

Original Research Article

<https://doi.org/10.20546/ijcmas.2019.809.103>

## Studies on Genetic Divergence in Byadgi Dabbi Chilli Genotypes (*Capsicum annum* L.)

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### ABSTRACT

#### Keywords

*Capsicum annum* L., Genetic divergence, D<sup>2</sup> analysis, Heterosis, cluster analysis

#### Article Info

##### Accepted:

15 August 2019

##### Available Online:

10 September 2019

A study on genetic diversity was conducted with 29 Chili (*Capsicum annum* L.) genotypes through Mohalanobis's D<sup>2</sup> analysis. Cluster analysis was used for grouping of 29 chilli genotypes and the genotypes were fallen into six clusters. The maximum number of 22 genotypes was included in cluster-I followed by cluster-III with 3 genotypes, Cluster-II, IV, V and VI had one genotype each. The highest inter-cluster distance was observed between cluster I and VI which indicated maximum exploitation of heterosis on hybridization. The least inter cluster distance was observed between cluster II and V. Cluster III (D<sup>2</sup>=197.76) have exhibited highest intra cluster distance followed by cluster I (D<sup>2</sup>=193.37). Cluster II, IV, V and VI had only one genotype and hence, the intra cluster distance of this cluster was zero. The contribution of various characters towards the total divergence was recorded the highest for capsacin (60.34%) followed by number of seeds per fruit (18.23%), dry fruit yield per hectare (9.61%), dry fruit yield per plant (7.64%), weight of 100 dry fruits (2.71%), fruit length and fruit diameter (0.49%), plant spread at 60 DAT (E-W) and fruit yield per plot (0.25%). Thus, it can be concluded that, selection for these traits will be beneficial for future improvement programme of chilli.

### Introduction

Chilli (*Capsicum annum* L.) is a popular vegetable and spice crop of India and many parts of the world. It provides a wide range of variability and diversity with a tremendous scope for genetic studies and improvement by breeding. 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). 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). In order to benefit transgressive segregation, the knowledge of genetic distance between parents is necessary (Khodadabi *et al.*, 2011). 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). Thus, main objective of this study was to analyse the potential genetic diversity among genotypes of chilli and to classify the genotypes into different groups based on cluster analysis and selection of suitable genotypes for further chilli hybridization programme.

## Materials and Methods

Field experiment was conducted with 29 Byadgi Dabbi genotypes during *kharif* 2018-19 at HREC, Devihosur, Haveri of University of Horticultural Sciences, Bagalkot. The experiment was laid out in randomized complete block design (RCBD) with two replications with spacing of 60x60 cm row to row and plant to plant. All the recommended package of practices and plant protection measures were followed to raise the crop healthy. Five plants were randomly selected from each genotype and replication and observations were recorded on different growth, yield and quality parameters. The data obtained for different growth, yield and quality parameters were used to select the desirable parents for hybridization. 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 Mahalanobis (1936)  $D^2$  statistics.

## Results and Discussion

The study of genetic divergence among genotypes under study was performed for all possible pair of characters and as an outcome, 29 genotypes were grouped into six different clusters using Mahalanobis  $D^2$  statistics. The clustering helps to identify genotypes that share the same characteristics 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 22 genotypes was included in cluster-I followed by cluster-III with three genotypes and Cluster-II, Cluster-IV, Cluster-V and Cluster-VI had one genotype each (Table 1). Hence, the genotypes studied were reliable enough for hybridization and selection. Similar opinions were also exhibited by Sahu *et al.* (2016).

## Intra and inter-cluster distances

Cluster III with three genotypes showed maximum intra-cluster distance ( $D^2=197.76$ ) followed by cluster I ( $D^2= 193.37$ ) which indicates diversity present within the cluster (Table 2). Cluster II, IV, V, VI had only one genotype and hence, the intra cluster distance was zero, which indicates very minimum diversity was found within the cluster. The maximum inter-cluster distance was observed between cluster I and VI followed by cluster II and VI (Table 2). Thus, highly divergent genotypes produce a wide range of variability that enables further selection. Therefore, the genotypes belonging to cluster I and VI 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 least inter-cluster distance was observed between cluster I and II followed by cluster II and V. The minimum inter cluster  $D^2$  value recorded between cluster I and II indicate the close genetic makeup of genotypes included in these clusters which suggests the lower degree of divergence in the genotypes. The findings of inter and intra cluster distances are in conformity with earlier works of Mishra *et al.* (2004), Farhad *et al.* (2010), Kumar *et al.* (2010) and Lahbib *et al.* (2012).

The relative contribution of different characters to genetic divergence depicted that Capsaicin (60.34%) contributed maximum to the total divergence. Which was followed by number of seeds per fruit, dry fruit yield per hectare, dry fruit yield per plant, weight of 100 dry fruits, fruit length, fruit diameter, plant spread at 60 DAT (E-W) and fruit yield per plot. 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 programmer of chilli. Similar findings have been reported by Sahu *et al.* (2016). However rest of the characters exhibited nil contribution to total genetic distance (Table 3).

### **Performance of cluster**

The mean performance of genotypes belonging to different clusters for different characters is shown in the Table 4. The component of cluster mean for plant height at 60 DAT was highest in the cluster III followed by cluster I. In case of plant height at 90 DAT cluster II possesses the highest average performance followed by cluster III. The highest cluster mean for plant height at 120 DAT was observed in cluster VI followed by cluster III. Highest cluster mean for plant spread (N-S) at 60 DAT was observed in the cluster II followed by cluster III. The highest mean for plant spread (E-W) 60 DAT was observed in cluster II followed by cluster III.

Highest cluster mean for plant spread (E-W) 120 DAT was observed in the cluster I followed by cluster III. Highest cluster mean for plant spread (N-S) 120 DAT was observed in the cluster III followed by cluster V. Number of primary branches was recorded highest in cluster V followed by cluster I. Secondary branches exhibited highest cluster mean for cluster IV followed by cluster III.

Days to first flowering showed highest cluster mean for cluster IV followed by cluster V. Days to 50 per cent flowering exhibited highest cluster mean for cluster II followed by cluster V. Number of fruits per plant was highest in cluster III followed by cluster II.

Average fruit weight showed the highest mean performance in cluster III followed by cluster VI. The highest cluster mean for fruit length was observed in cluster III followed by cluster I. Fruit diameter was highest in cluster II followed by cluster IV. Fruit yield per plant showed highest cluster mean in cluster III followed by cluster II. The highest cluster mean for fruit yield per plot observed in cluster III followed by cluster II. In case of fruit yield per hectare the highest mean performance of genotype was observed in cluster III followed by cluster II. The highest cluster mean for weight of 100 dry fruits was recorded in cluster IV followed by cluster V. The highest cluster mean for number of seeds per fruit was observed in cluster V followed by cluster I. In case of capsaicin the highest mean performance of genotype was observed in cluster VI followed by cluster III. This is in conformity with the findings of other researchers Datta and Jana, (2011), Hasan *et al.* (2014), Srinivas *et al.* (2015).

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 observed between the clusters I and IV indicated that the accessions included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregating population for obtaining desirable combination.

**Table.1** Cluster composition based on D<sup>2</sup> values in chilli (*cv. Byadgi Dabbi*)

Cluster number	Number of genotypes	Genotypes included
<b>I</b>	22	DKHBD-3, DKK-G-1, DKHDD-4, DKK-G-2, DKS-ND-1, DKK-DD-8, DKSDD-5, DKHBD-9, DKK-DD-6, GSK-DD-3, GSK-ND-4, DKK-G-3, DKHBD-1, DKHBD-4, DKHBD-2-2, DKHBD-6, DKHBD-7, DKK-DD-7, DKHBD-5, GSK-ND-3, DKHBD-3, DKS-DD-1
<b>II</b>	1	GSK-BD-1
<b>III</b>	3	DKS-ND-2, DKHBD-2-1, DKS-DD-2
<b>IV</b>	1	DKKKBK-4
<b>V</b>	1	DKHBD-8
<b>VI</b>	1	GSK-ND-5

**Table.2** Intra cluster and inter cluster D<sup>2</sup> values in chilli (*cv. Byadgi Dabbi*)

Clusters	<b>I</b>	<b>II</b>	<b>III</b>	<b>IV</b>	<b>V</b>	<b>VI</b>
<b>I</b>	<b>193.97</b>	354.86	1362.27	509.03	788.20	12054.12
<b>II</b>		<b>0.00</b>	491.67	182.10	281.94	8960.47
<b>III</b>			<b>197.76</b>	565.66	399.46	5970.01
<b>IV</b>				<b>0.00</b>	358.05	8900.20
<b>V</b>					<b>0.00</b>	7216.79
<b>VI</b>						<b>0.00</b>

**Table.3** Per cent contribution of the different characters to the total divergence in chilli (*cv. Byadgi Dabbi*)

<b>Sl. No.</b>	<b>Source</b>	<b>Times ranked 1st</b>	<b>Contribution %</b>
1	Plant height 60 days	0	0.00
2	Plant height 90 days	0	0.00
3	Plant height 120 days	0	0.00
4	Plant Spread at 60 days E-W	1	0.25
5	Plant Spread at 60 days N-S	0	0.00
6	Plant Spread 120 days E-W	0	0.00
7	Plant Spread at 120 days N-S	0	0.00
8	No. of primary branches	0	0.00
9	No .of secondary branches	0	0.00
10	Days to first flowering	0	0.00
11	Days to 50% flowering	0	0.00
12	Number of fruits per plant	0	0.00
13	Fruit length	2	0.49
14	Fruit diameter	2	0.49
15	Average dry fruit weight	0	0.00
16	Dry fruit yield per plant	31	7.64
17	Fruit yield per plot	1	0.25
18	Dry fruit yield per hectare	39	9.61
19	Weight of 100 dry fruits	11	2.71
20	Number of seeds per fruit	74	18.23
21	Capsaicin	245	60.34

**Table.4** The mean values of 21 characters for 6 clusters formed by 29 genotypes in chilli (*cv. Byadgi Dabbi*)

Sl. No.	Character	Clusters					
		I	II	III	IV	V	VI
1.	Plant height at 60 DAT (cm)	50.56	49.49	51.40	48.79	49.00	49.36
2.	Plant height at 90 DAT (cm)	60.65	70.31	65.30	57.28	59.29	63.81
3.	Plant height at 120 DAT (cm)	67.03	71.48	71.96	59.22	63.48	75.75
4.	Plant spread from E-W at 60 DAT (cm)	46.83	50.76	48.97	47.21	47.73	48.87
5.	Plant spread from N-S at 60 DAT (cm)	33.49	29.81	34.91	33.04	32.59	30.70
6.	Plant spread from E-W at 120 DAT (cm)	42.00	49.46	48.09	42.89	45.09	37.73
7.	Plant spread from N-S at 120 DAT (cm)	40.48	42.82	44.07	41.61	43.04	36.84
8.	Number of primary branches per plant	3.63	3.30	3.40	3.60	4.50	3.40
9.	Number of secondary branches per plant	7.97	8.00	9.37	10.00	6.70	6.50
10.	Days to first flowering	31.70	30.00	33.67	34.50	34.00	31.00
11.	Days to 50 per cent flowering	42.19	43.50	40.83	35.50	43.50	41.50
12.	Number of fruits per plant	11.16	11.70	15.49	9.50	9.50	8.00
13.	Average Fruit weight (g)	1.76	1.78	1.91	1.67	1.48	1.78
14.	Fruit length (cm)	7.86	7.36	8.01	6.37	7.49	6.95
15.	Fruit diameter (cm)	14.94	16.70	15.27	16.28	13.54	13.72
16.	fruit yield/plant (g)	27.14	30.34	39.14	21.89	22.68	22.36
17.	Fruit yield per plot(kg)	0.69	0.77	0.99	0.62	0.48	0.52
18.	Dry fruit yield per ha(q/ha)	8.36	9.91	12.04	7.51	5.70	6.33
19.	Weight of 100 dry fruits (g)	125.22	123.73	124.79	171.96	149.04	123.30
20.	Number of seeds per fruit	104.65	96.50	80.95	81.22	127.33	104.00
21.	Capsaicin (SHU)	6497.55	12220.00	19436.33	12015.00	17160.00	51253.00

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### How to cite this article:

Sushmitha, A., T.B. Allolli, V.M. Ganiger, P.S. Ajjappalavar, J.B. Shashikanth Evoor, J.B. Gopali and Abdul Kareem. 2019. Studies on Genetic Divergence in Byadgi Dabbi Chilli Genotypes (*Capsicum annum* L.). *Int.J.Curr.Microbiol.App.Sci*. 8(09): 861-867. doi: <https://doi.org/10.20546/ijcmas.2019.809.103>