Electronic Journal of Plant Breeding, 8(4): 1247-1257 (Dec 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00179.X

Research Article

Breeding Strategies Based on Diversity Analysis in Advance Breeding Lines of Chilli (*Capsicum annuum* var. *annuum* L.)

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(Received: 28 Sep 2017; Revised: 4 Dec 2017; Accepted: 6 Dec 2017)

Abstract
An attempt was made to determine the degree of divergence in 64 genotypes of chilli which were evaluated in a Randomized Complete Block Design with three replications during summer–rainy season 2015. The observations were recorded on 17 biometrical traits including 14 quantitative and three qualitative traits. A considerable amount of genetic diversity was observed among the genotypes, arranged in eight clusters with maximum in cluster II and four were mono-genotypic cluster. Leaf length contributed maximum towards total genetic divergence followed by fruit length, primary branches/plant, plant height, capsaicin content, fresh fruit yield/plant, pedicel length, oleoresin content and fruit girth. Based on intra and inter cluster distance and mean performance for desirable attributes, Nine genotypes namely, DPCh–17, DPCh–39', 'DPCh–12, DPCh–9, DPCh–35, DPCh–45, DPCh–5, DPCh–28 and DPCh–43 from diverse clusters along with 'DPCh–10, DPCh–36, DPCh–8 and DPCh–15 from mono-genotypic groups offer promise for their direct use as varieties and as potential parents in future breeding programmes to isolate transgressive segregants.
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Key words
Chilli, genetic divergence, D^2, distance, cluster, transgressive segregants

Introduction

Chilli or Hot pepper (*Capsicum annuum* var. *annuum* L.), belongs to the family Solanaceae and is one of the common and remunerative cash crops grown for its green and dry red fruits especially as spice in Indian subcontinent. It forms an indispensable adjunct in every house of the tropical world. It is used in many ways such as vegetable, spice, pickle, condiment and also for medicinal and ornamental purposes. The green chilli fruits are rich source of ascorbic acid, phytonutrients, carotenoids and rutin which are of immense importance in pharmaceutical needs (Purseglove, 1977). The 'capsaicin' causing pungency carries diverse prophylactic and therapeutic properties and is used in allopathic and ayurvedic medicines.

Today, India has emerged as the major producer, consumer and exporter of chilli. It is presently grown extensively throughout the country both under rainfed and irrigated conditions in almost all the states and contributes almost one fourth of the world production. It covers an area of 792 million hectares with annual production of 1376 million tonnes during 2014–15 (Anonymous, 2015a). Chilli was exported to the tune of 3, 12,500 metric tonnes worth Rs. 27, 223 million during 2014–15 that contributed about 38 per cent of the total spice export from India and 16 per cent share of the world spice trade (Anonymous, 2015b).

India has immense potential to grow and export different types of chillies required by various markets around the world. Indian chilli exports nowadays, is facing severe competition in the international market from other chilli growing countries along with high domestic consumption. On the other hand, the average yield is low due to various constraints such as non–availability of suitable cultivars/hybrids, biotic and abiotic stresses and genetic drift in the age old popular cultivars. Chilli production has also suffered a lot due to extensive and continuous cultivation of one or two specific cultivars for fresh as well as dry fruits which has resulted in plethora of disease infestation. Thus, there is a pressing demand to develop high yielding varieties/hybrids with good quality attributes to enhance the productivity.

One major approach to develop high yielding cultivars through breeding is to maximize the genetic diversity between parental genotypes that is usually estimated by measurements of morphological and physiological differences. Knowledge about levels and patterns of genetic diversity can be an invaluable aid in crop breeding for diverse applications namely, genetic variability in cultivars (Mohammadi and Prasanna, 2003), identification of diverse parental combinations to generate segregating progenies with diverse back ground (Barrett and Kidwell, 1998), and introgression of desirable genes from variable germplasm into the existing genetic base (Thompson and Nelson, 1998). An understanding of the genetic relationships among the genotypes can be useful in planning crosses, assigning lines to specific heterotic groups, and in precise identification with respect to plant varietal protection (Evgenidis *et al*., 2011).

Genetic diversity is the main source of variability in any crop improvement program. It serves as a

DOI: 10.5958/0975-928X.2017.00179.X

reservoir for identifying superior alleles controlling key agronomic and quality traits. The improvement potential of any crop is proportional to the magnitude of genetic variability in the germplasm (Singh *et al*., 2009) which provides the possibility to improve the yield and quality through strategic breeding programme. Genetic diversity of germplasm determines their potential for improved efficiency and thereby, utilizing diverse genetic material in breeding programme which may eventually resulted in enhanced crop production. The use of different plant breeding techniques can result in uniform plant types which are more efficient by means of different goals including enhanced yield along with desirable traits. This requires much more research to be executed to specify the most optimized methods for utilization in the production of efficient plants (Fu and Somers, 2009) and necessitate to conduct breeding experiments to meet the objectives (Martin *et al*., 2008; Van de Wouw *et al*., 2010).

One of the important breeding approaches is based on hybridization followed by selection in the subsequent generations. The main issue in hybridization programme is to estimate the relationship between parents before initiating the crossing *i.e.* choice of parents is the first crucial step in plant breeding program. Euclidean distance can theoretically estimated the genetic distance between parents to maximize the transgressive segregation (Hoque and Rahman, 2006). An understanding of genetic diversity among the parents is essential to obtain desirable transgressive segregants since diverse parents leads to high heterosis (Khodadadi *et al*., 2011). Inclusion of diverse parents in hybridization programs provide an opportunity of combining desirable genes and hence resulted in isolation of superior lines with requisite traits (Ceolin *et al.*, 2007). Cluster analysis is the one of the most suitable approach in identifying variability in germplasm, lessen the number of breeding lines by eliminating duplicates from the large germplasm and thereby suggests appropriate parents to be involved in conventional breeding (Eivazi *et al*., 2007).

Keeping this in view, initiatives have been taken to isolate transgressive segregants with high yield and desirable plant/fruit attributes from different intervarietal crosses involving diverse parents. In the present study, 64 progenies derived from ten diverse crosses of chilli were used to gather information on genetic diversity. This information shall enable the breeders to make informed decisions about suitable parents while planning breeding programme for high yield along with desirable horticultural traits.

Materials and methods

The present investigation was undertaken at the Experimental Farm of Department of Vegetable Science and Floriculture, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur during summer 2015. It was situated at an elevation of 1, 290.8 m above mean sea level with 32^0 6′ N latitude and 76^0 3′ E longitudes. The location is characterized by humid and temperate climate with an annual rainfall of 2,500 mm of which 80 per cent is received during June to September and represents the mid–hill zone of Himachal Pradesh. The soil is classified as Alfisols typic Hapludalf clay having a pH of 5.7.

The experimental material for present study comprised of 64 genotypes of chilli including 58 advance breeding lines (F_5) derived from ten intervarietal crosses and six varieties (Table 1). These genotypes were sown during mid of March 2015 in the nursery bed of size 3 m × 1 m× 15 cm. The seedlings were ready for transplanting Cm 50 DAS. The seedlings of the 64 genotypes were transplanted during mid of May 2015 in Randomized Complete Block Design with three replications. Each genotype was planted in two rows of 2.25 m length consisting of ten plants in each replication with inter and intra row spacing of 45 cm, respectively.

The data were recorded on five randomly selected plants in each genotype over the replications for different traits *viz.*, days to flowering, days to first picking, fruit length (cm), fruit girth (cm), pedicel length (cm), leaf length (cm), leaf width (cm), plant height (cm), number of primary branches/plant, number of marketable fruits/plant, average fruit weight (g), marketable green fruit yield/plant (g), harvest duration (days) and dry fruit yield/plant (g), following minimal descriptors as suggested by Sharma et al. (2016). The quality parameters were estimated for ascorbic acid content (mg/100g) as described by Ranganna (1977), oleoresin content (ASTA Units) as per procedure given by A.O.A.C. (1980) and capsaicin content (%) using method by Bajaj (1980). D^2 statistic (Mahalanobis 1936; Rao 1952) was used to analyze the data using statistical software WINDOSTAT 8.0 developed by Indostat Services. Grouping of genotypes was done following Tocher's method (Rao 1952).

Results and discussion

The analysis of variance revealed that mean squares due to genotypes were significant for all yield attributing traits including fruit yield and quality traits (Table 2), indicating the presence of significant variability in the genotypes for all the characters. Non-hierarchical Euclidean cluster analysis leads to grouping of 64 genotypes into eight clusters, where in four clusters were

DOI: 10.5958/0975-928X.2017.00179.X

monogenotypic (solitary) and remaining four were polygenotypic (Table 3 and Fig 1). The cluster II was the largest consisting of 32 genotypes with 50.00 per cent constitution followed by cluster I with thirteen, cluster III with eight and cluster VI with seven genotypes. The remaining four clusters namely, IV ('DPCh-4'), V ('DPCh-15'), VII ('DPCh-36') and VIII ('DPCh-8') were monogenotypic with only one genotype suggesting diverse origin of these genotypes. Different clustering patterns of arrangement of genotypes have also been reported by Yatung *et al*. (2014) with different genetic material in their studies on chilli. Pandit and Adhikary (2014) and Janaki *et al*. (2015) suggested that monogenotypic clusters were more divergent from others.

The intra-cluster distance varied from 0 to 13.54 with the highest in cluster VI followed by 11.38 in cluster III, 10.63 in cluster II and 9.54 in cluster I while monogenotypic clusters had intra-cluster distance with zero, (Table 4). The chances of developing good segregants by hybridization among parents within cluster would be low since they have low intra-cluster distance. 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 inter-cluster distance ranged from 10.42 to 22.43 (Table 3). The highest inter-cluster genetic divergence was recorded between clusters IV and VII followed by I and III, VII and VIII, and that of III and VII. The inter-cluster proximity was minimum between clusters IV and V followed by IV and VIII, II and V, and V and VI. This clearly indicates that the genotypes included in the clusters with high inter-cluster distance showed sufficient genetic diversity and selection of parents from these diverse clusters would be useful in hybridization programme for improving yield and other desirable horticultural traits. The crosses involving the diverse genotypes would be expected to manifest maximum heterosis and are more likely to evolve desirable recombinants in segregating generations. The minimum inter-cluster distance was observed between genotypes of cluster IV and V which can be used as parents in hybridization programme (Khodadadi *et al*., 2011). The genotypes of cluster IV and VIII and cluster V and VI also showed minimum inter-cluster distance. The low inter-cluster distance between these cluster pairs suggested close proximity of genotypes grouped in these clusters with respect to their genetic constitution. The genotypes grouped into the same cluster presumably diverge very little from one another and crossing of genotypes belonging to the same cluster is not expected to yield desirable segregants. Based on inter-cluster distance, Kumar *et al*., (2012) have also suggested selection of parents from diverse clusters for utilization in hybridization programme to obtain desirable transgressive segregants. Thus, crosses between the genotypes from clusters VI and I, I and VIII or VI and II can be used in chilli breeding to exploit maximum heterosis to obtain heterotic hybrids and desirable segregants.

The composition of cluster means for different characters showed considerable differences among the genotypes for characters studied (Table 5). Cluster IV was observed to be important with maximum cluster means for the most valuable traits *viz.*, earliest flowering, number of marketable fruits/plant, green fruit yield/plant, dry fruit yield/plant and capsaicin content along with desirable cluster means for early fruit harvest, pedicel length, primary branches/plant, average fruit weight and harvest duration. On the same line, cluster VIII showed desirable means for earliest fruits picking, minimum pedicel length and maximum plant height besides it showed good performance for green fruits yield, fruit length, fruit girth and primary branches/plant. In addition, cluster VII showed maximum cluster means for fruit girth, leaf length, average fruit weight and ascorbic acid content while it showed desirable cluster means for harvest duration and leaf width. Cluster I revealed maximum mean values for fruit length, leaf width and harvest duration. Hence, different clusters of genotypes on the basis of means revealed divergence for different characters and can be utilized as indicators for selecting diverse parents for specific trait in hybridization programmes (Farhad *et al*., 2008; Smitha and Basavaraja, 2013).

It is worth mentioning that dilution of superiority of a particular line for a trait in question could be affected by the inferior or moderate line which is grouped in the same cluster with that trait, while calculating cluster mean (Million, 2012). Hence, it would be imperative to select parents on the basis of extent of genetic divergence with respect to a trait in question besides selecting genotypes with higher inter-cluster distance.

The role of specific trait towards genetic diversity was calculated on the basis of number of times it ranked first (Table 6). Out of 15 traits, 75% of the total variation was elucidated by seven traits. Leaf length contributed maximum towards total genetic divergence followed by fruit length, primary branches/plant, plant height, capsaicin content, fresh fruit yield/plant, pedicel length, oleoresin content and fruit girth. Leaf width, average fruit weight and marketable fruits/plant also contributed to the desirable extent. Therefore, these parameters can be used in selecting genetically diverse parents for hybridization to create variability in the population (Sirshat *et al*., 2006; Farhad *et al*.,

 DOI: 10.5958/0975-928X.2017.00179.X

2008; Datta and Jana, 2010) towards total genetic divergence.

Conclusion

In autogamous species, such as chilli, the genetic variance is expected to derive mainly from additive effects. Heterosis may not be of direct interest, but heterotic crosses could produce desirable transgressive segregants. Therefore, selection of genotypes as superior and diverse parents for hybridization programme should be based on diverse clusters. Accordingly, best performing genotypes *viz.*, DPCh-17, DPCh-39,DPCh-12' and 'DPCh-9 from cluster II, DPCh-35 and DPCh-45 from cluster I DPCh-5 from cluster III, DPCh-28 and 'DPCh-43 from cluster VI along with 'DPCh-10, DPCh-36, DPCh-8 and 'DPCh-15' grouped in monogenotypic clusters offer promise for their direct use as varieties and as potential parents in future breeding programmes to isolate transgressive segregants. The genetically divergent genotypes may be used as mapping populations to detect diversity at molecular level and also to identify molecular markers linked to desirable traits for marker assisted selection (MAS). Hence, it can be concluded that evaluation of genetic diversity can be useful for the selection of the most efficient genotypes for designing breeding strategy to create genetic variability in the existing germplasm pool of chilli.

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DOI: 10.5958/0975-928X.2017.00179.X

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Electronic Journal of Plant Breeding, 8(4): 1247-1257 (Dec 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00179.X

Table 1. List of genotypes along with their pedigree.

S. No.	Genotypes	Pedigree/Crosses	S. No.	Genotypes	Pedigree/Crosses
1	DPCh–1	PSSu–1–F_5–1 (Pusa Sadabahar × Surajmukhi)	33	DPCh–33	PjAn–3–F5–2 (Pusa Jwala × Anugraha)
2	DPCh–2	PSSu–1–F_5–2 (Pusa Sadabahar × Surajmukhi)	34	DPCh–34	LCA–Pc–1–F_5–1 (LCA–436 × Pant C–1)
3	DPCh–3	PSSu–I–F_5–3 (Pusa Sadabahar ×Surajmukhi)	35	DPCh–35	LCA–Pc–3–F_5–1 (LCA–436 × Pant C–1)
4	DPCh–4	PSSu–2–F_5–1 (Pusa Sadabahar × Surajmukhi)	36	DPCh–36	LCA–Pc–3–F_5–2 (LCA–436 × Pant C–1)
5	DPCh–5	PSSu–2–F_5–2 (Pusa Sadabahar × Surajmukhi)	37	DPCh–37	LCA–Pc–3–F_5–3 (LCA–436 × Pant C–1)
6	DPCh–6	PSSu–2–F_5–3 (Pusa Sadabahar × Surajmukhi)	38	DPCh–38	LCA–Pc–5–F_5–1 (LCA–436 × Pant C–1)
7	DPCh–7	CSSu–1–F_5–1 (Chilli Sonal × Surajmukhi)	39	DPCh–39	LCA–Pc–5–F_5–2 (LCA–436 × Pant C–1)
8	DPCh–8	CSSu–2–F_5–1 (Chilli Sonal ×Surajmukhi)	40	DPCh–40	LCA–Pc–6–F_5–1 (LCA–436 × Pant C–1)
9	DPCh–9	CSSu–2–F_5–2 (Chilli Sonal × Surajmukhi)	41	DPCh–41	H–2–3–5–1–1 (Private Sector hybrids–1)
10	DPCh–10	CSSu–2–F_5–3 (Chilli Sonal × Surajmukhi)	42	DPCh–42	H–2–4–1–1 (Private Sector hybrids–1)
11	DPCh–11	CSSu–2–F_5–4 (Chilli Sonal × Surajmukhi)	43	DPCh–43	H–2–5–1–1(Private Sector hybrids–1)
12	DPCh–12	CSSu–2–F_5–5 (Chilli Sonal × Surajmukhi)	44	DPCh–44	H–2–5–2–1(Private Sector hybrids–1)
13	DPCh–13	CSSu–3–F_5–1 (Chilli Sonal × Surajmukhi)	45	DPCh–45	H–2–5–3–1(Private Sector hybrids–1)
14	DPCh–14	CSSu–5–F_5–1 (Chilli Sonal × Surajmukhi)	46	DPCh–46	H–3–1–1–1(Private Sector hybrids–2)
15	DPCh–15	CSSu–6–F_5–1 (Chilli Sonal × Surajmukhi)	47	DPCh–47	H–3–1–2–1(Private Sector hybrids–2)
16	DPCh–16	ALSu–1–F_5–1 (Arka Lohit ×Surajmukhi)	48	DPCh–48	H–3–4–1–1(Private Sector hybrids–2)
17	DPCh–17	ALSu–1–F_5–2 (Arka Lohit × Surajmukhi)	49	DPCh–49	H–3–4–2–1(Private Sector hybrids–2)
18	DPCh–18	ALSu–1–F_5–3 (Arka Lohit × Surajmukhi)	50	DPCh–50	H–11–2–5–1–1–1(Private Sector hybrids–3)
19	DPCh–19	ALSu–2–F_5–1(Arka Lohit × Surajmukhi)	51	DPCh–51	H–11–2–5–1–3–1(Private Sector hybrids–2)
20	DPCh–20	ALSu–2–F_5–2 (Arka Lohit × Surajmukhi)	52	DPCh–52	H–11–5–2–1–1(Private Sector hybrids–2)
21	DPCh–21	ALSu–3–F_5–1 (Arka Lohit × Surajmukhi)	53	DPCh–53	H–11–5–2–1–2–1(Private Sector hybrids–2)
22	DPCh–22	ALSu–3–F_5–2 (Arka Lohit × Surajmukhi)	54	DPCh–54	H–11–5–2–1–2–3 (Private Sector hybrids–2)
23	DPCh–23	ALSu–3–F_5–3 (Arka Lohit × Surajmukhi)	55	DPCh–55	H–11–5–4–1–1 (Private Sector hybrids–2)
24	DPCh–24	ALSu–4–F_5–1 (Arka Lohit × Surajmukhi)	56	DPCh–56	H–11–6–1–1(Private Sector hybrids–2)
25	DPCh–25	ALSu–6–F_5–1 (Arka Lohit × Surajmukhi)	57	DPCh–57	PAU–Pc–1–F_5–1 (PAU Sel × Pant C–1)
26	DPCh–26	ALSu–6–F_5–2 (Arka Lohit × Surajmukhi)	58	DPCh–58	PAU–Pc–1–F_5–2 (PAU Sel × Pant C–1
27	DPCh–27	PjSu–1–F_5–1 (Pusa Jwala ×Surajmukhi)	59	Arka Lohit	Released variety from IIHR, Bangaluru
28	DPCh–28	PjSu–1–F_5–2 (Pusa Jwala × Surajmukhi)	60	Pusa Sadabahar	Released variety from IARI, New Delhi
29	DPCh–29	PjSu–2–F_5–1 (Pusa Jwala × Surajmukhi)	61	Sel. 352	Improved variety from PAU, Ludhiana
30	DPCh–30	PjAn–1–F_5–1 (Pusa Jwala × Surajmukhi)	62	Surajmukhi	CSKHPKV, Palampur
31	DPCh–31	PjAn–2–F_5–1 (Pusa Jwala × Surajmukhi)	63	LCA–206	Improved from LAM Station, Andhra Pradesh
32	DPCh–32	PjAn–3–F_5–1 (Pusa Jwala × Surajmukhi)	64	Chilli Sonal	Improved variety from PAU, Ludhiana

Electronic Journal of Plant Breeding, 8(4): 1247-1257 (Dec 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00179.X

Table 2. Analysis of variance for yield and yield contributing, and quality traits in chilli

Traits	Replication	Genotypes	Error
df	**2**	**63**	**126**
I. Yield and yield contributing traits			
ays to flowering	18.07	71.12*	3.58
Days to first harvest	23.73	80.62*	4.26
Fruit length (cm)	0.84	22.43*	0.12
Fruit girth(cm)	0.10	1.94*	0.03
Pedicel length (cm)	0.02	1.36*	0.05
Leaf length (cm)	0.37	14.58*	0.10
Leaf width(cm)	0.03	2.55*	0.05
Plant height (cm)	62.22	274.17*	4.19
Primary branches per plant	0.76	6.01*	0.09
Number of marketable fruits per plant	1.12	441.55*	13.25
Average fruit weight (g)	0.006	4.37*	0.13
Marketable green fruit yield per plant (g)	303.38	15504.27*	140.69
Harvest duration (days)	1.47	26.34*	1.99
Dry fruit yield per plant (g)	156.67	298.89*	11.39
II. Quality traits			
Ascorbic acid content (mg/100g)	200.49	245.90*	10.18
Oleoresin (ASTA Units)	15.53	339.52*	8.03
Capsaicin content (%)			
	0.003	0.061*	0.001

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Table 3. Clustering pattern in 64 genotypes

Cluster number	Number of genotypes	Genotypes
I	13	DPCh–25,DPCh–26, DPCh–27, DPCh–42, DPCh–37, DPCh–38, DPCh–35, DPCh–32, DPCh–31, DPCh–34, DP33, DP44, DPCh–45
II	32	DPCh–24, DPCh–55, DPCh–23, DPCh–41, DPCh–22, DPCh–39, DPCh–51, DPCh–50, DPCh–30, DPCh–47, DPCh–12, DPCh–11, DPCh–18, DPCh–57, DPCh–56, DPCh–6, DPCh–54, DPCh–48, DPCh–9, DPCh–49, DPCh–21, Chilli Sonal, DPCh–17, DPCh–52, DPCh–53, DPCh–16, Selection –352, LCA–206, DPCh–58, Surajmukhi, DPCh–7, DPCh–20
III	8	DPCh–2, DPCh–4, DPCh–1, Pusa Sadabahar, DPCh–5, DPCh–3, Arka Lohit DPCh–19
IV	1	DPCh–10
V	1	DPCh–15
VI	7	DPCh–28, DPCh–29, DPCh–45, DPCh–13, DPCh–40, DPCh–43, DPCh–14
VII	1	DPCh–36
VIII	1	DPCh–8

Total 64

Table 4. Average intra (in bold) and inter cluster D^2 distance

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**9.54**	18.80	22.08	18.82	15.08	14.30	13.53	16.62
II		**10.63**	13.15	13.21	12.25	15.01	18.69	15.18
III			**11.38**	16.15	14.95	18.05	20.18	20.11
IV				**0.00**	10.42	15.10	22.43	11.12
V					**0.00**	12.90	16.44	14.47
VI						**13.54**	16.17	15.95
VII							**0.00**	20.74
VIII								**0.00**

 DOI: 10.5958/0975-928X.2017.00179.X

Table 5. Cluster means for different traits in chilli

Traits / Clusters	I	II	III	IV	V	VI	VII	VIII	Mean	Minimum	Maximum
Days to flowering	44.18	45.74	51.54	38.67	39.67	41.00	47.33	42.67	43.85	38.67	51.54
Days to first picking	56.08	59.49	65.54	53.00	52.67	56.10	59.33	52.33	56.81	52.33	65.54
Fruit length (cm)	11.59	6.69	5.99	7.79	8.05	8.14	9.08	10.28	8.45	5.99	11.59
Fruit girth (cm)	4.50	3.69	3.25	3.36	3.36	4.56	6.08	4.38	4.14	3.25	6.08
Pedicel length (cm)	4.65	3.64	3.72	3.88	5.61	3.87	5.90	3.50	4.34	3.50	5.90
Leaf length (cm)	12.58	8.28	8.97	7.55	9.78	10.81	13.10	6.88	9.74	6.88	13.1
Leaf width (cm)	5.09	3.51	4.22	2.69	2.60	4.29	5.08	2.69	3.77	2.60	5.09
Plant height (cm)	73.23	65.26	53.85	60.51	64.56	66.66	57.67	81.44	65.39	53.85	81.44
Primary branches/ plant	2.62	3.30	6.20	3.47	3.40	2.60	3.40	3.47	3.55	2.60	6.20
Marketable fruits/ plant	50.77	53.15	61.06	87.76	76.10	61.19	27.71	49.16	58.36	27.71	87.76
Average fruit weight (g)	5.75	3.61	3.06	3.81	3.40	4.61	6.64	6.57	4.68	3.06	6.64
Marketable green fruit yield/ plant (g)	288.43	191.02	182.22	335	259.33	287.52	182.67	323	256.14	182.22	335
Harvest duration (days)	61.26	59.34	59.46	59.67	56.33	58.57	60	60.33	59.37	56.33	61.26
Dry fruit yield/ plant (g)	40.62	27.66	23.58	41.33	34.67	40.81	28.33	40.33	34.66	23.58	41.33
Ascorbic acid (mg/100g)	113.58	107.71	101.96	104.73	115.53	115.05	125.93	112.97	112.18	101.96	125.93
Oleoresin (ASTA Units)	57.81	53.95	59.58	39.91	65.9	63.94	60.68	39.91	55.21	39.91	65.9
Capsaicin (%)	0.47	0.65	0.66	0.81	0.62	0.55	0.38	0.74	0.61	0.38	0.81

Max–Maximum; Min–Minimum

Electronic Journal of Plant Breeding, 8(4): 1247-1257 (Dec 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00179.X

Table 6. Relative contribution (%) of Individual traits to the genetic divergence among chilli genotypes

Traits	Nunber of times ranked first	Contribution (%)
Days to flowering	10	0.50%
Days to first picking	18	0.89%
Fruit length	299	14.83%
Fruit girth	119	5.90%
Pedicel length	133	6.60%
Leaf length	365	18.11%
Leaf width	85	4.22%
Plant height	187	9.28%
Primary branches/plant	231	11.46%
Number of marketable fruits/ plant	47	2.33%
Average fruit weight	54	2.68%
Harvest duration	8	0.40%
Marketable green fruit yields/ plant	141	6.99%
Dry fruit yields/ plant	1	0.05%
Ascorbic acid content	23	1.14%
Oleoresin content	129	6.40%
Capsaicin content	166	8.23%

Electronic Journal of Plant Breeding, 8(4): 1247-1257 (Dec 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00179.X

Fig 1: Dendrogram showing grouping of sixty four chilli genotypes based on D^2 statistics using Tocher's method