00

Supplementary Table 3. The nearest and farthest clusters from each cluster based on D^2 values in chilli genotypes

Cluster number	Nearest cluster with D^2 values	Farthest cluster with D^2 values
I	III (619.86)	II (2289.29)
II	V (1067.69)	IV (4387.88)
III	I (619.86)	VI (1930.75)
IV	I (1420.32)	V (4626.16)
V	II (1067.69)	IV (4626.16)
VI	I (946.28)	IV (3776.11)

Supplementary Table 4. Mean values of clusters for 17 characters in 35 chilli genotypes (Tocher's method)

Clusters	Plant height (cm)	Plant spread (cm²)	No. of primary branches per plant	Days to first flowering	Days to 50% flowering	Days to first harvest	Days to last harvest	Fruit length (cm)	Fruit Diameter (cm)	No. of fruits per plant	Fruit weight (g)	Fruit yield per plant (Kg)	Fruit yield Per plot (Kg)	Ascorbic acid (mg/100g)	Chlorophyll (%)	Capsaicin (%)	Capsanthin (ASTA units)
I	55.15	3494.92	3.38	57.59	62.35	91.19	147.73	8.03	1.08	70.23	3.99	0.27	3.80	67.26	1.95	0.48	233.25
II	59.68	5051.79	3.30	56.31	62.00	89.50	158.92	9.22	1.12	81.33	4.83	0.35	4.95	182.54	1.81	0.38	246.97
III	59.93	3073.12	3.11	52.89	60.57	83.76	152.05	7.42	1.33	68.95	5.76	0.32	4.45	109.03	1.93	0.46	269.80
IV	68.59	4491.33	3.46	61.88	66.33	91.22	151.00	8.57	1.01	94.33	3.52	0.33	4.62	53.53	1.87	0.59	336.25
V	56.73	3897.15	3.24	62.09	63.92	93.67	153.92	9.82	1.12	67.42	5.85	0.34	4.80	127.27	1.79	0.47	168.77
VI	84.83	6712.00	5.13	56.00	65.33	98.00	162.33	2.77	2.06	55.33	6.08	0.33	4.67	46.24	2.08	0.25	138.40