Vegetable Science (2016) 43 (2) : 243-247

Genetic divergence in Chilli (*Capsicum annuum* L.) germplasm based on quantitative traits

K Srivastava*, S Vijaya Gowthamee and HR Bhandari

Received: November 2016 / Accepted: January 2017

Abstract

Genetic divergence using Mahalanobis D^2 statistics was studied using 13 yield traits in 37 genotypes of chilli (*Capsicum annuum* L.). D^2 analysis clustered the genotypes into seven groups and indicated sufficient diversity among the genotypes tested. Cluster-I was the biggest cluster with 13 genotypes followed by cluster-IV with 11 genotypes. Cluster-III recorded maximum intra-cluster distance (51.85). Maximum inter-cluster distance (345.23) was recorded between cluster-IV and VII. Cluster-VII and cluster-III recorded desirable mean values for six and three traits, respectively. Among 13 yield traits studied, fresh fruit yield/ plant, number of seeds/pod and fruit diameter had the maximum contribution towards genetic diversity. The traits number of primary branches/plant, number of secondary branches/plant and fresh fruit weight/pod had no contribution towards genetic divergence. The diverse lines may be utilized in crop improvement by exploiting heterosis or by transgressive breeding.

Keywords: Chilli, Quantitative traits, Cluster analysis, Genetic diversity

Introduction

Chilli (*Capsicum annuum* L.), a member of family solanaceae is one of the important vegetable and spice crops in India. It is cultivated for its fruits and is mostly valued for pungency, colour and flavour. Chilli fruits are an important constituent of diet on account of high vitamin content, minerals, fibres, etc and find itself its place in allopathic and ayurvedic medicines. It is much valued in processing and beverage industries for its flavour. The natural colour extracts of chilli are also finding their increased value in place of artificial colours in food items (Kumar *et al*. 2006). Thus, chilli has diverse uses as vegetables, spice, condiment, culinary supplement, medicine and ornamental plants. Being the largest chilli producer, India has vast potentiality to increase the production, in order to promote export besides meeting its domestic requirements. However, despite continuous efforts at various levels, chilli productivity did not gain momentum due to number of constraints such as non-availability of suitable cultivars/ hybrids, biotic and abiotic stresses, genetic drift in cultivars and development of new pathogenic races (Sharma and Singh 2009). Therefore, there is a demand to develop high yielding varieties or hybrids enriched with good quality attributes through genetic reconstructing of the chilli germplasm for enhancing the productivity.

Existence of genetic diversity is the pre-requisite of genetic enhancement of any crop. It is also essential for natural selection to act and to support the survival of the fittest. In human-directed plant evolution, genetic diversity is of considerable importance to manipulate the plant phenotype in a direction beneficial to human. It has become more important in context of changing climatic scenario as they may act as the base on which new selections for changed environments can be made. Yield improvement in any crop can be achieved using efficient utilization of germplasm resources which, in turn requires adequate knowledge on genetic diversity. As yield is regarded as a 'super trait' influenced by many components, direct selection for yield is not effective. In order to have a clear picture of yield components for effective selection programme, there is a need to study genetic diversity for component traits of yield also.

Genetic diversity is routinely assessed by phenotypic evaluation of germplasm lines in terms of economic traits. Phenotypic evaluation is cheap, direct and doesn't require sophisticated techniques. It is based on multiple traits and provides the criteria for selection of divergent lines

Department of Genetics & Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, UP
*Corresponding author, Email: karstav7@gmail.com

for their subsequent use in crop improvement programmes. In this context, a comprehensive study was undertaken to study genetic diversity using phenotypic evaluation in order to understand the genetic diversity and genetic relationship among chilli cultivars.

Materials and Methods

The experimental material comprised of 37 diverse genotypes of chilli received from different universities and institutes and are listed in Table 1. The experiment was carried out at Institute of Agricultural Sciences, Banaras Hindu University (BHU), Varanasi, Uttar Pradesh situated at 83.03°E longitude and 25.02°N latitude and at an altitude of 128.93m above mean sea level in the North Gangetic zone of India. Field experiment was carried out during *Kharif* season 2010-11 at Vegetable Research Farm, Institute of Agricultural Sciences, BHU, Varanasi. The experiment was laid out in randomized complete block design (RCBD) with three replications. The spacing of 60 cm (row to row) and 45 cm (plant to plant) was followed. Each genotype was sown in two rows per replication ensuring sufficient plants for observation and data recording. All the standard cultural procedures were followed to maintain a good plant stand. Observations were recorded from five randomly selected plants for 13 traits *viz*., days to 50 per cent flowering (DFF), plant height (PH), number of primary branches per plant (PBP), number of secondary branches per plant (SBP), fruit length (FL), fruit diameter (FD), number of fruits per plant (FPP), fresh fruit weight (FFW), dry fruit weight (DFW), fresh yield per plant (FY), dry yield per plant, number of seeds per fruit (SNPF) and test weight (TW). The mean values for all the 13 traits were used for statistical analysis. The data was analysed using Analysis of Variance (Panse and Sukhatme 1967). The character contribution towards genetic divergence was computed using the method given by Singh and Chaudhary (1977). Percentage contribution towards genetic divergence was calculated using the following formula

$$\text{Percentage contribution of the character} = \left(\frac{N}{M}\right) \times 100$$

Where,

N = Number of genotype combinations where the character was ranked first.

M = All possible combinations of number of genotypes considered.

The genetic divergence was worked out among the genotypes using Mahalanobis D^2 statistics (Mahalanobis, 1936) and the D^2 values were calculated as follows:

$$D_{ij}^2 = \sum_{t=1} (Y_i^t - Y_j^t)^2$$

Where,

D_{ij}^2 is the distance between ith and jth genotypes,

Y_i^t is uncorrelated mean value of ith genotype for character 't', and

Y_j^t is uncorrelated mean value of jth genotype for character 't'.

The average intra and inter cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

$$\text{Square of intra – cluster distance} = \sum D_i^2/n$$

$$\text{Square of intra – cluster distance} = \sum D_i^2/n_i\, n_j$$

Where,

D_i^2 = Sum of distance between all possible combinations,

n= Number of all possible combinations,

n_i = Number of entries in cluster i, and

n_j = Number of entries in cluster j

The genotypes were grouped into different clusters by employing Tocher's method as outlined by Rao (1952).

Results and Discussion

Genetic divergence among 37 genotypes of chilli was studied using D^2 statistics (Mahalanobis 1936). The analysis employed Mahalnobis Euclidean^2 Distance by Ward's method so as to group the genotypes into different clusters. χ^2 test applied was significant indicating significant difference between the means in respect of pooled effect of 13 traits under study. Hence, further analysis was carried out for estimating D^2-values to study genetic divergence.

Distribution of genotypes into different clusters by Ward's method in chilli is presented in Table-2. The cluster diagram, indicating dispersion of genotypes under divergent clusters, is presented in Fig.1. Thirty seven chilli genotypes were grouped into seven different clusters based on the inter-genetic distances. Cluster-I constituted maximum number (13) of genotypes followed by cluster-2 consisting of five genotypes, clusters-III consisting of two genotypes, cluster 4

Table 1: List of chilli genotypes under study

S. No.	Genotype	Source	S. No.	Genotype	Source
1	EC 566320	NBPGR, New Delhi.	20	SM20	IIVR, Varanasi
2	EC 519630	NBPGR, New Delhi.	21	WALIA	IIVR, Varanasi
3	EC 566301	NBPGR, New Delhi.	22	ARKA ABHIR	IIHR, Bangalore
4	EC979626	NBPGR, New Delhi.	23	SOLAN LOCAL	Local Collection, Himachal Pradesh
5	EC257216	NBPGR, New Delhi.	24	NO 495	ANGRAU, A.P
6	EC570008	NBPGR, New Delhi.	25	AKC 89138	ANGRAU, A.P
7	EC560314	NBPGR, New Delhi.	26	SHP 7 YELLOW	IIVR, Varanasi
8	IC413714	NBPGR, New Delhi.	27	NO 8	IIVR, Varanasi
9	IC119414	NBPGR, New Delhi.	28	DABBI	ANGRAU, A.P
10	IC119298	NBPGR, New Delhi.	29	SEL 9	IIVR, Varanasi
11	IC382266	NBPGR, New Delhi.	30	SEL 17-1-4	IIVR, Varanasi
12	IC119321	NBPGR, New Delhi.	31	PANT C1	GBPUA&T, Pantnagar
13	IC119361	NBPGR, New Delhi.	32	TIWAN 2	AVRDC, Taiwan
14	IC397471	NBPGR, New Delhi.	33	KDCS 810	IIVR, Varanasi
15	IC1402	NBPGR, New Delhi.	34	PBC 535	IIVR, Varanasi
16	IC413702	NBPGR, New Delhi.	35	KTPL 19	Katrain, H.P
17	IC119327	NBPGR, New Delhi.	36	BULLET 2	IIVR, Varanasi
18	IC113368	NBPGR, New Delhi.	37	KADDI	ANGRAU, A.P
19	IC113367	NBPGR, New Delhi.			

Table 2: Distribution of 37 genotypes of chilli in different clusters by Ward's method.

Cluster	Genotypes included	Number
1	EC 566320, EC560314, EC979626, EC 566301, IC119327, IC113368, IC119298, IC113367, IC119361, SM20, PBC 535, IC413702, KADDI.	13
2	EC 519630, IC119321, IC1402, KDCS 810, WALIA.	5
3	IC413714, ARKA ABHIR	2
4	EC257216, EC570008, IC397471, SHP 7 YELLOW, NO 8, BULLET-2, DABBI, IC382266, AKC-89138, PANT C-1, TIWAN-2	11
5	NO 495, KTPL 19, IC119414, SEL 17-1-4	4
6	SEL 9	1
7	SOLAN LOCAL	1

consisting of eleven genotypes, cluster 5 consisting of four genotypes and cluster 6 and 7 consisting of one genotype each. This is in agreement with reports of Smitha and Basavaraja (2006) and Dutonde *et al*. (2008) who reported eight and seven clusters in 40 genotypes of chilli, respectively. In contrast, Hasan *et al*. (2015) reported five clusters in 13 genotypes indicating more divergent lines under the study.

Average intra- and inter-cluster distances among seven clusters are presented in Table-3. The average intra-cluster distance did not exceed average inter-cluster distance. The intra-cluster distances ranged from 0 (cluster-VI and VII) to 51.85 (cluster-III). Highest value of intra-cluster distance in cluster-III indicated the presence of genetically diverse lines in the cluster. The inter cluster D^2 value was maximum (345.23) between cluster-IV and VII followed by cluster-V and VII with high values (330.58). The minimum distance observed was (42.59) between cluster-I and II followed by clusters-II and IV with value (51.14) which indicated close relationship among the genotypes involved. Genotypes within a cluster may be considered less divergent and crossing between them may not be beneficial. Maximum heterosis can be achieved by selecting genotypes from clusters with maximum inter-cluster distance. Janaki *et al*. (2016) suggested that the genotypes from clusters with smaller values of inter-cluster distance can be used for backcrossing.

Table 3: Estimates of average intra- (bold) and Inter-cluster distance (D^2) values among seven clusters of 37 chilli genotypes by Ward's method

Cluster	I	II	III	IV	V	VI	VII
I	34.60	42.59	57.48	51.21	61.48	67.16	318.57
II		34.08	67.97	51.14	72.26	78.24	324.28
III			51.85	87.01	88.38	77.53	290.55
IV				37.60	56.95	70.50	345.23
V					48.74	61.69	330.58
VI						0	300.05
VII							0

Comparison of cluster means for the different characters (Table-4) indicated considerable differences between clusters for all the characters. Cluster-I containing thirteen genotypes was characterized by exhibiting highest value (10.32 cm) for fruit length. Cluster-II containing five genotypes was characterized by exhibiting minimum values for days to 50% flowering (63.11), fruit diameter (0.94 cm) and number of seeds/ pod (55.57). Cluster-III, containing two genotypes, was characterized by exhibiting maximum value for plant

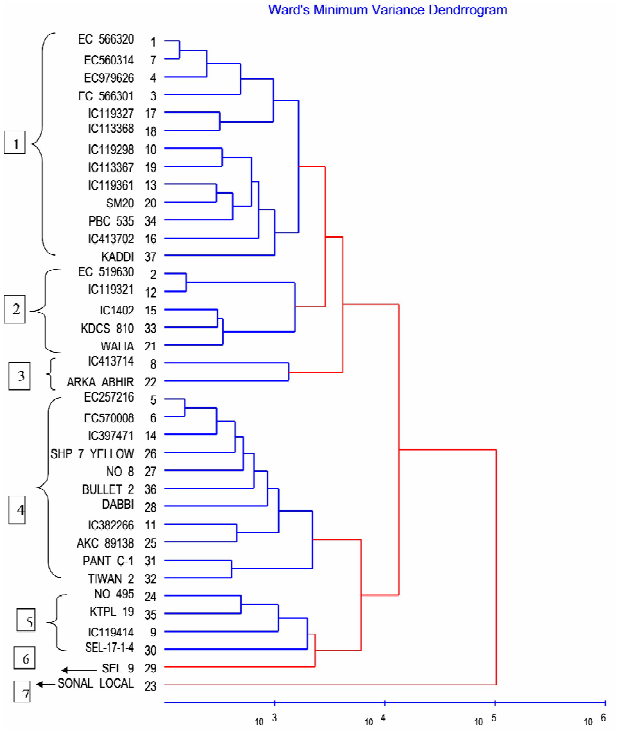

Fig. 1. Dendrogram of 37 genotypes of chilli based on D^2 statistics

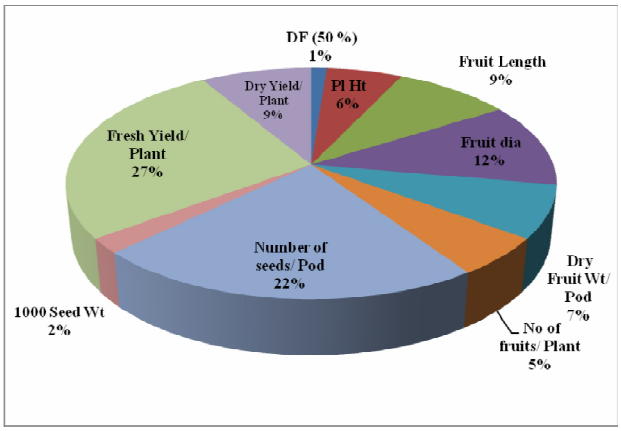

Fig.2: Contribution of different characters towards diversity in chilli germplasm

height (74.5 cm), number of fruits/plant (65.1), test weight (5.35 g) and minimum value for number of secondary branches/plant (9.06). Cluster- IV containing eleven genotypes was characterized by lowest fresh fruit weight per pod (2.26g), dry fruit weight per pod (0.63g), fresh yield per plant (101.9g) and dry yield per plant (30.45 g). Cluster-V containing four genotypes was characterized by highest fruit girth (3.53 cm) and lowest test weight (4.03 g). Cluster-VI containing one genotype was characterized by highest days to 50% flowering (73.93), number of seeds per pod (180.86). It exhibited minimum values for fruit length (3.88 cm) and number of primary branches (3.73). Cluster-VII containing one genotype was characterized by highest values for number of primary branches (4.33), number of secondary branches per plant (12.86), fresh fruit weight per pod (24.75 g), dry fruit weight per pod (5.58), fresh yield per plant (524.13) and dry yield per plant (101.85). However, this cluster had lowest plant height (48.33 cm). It is desirable to select genotypes from clusters having high cluster means and also with high fruit yield as parents for future recombination breeding programmes.

Genetic diversity study indicated that among the 13 characters studied, the highest contribution towards the genetic diversity was by fresh yield per plant (26.58%), followed by number of seeds per pod (22.22%) and fruit diameter (11.7%) (Fig. 2). Fruit diameter was reported to contribute maximum towards divergence in chilli by Janaki *et al.* (2016). Present study reported no contribution of three traits viz., number of primary branches/plant, number of secondary branches/plant and fresh fruit weight/pod had towards genetic divergence. This is in agreement with reports of Janaki et al. (2016) who reported no contribution of number of primary branches toward genetic divergence. Other traits *viz.* fruit length, dry yield, number of fruits per plant and

Table 4: Mean values of different clusters in respect to13 parameters in chilli.

Characters	Mean						
	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI	Cluster-VII
Days to 50 % flr	66.96	63.11	68.10	66.53	65.00	73.93	64.40
Pl Ht (cm)	68.45	56.88	74.50	65.57	63.63	50.73	48.33
No. of Pri Branch	3.88	4.03	4.07	4.10	4.20	3.73	4.33
No. of Sec Branch	10.36	10.68	9.07	11.06	9.28	11.53	12.87
Fruit Lt (cm)	10.32	6.81	8.84	7.02	7.95	3.88	4.19
Fresh Frt Wt/ Pod (gm)	3.33	2.84	4.44	2.27	3.17	4.36	24.75
Fruit Girth (cm)	1.36	0.94	1.30	1.46	3.54	1.47	1.17
Dry Frt Wt/ Pod (gm)	0.91	0.78	1.14	0.63	0.91	1.27	5.59
No of Fruits/ Plant	54.58	59.07	65.10	47.55	37.68	30.87	21.20
No of Seeds/ Pod	92.75	55.57	102.27	98.76	133.25	180.87	146.60
1000 Seed Wt	4.86	4.11	5.36	4.64	4.04	4.29	4.17
Fresh Yield/ Plant	176.38	170.37	294.13	101.91	123.70	136.06	524.13
Dry Yield/ Plant (gm)	49.35	46.57	72.10	30.45	34.04	46.40	101.85

plant height had small contributions towards genetic divergence. In contrast, number of fruits/plant was reported to have the highest contribution towards genetic divergence (Smitha and Basavaraja, 2006; Hasan et al., 2015).

Conclusion

Mahalanobis D^2 statistics study by Ward's method distributed 37 genotypes into 7 clusters. The maximum inter cluster distance was observed between cluster-IV and VII. Crossing between genotypes of these clusters can yield maximum heterosis or desirable segregants. Cluster-VII exhibited highest mean values for maximum (five) traits namely number of secondary branches/plant, fresh fruit weight/pod, dry fruit weight/pod, fresh fruit yield/plant and dry fruit yield/plant and minimum value for days to 50% flowering. Cluster-III exhibited maximum mean values for plant height, number of fruits/plant and 1000 seed weight. The genotypes from these two clusters can be used as prospective donors for above traits. Crosses can be attempted between genotypes of these clusters for combining desirable traits. Fresh yield/plant and number of seeds/pod contributed maximum towards genetic divergence. Number of primary branches/plant, number of secondary branches/plant and fresh fruit weight/pod had no contribution towards genetic divergence. These traits can be considered as the indication of genetic diversity in the germplasm lines.

सारांश

मिर्च की 37 प्रभेदों में 13 उपज घटकों के प्रयोग द्वारा आनुवांशिक प्रसरण विश्लेषण महालानोबिस डी वर्ग विधि से किया गया। डी वर्ग विश्लेषण ने प्रभेदों को कुल 7 समूहों में समायोजित किया एवं प्रभेदों में पर्याप्त प्रसरण को इंगित किया। समूह–1, 13 प्रभेदों के साथ सबसे बड़ा समूह था। समूह–4, 11 प्रभेदों के साथ दूसरा बड़ा समूह था। समूह–3 की आंतरिक दूरी सबसे ज्यादा (51.85) पाई गई। दो समूहों के बीच सबसे ज्यादा दूरी (345.23) समूह–4 एवं समूह–7 के बीच पायी गयी। अध्ययनरत् 13 उपज घटकों में प्रति पौधा ताजा फल उपज, प्रति फल बीजों की संख्या एवं फल व्यास का प्रसरण में अधिकतम योगदान था। प्रति पौधा प्राथमिक शाखा की संख्या, प्रति पौध द्वितीयक शाखा की सख्या एवं प्रति फल ताजा फल भार का आनुवांशिक प्रसरण में कोई योगदान नहीं था। प्रसरित प्रभेदों का उपयोग फसल सधार हेतु ओज एवं अतिक्रमणीय प्रजनन के द्वारा की जा सकती है।

References

Dutonde SN, Bhalekar MN, Patil BT, Kshirsagar DB and Dhumal SS (2008) Genetic diversity in chilli (*Capsicum annuum* L.). Agric Sci Digest 28 (1): 45–47.

Hasan Rokib, Mahmudul Huque AKM, Kamal Hossain M and Alam N (2015) Assessment of genetic divergence in chilli (*Capsicum annuum* L.) genotypes. Plant Gene Trait 6(3): 1-5.

Janaki M, Naram Naidu L, Venkata Ramana C and Paratpara Rao M (2016) Genetic divergence among chilli (*Capsicum annuum* L.) genotypes based on quantitative and qualitative traits. Int J Sci Nat (1): 181-189.

Kumar S, Kumar R and Singh J (2006) Cayenne/American pepper (*Capsicum* species). In: Peter KV (ed) Handbook of herbs and spices. Woodhead, Cambridge, pp 299-312.

Mahalanobis PC (1936) On the generalised distance in statistics. Proc Natl Acad Sci India 2: 49-55.

Panse VG and Sukathme PV (1967) Statistical Methods for Agricultural Workers, ICAR, New Delhi, pp 145.

Rao CR (1952) Advanced Statistical Methods in Biometrical Research. John Wiley and Sons Inc New York, 236-272.

Sharma M and Singh Y (2009) Genetic divergence in chilli (*Capsicum annuum* L.) for green yield and its contributing traits under mid hill conditions of Himachal Pradesh. Himachal J Agril Res 35(2): 180-182.

Singh RK and Chaudhary BD (1977) Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, pp 215-218.

Smitha RP and Basavraja N (2006) Genetic divergence studies in chilli (*Capsicum annuum* L.). Karnataka J Agric Sci 19(4): 975-977.