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## Studies on genetic divergence in chilli genotypes (*Capsicum annum* L.)

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### Abstract

Sixteen genotypes of chilli were tested for genetic divergence using D<sup>2</sup> analysis in order to ascertain the nature and magnitude of genetic diversity present in the material. Genetic divergence among sixteen genotypes based on fruit yield and its component characters were grouped into three clusters. The maximum number of nine genotypes was included in cluster-III followed by five genotypes in cluster-I. The highest inter-cluster divergence was observed between the clusters II and III (5.531) which indicated maximum exploitation of heterosis on hybridization. The contribution of various characters towards the total divergence was recorded the highest for fruit girth (40.83 per cent), dry weight of fruits (21.66 per cent), fruit yield per plant (10.83 per cent) and dry matter % of fruits (11 per cent). Thus, it can be concluded that, selection for these traits will be beneficial for future improvement programme of chilli.

**Keywords:** *Capsicum annum* L., genetic divergence, d<sup>2</sup> analysis, heterosis, cluster analysis

### Introduction

Chilli (*Capsicum annum* L.) is known as the universal spice of India and has diverse utilities as a spice, condiment, and culinary supplement, and medicine, vegetable and ornamental plant. The important chilli growing states are Andhra Pradesh, Karnataka, Maharashtra, Orissa, Tamil Nadu and Madhya Pradesh. A wide variability in chilli fruit morphology, pungency, bearing habit and crop duration is found throughout India (Asati and Yadav, 2004) [1]. Genetic divergence existing in the population helps in the selection of suitable parents for utilization in any crop breeding programme leading to reduction in the number of crosses (Guerra *et al.*, 1999) [3]. The information on the nature and degree of genetic divergence is essential for the breeder to choose the right type of parents for hybridization in heterosis breeding (Farhad *et al.*, 2010; Khodadabi *et al.*, 2011) [2, 6]. In order to benefit transgressive segregation, the knowledge of genetic distance between parents is necessary (Khodadabi *et al.*, 2011) [6]. Hybrids produced from distantly related parents are expected to exhibit higher heterosis and minimize the inherent field genetic vulnerability than those from closely related parents (Lahbib *et al.*, 2012) [8]. In case of D<sup>2</sup> analysis, one can only know the intra-cluster distance but not relative position of the genotypes in the respective cluster. Principal component analysis facilitates in-depth analysis of genetic divergence between genotypes in terms of spatial distance. Thus, main objective of this study was to analyze the potential genetic diversity among genotypes of chilli and to classify the genotypes into different groups based on cluster analysis and principal component analysis and selection of suitable genotypes for further chilli hybridization programme.

### Materials and Methods

The present experiment was conducted at Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur during *rabi* season of 2016-17 in order to evaluate the performance of sixteen genotypes of chilli for various yield and its component traits under field condition with three replications of each genotype. Each plot measuring 4.2 x 3.5 m<sup>2</sup> had six rows spaced at 60 cm apart with intra-row spacing of 50 cm. The chilli seeds were planted during second week of September, 2016. The recommended dose of fertilizer *i.e.* nitrogen 150 Kg, phosphorus 75 Kg and potassium 60 Kg per hectare was applied. Half nitrogen was applied at the time of planting and remaining was applied in two splits *i.e.*, at 30 and 60 DAP. Crop was visited regularly throughout the growing season and intercultural operations such as weeding, irrigation and plant protection measures were performed as and when necessary. The study was carried out on the basis of observations recorded from five randomly selected plants in each plot. The data obtained for different growth and yield parameters was used to select the desirable parents for hybridization (Table 3). The genotypes were grouped into a number of clusters using Tocher's method as described by Rao (1952) and the most divergent ones were selected using the

Mahalanobis (1936)  $D^2$  statistics. The population of different genotypes was arranged in order of their relative distances from each other. For including a particular genotype in the clusters, a level of  $D^2$  was fixed by taking the maximum  $D^2$  values between any two populations in the first row of the table where  $D^2$ -values were arranged in increasing order of magnitude. The maximum numbers of possible pairs were calculated from sixteen genotypes considering all the traits. This analysis was carried out through computer software SPAR-1.

### Result and Discussion

The study of genetic divergence among genotypes under study was performed for all possible pair of character and as

an outcome, sixteen genotypes were grouped into three different clusters using Mahalanobis  $D^2$  statistics. The clustering helps to identify genotypes that share the same characteristics and/or that are closely related and vice versa. The cluster analysis groups different genotypes on the basis of similarities and thus provides the hierarchical classification. From the clustering pattern, it was observed that the genotypes from different region were independent of their genetic origin. The maximum number of nine genotypes was included in cluster-III followed by five genotypes in cluster-I and two genotypes in cluster-II (table 1). Hence, the genotypes studied were reliable enough for hybridization and selection. Similar opinions were also exhibited by Sahu *et al.* (2016) [12].

**Table 1:** Clustering pattern of different genotypes of chilli

Cluster Number	Number of genotype included	Name of genotypes
1	5	2016/CHIVAR-4, 2014/CHIVAR-4, 2014/CHIVAR-5, 2014/CHIVAR-7, 2014/CHIVAR-9
2	2	2016/CHIVAR-5, 2016/CHIVAR-8
3	9	2016/CHIVAR-3, 2016/CHIVAR-6, 2014/CHIVAR-2, 2014/CHIVAR-3, LCA-334, Kashi Anmol-2, 2014/CHIVAR-6, 2014/CHIVAR-8, 2014/CHIVAR-10

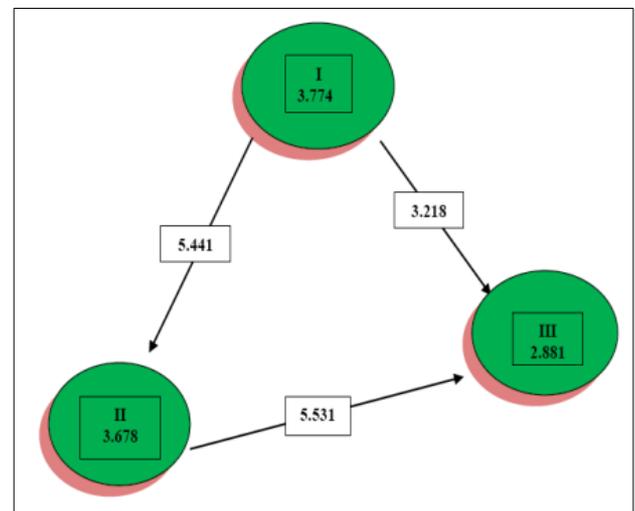
### Intra and inter-cluster distances

The intra cluster divergence values ranged (fig.1.) from 2.881 to 3.774 (Table 2). The highest intra cluster distance was observed in cluster I (3.774) followed by cluster II (3.678) and lowest in cluster III (2.881). However, the inter-cluster divergence values varied from 3.218 to 5.531. The maximum inter-cluster divergence was observed between the clusters II and III (5.531) followed by cluster I and II (5.441) and the minimum inter-cluster distance was observed in between cluster I and III (3.218). Thus, highly divergent genotypes produce a wide range of variability that enables further selection. Therefore, the genotypes belonging to cluster II and III may be considered as parents for hybridization programme because genotypes within these clusters have high degree of divergence and would produce more desirable breeding materials for achieving maximum genetic advance. The findings of inter and intra cluster distances are in conformity with earlier works of Mishra *et al.*, (2004) [10], Farhad *et al.* (2010) [2], Kumar *et al.* (2010), and Lahbib *et al.* (2012) [8]. 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. Consequently, a crossing programme should be conducted with putative parents. Critical assessment of clusters showed that clusters were heterogeneous within themselves and between each other based on major character relation. The inter cluster distance were greater than the intra cluster distance revealing that considerable amount of genetic diversity existed among the genotypes Janaki *et al.* (2016) [5].

**Table 2:** Inter and intra cluster distances

Cluster Number	I	II	III
1	3.774	5.441	3.218
2		3.678	5.531
3			2.881

\* Diagonal bold values indicate intra cluster distances



**Fig 1:** Diagram showing inter and intra cluster  $D^2$  values of different cluster in chilli.

### Performance of cluster

The mean performance of genotypes belonging to different clusters for different characters is shown in the Table 3. The component of cluster mean for the Days to first flowering was highest in cluster-III followed by cluster-II. In case of Days to 50 % flowering cluster-III possesses the highest average performance followed by cluster-II. The highest mean for number of Plant height (cm) was observed in cluster-I followed by cluster-II. Number of primary branches was recorded highest in cluster-I followed by cluster-III and cluster-II. Stem girth (cm) exhibited highest cluster mean for cluster-II followed by cluster-III \ and lowest for cluster-I. Days to first picking showed highest cluster mean for cluster-III followed by cluster-II and lowest for cluster-II. Fruit length (cm) exhibited highest cluster mean for cluster-I and lowest for cluster-II. Fruit girth (cm), exhibited the highest mean performance in cluster-II and lowest for cluster-III, whereas,

The stalk length (cm), was observed in cluster-I followed by cluster-II and lowest in cluster-III. The genotype with highest number of seeds per fruit, was grouped into cluster-I and lowest was observed in cluster-II. Number of fruits per plant showed the highest mean performance in cluster-III and lowest in cluster-II. The highest cluster mean for fresh weight of fruits (gm), was recorded in cluster-II and lowest for cluster-III. The highest dry weight of fruits (gm), was observed in cluster-II and lowest in cluster-III. In case of number of picking the highest mean performance of genotype was observed in cluster-III and lowest in cluster-II. The highest cluster mean for dry matter % of fruits was recorded

in cluster-II and lowest for cluster-III. The highest cluster mean for fruit yield per plant (gm), was recorded in cluster-I and lowest for cluster-II. The highest fruit yield per ha (q) was observed in cluster-I and lowest in cluster-II. In case of number of picking the highest mean performance of genotype was observed in cluster-III and lowest in cluster-II. The highest cluster mean for dry matter % of fruits was recorded in cluster-II and lowest for cluster-III. The highest cluster mean for fruit yield per plant (gm), was recorded in cluster-I and lowest for cluster-II. The highest fruit yield per ha (q) was observed in cluster-I and lowest in cluster-II.

**Table 3:** Mean performance of genotypes in individual cluster for different yield traits.

Cluster No.	Entries	Characters																
		Days to first flowering	Days to 50 % flowering	Plant height (cm)	Number of primary branches	Stem girth (cm)	Days to first picking	Fruit length (cm)	Fruit girth (cm)	Stalk length (cm)	Number of seeds per fruit	Number of fruits per plant	Fresh weight of fruits (gm)	Dry weight of fruits (gm)	Number of pickings	Dry matter % of fruits	Fruit yield per plant (gm)	Fruit yield per ha (q)
1	5	44.80	52.80	58.73	7.95	3.97	96.80	10.41	3.73	4.04	68.95	116.32	30.02	4.73	4.93	16.55	344.36	107.33
2	2	46.50	57.17	54.77	3.83	4.80	96.83	7.73	6.23	3.62	56.00	96.57	34.47	7.38	4.50	21.57	188.74	58.94
3	9	48.85	64.00	52.99	6.27	4.03	101.56	8.47	3.36	3.59	63.70	123.69	22.02	2.42	5.22	11.22	303.61	96.88

### Desirable genotypes based on cluster performance

The genotypes belonging to different clusters with highest mean performance for all the characters under consideration are presented in Table 4. Among them, 2014/CHIVAR-9 included in cluster-I possessed the highest values for maximum number of characters *viz.* fruit length fresh weight of fruits, dry weight of fruits, fruit yield per plant, fruit yield per plot and fruit yield per ha. Highest days to first flowering were observed in 2014/CHIVAR-8 of cluster-III, whereas, Days to 50 % flowering and number of fruits per plant was observed in genotype Kashi Anmol-2 included in cluster-II. The genotype 2016/CHIVAR-4 belonging to cluster-I was recorded with highest values for the characters namely Plant height, number of primary branches and stalk length. Highest dry matter % of fruits was observed in 2016/CHIVAR-5 of cluster-II, whereas maximum number of pickings was observed in the genotype 2014/CHIVAR-10 included in the cluster-III. In case of the genotype 2016/CHIVAR-8 belonging to cluster-II possessed highest value of Stem girth and Fruit girth. Days to first picking was observed highest in the genotype 2016/CHIVAR-6 belonging to the cluster-III, whereas maximum number of seeds per fruit was observed in the genotype 2014/CHIVAR-3 included in the cluster-III. In present investigation, genotypes originating from different geographical regions were grouped together under same cluster and cultivars from same geographical origin were accommodated in different clusters. This demonstrated that

geographical distribution was not related to genetic diversity. Kumar *et al.* (2010) [7] with twenty five genotypes; Farhad *et al.* (2010) [2] with forty five genotypes; Sahu *et al.* (2016) [12] with nineteen genotypes and Janaki *et al.* (2016) [5] with sixty three genotypes also observed that clustering pattern was not influenced by geographic distribution of genotypes.

Therefore, present findings suggest the existence of genetic divergence in population of chilli. This may perhaps be due to the free exchange of breeding materials from one location to another. Besides, it may be due to the fact that the nature of selection pressure operating under respective domestic conditions might be similar across geographic barriers. Thus, it is evident that geographical diversity, though important may not be the sole factor determining genetic divergence and the factors other than geographic diversity might have been responsible for the grouping of the genotypes. Based on the findings of present experiment, it can be concluded that inter-crossing among the genotype belonging to genetically diverse clusters and showing superior mean performance might prove beneficial for obtaining desirable segregants in the coming generation. Keeping in view the result of cluster analysis, genotypes namely 2014/CHIVAR-9 and 2016/CHIVAR-4 of cluster-I, 2016/CHIVAR-5 of cluster-II, Kashi Anmol-2 and 2014/CHIVAR-6 of cluster-III possessing superiority among genotypes may be utilized as parents in hybridization programmer for obtaining desirable combination.

**Table 4:** Desirable genotypes for important traits of chilli based on individual clusters

Characters	Cluster-I	Cluster-II	Cluster-III
Days to first flowering	2016/CHIVAR-4 (35)	2016/CHIVAR-5 (36.67)	2014/CHIVAR-8 (41.00)
Days to 50 % flowering	2016/CHIVAR-4 (43.67)	2016/CHIVAR-5 (45.33)	Kashi Anmol-2 (57)
Plant height (cm)	2016/CHIVAR-4 (66.50)	2016/CHIVAR-5 (57.30)	2014/CHIVAR-8 (64.77)
Number of primary branches	2016/CHIVAR-4 (9.73)	2016/CHIVAR-5 (4.60)	2014/CHIVAR-10 (9.33)
Stem girth (cm)	2014/CHIVAR-9 (4.46)	2016/CHIVAR-8 (4.88)	2014/CHIVAR-6 (4.48)
Days to first picking	2016/CHIVAR-4 (91.33)	2016/CHIVAR-5 (91)	2016/CHIVAR-6 (98)
Fruit length (cm)	2014/CHIVAR-9 (13.84)	2016/CHIVAR-5 (8.09)	2014/CHIVAR-6 (9.66)
Fruit girth (cm)	2014/CHIVAR-9 (4.50)	2016/CHIVAR-8 (7.93)	2014/CHIVAR-6 (4.20)
Stalk length (cm)	2014/CHIVAR-4 (4.42)	2016/CHIVAR-5 (3.95)	2014/CHIVAR-8 (4.13)
Number of seeds per fruit	2014/CHIVAR-9 (82.73)	2016/CHIVAR-8 (78.33)	2014/CHIVAR-3 (84.20)
Number of fruits per plant	2014/CHIVAR-5 (145.47)	2016/CHIVAR-8 (104.33)	Kashi Anmol-2 (157.67)
Fresh weight of fruits (gm)	2014/CHIVAR-9 (48.33)	2016/CHIVAR-8 (37.87)	2014/CHIVAR-6 (33.23)
Dry weight of fruits (gm)	2014/CHIVAR-9 (8.83)	2016/CHIVAR-5 (8.67)	2014/CHIVAR-3 (4.00)
Number of pickings	2016/CHIVAR-4 (5.36)	2016/CHIVAR-5 (4.67)	2014/CHIVAR-10 (5.77)

Dry matter % of fruits	2016/CHIVAR-4 (24.73)	2016/CHIVAR-5 (27.43)	2014/CHIVAR-3 (18.77)
Fruit yield per plant (gm)	2014/CHIVAR-9 (414.99)	2016/CHIVAR-8 (199.67)	Kashi Anmol-2 (388.69)
Fruit yield per plot (kg)	2014/CHIVAR-9 (19.52)	2016/CHIVAR-8 (9.34)	Kashi Anmol-2 (18.50)
Fruit yield per ha (q)	2014/CHIVAR-9 (132.75)	2016/CHIVAR-8 (63.48)	Kashi Anmol-2 (125.80)

### Contribution of various characters towards the total divergence

Among the yield contributing characters, the maximum contribution towards divergence was made by fruit girth, dry weight of fruits, fruit yield per plant and dry matter % of fruits (Table-5). The characters contributing maximum

towards divergence needs to be given greater emphasis for selection of parents in the respective clusters for hybridization. Thus, it can be concluded that selection for these traits will be beneficial for future improvement programme of chilli. Similar findings have been reported by Sahu *et al.* (2016) [12].

**Table 5:** Contribution of each character to divergence

Characters	Days to first flowering	Days to 50 % flowering	Plant height (cm)	Number of primary branches	Stem girth (cm)	Days to first picking	Fruit length (cm)	Fruit girth (cm)	Stalk length (cm)	Number of seeds per fruit	Number of fruits per plant	Fresh weight of fruits (gm)	Dry weight of fruits (gm)	Number of pickings	Dry matter % of fruits	Fruit yield per plant (gm)	Fruit yield per ha (q)	Total
Number times appearing first time	0	0	6	5	1	3	1	49	0	1	0	0	26	1	12	13	2	120
Percent contribution	0	0	5	4.16	0.83	2.5	0.83	40.83	0	0.83	0	0	21.66	0.87	10	10.83	1.66	100

### Conclusion

The inter-crossing among the genotype belonging to genetically diverse clusters and showing superior mean performance might prove beneficial for obtaining desirable segregants in the coming generation. The genotypes namely 2014/CHIVAR-9 and 2016/CHIVAR-4 of cluster-I, 2016/CHIVAR-5 of cluster-II, Kashi Anmol-2 and 2014/CHIVAR-6 of cluster-III possessing superiority among genotypes may be utilized as parents in hybridization programme for obtaining desirable combination.

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