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Genetic variability studies in chilli (*Capsicum annum* L.)

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Abstract
A study was conducted to evaluate the nature and magnitude of genetic variability in 15 Chilli genotypes in a randomized block design with three replications. The analysis of variance revealed significant difference among 15 genotypes for all the character studied indicating the presence of sufficient variability in the studied material. Results revealed the presence of wide genetic variability. The genotypes were grouped into 5 clusters based on Mahalanobis D2 statistics using Torcher's method. The clustering pattern of genotypes revealed that the genetic diversity was independent of the geographical diversity. Among the 5 clusters, maximum numbers of genotypes were found in cluster II, while clusters IV and V was found to be mono-genotypic. Among the 14 quantitative characters studied, number of seeds/fruits constituted a maximum of 26% contribution to the divergence, followed by fruit weight(g). Ranking of genotypes based on intra-cluster mean performance for these characters which are major contributors of genetic diversity revealed its usefulness in selecting parents for heterosis breeding.

Keywords: Chilli, genetic variability, genetic advance, heritability, genetic divergence, d2 analysis

Introduction
Chilli or pepper (*Capsicum annuum* L.) belongs to family Solanaceae, which is emerging as one of the commercial vegetable crops at the global level. Chilli finds its place in spice as well as condiments. Chilli fruits are rich sources of vitamin C, vitamin A and E. The productivity of the crop is low due to many limiting factors such as lack of superior genotypes or improved cultivars for use in breeding programme to develop potential hybrids. So, there is need for development of new varieties and hybrids with high productivity. The critical assessment of nature and magnitude of variability in the germplasm stock is one of the important pre-requisites for formulating effective breeding methods as the genetic improvement of any crop depends on magnitude of genetic variability and the extent of heritability of economically important characters, though the part played by environment in the expression of such character also needs to be taken into account (Krishna *et al.*, 2007) [9]. Improvement in any crop is proportional to the magnitude of its genetic variability present in germplasm. Greater the variability in a population, there are the greater chance for effective selection for desirable types (Vavilov, 1951) [14]. When, variability is partitioned into heritable and non- heritable components, efficiency of selection is better understood.
Heritability is the portion of phenotypic variation which is transmitted from parent to progeny. Higher the heritable variation, greater will be the possibility of fixing the characters by selection. Hence, heritability studies are of foremost importance to judge whether the observed variation for a particular character is due to genotype or due to environment. Heritability estimates may not provide clear predictability of the breeding value. Thus, estimation of heritability accompanied with genetic advance is generally more useful than heritability alone in prediction of the resultant effect for selecting the best individuals (Johnson *et al.*, 1955) [6].
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) [3, 8]. In case of D^2 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. Keeping foregoing points in view, a total of 15 genotypes of chilli were evaluated for the study of study variability, heritability, genetic advance and genetic divergence.

Materials and Methods

Fifteen genotypes of chilli selected from the germplasm collection obtained from IIHR Bangalore and farmers varieties were grown in Randomized Block Design with three replications during *rabi* 2019-2020 at the Horticulture Research Farm in the Department of Horticulture, SHUATS, Prayagraj, UP, India. The unit plot size was 3 m^2 with row-to-row and plant-to-plant spacing being 60 cm and 30 cm respectively. Agronomic practices were followed to raise a good crop. Five competitive plant were randomly selected in each entry for recording observation on Plant height (cm), Number of Branches per plant, Plant Spread E-W (cm), Plant Spread N-S (cm), Days to first flower Initiation, Number of Fruits per plant, Fruit length (cm), Fruit Diameter (cm), Fruit Weight (g), Number of Seeds per fruit, Fruit yield per plant (g), Fruit yield per plot (kg), Fruit yield (t/ha) However, observations were recorded on plot basis for days to 50% flowering. The data recorded during observation was used for analysis to test the level of significance as per method given by (Chandel, 1984) [2]. The data were analyzed to work out various components coefficient of variation and heritability in broad sense and expected genetic advance as percent of Mean were estimated as suggested by (Johnson *et al.,* 1955) [6] respectively. The data were subjected to multivariate analysis of genetic divergence using Mahalanobis D^2 statistics. Grouping of entries was done by Torcher's method.

Results and Discussion

The analysis of variance (ANOVA) (Table 1) revealed considerable amount of variability for the fourteen traits studied suggesting sample scope to identify desirable each genotypes. The study on genetic variability parameters (Table 2) revealed that the magnitude of GCV and PCV was highest for Fruits yield per plant (g) (45.94) and Fruit yield per plot (kg) (45.86) respectively indicating the presence of high amount of variation and role of environment on the expression of these traits. The heritability estimates were found to be high (more than 60%) for plant height (cm) (99.50), Number of Branches per plant (79.30), Plant Spread E-W (cm) (91.50), Plant Spread N-S (cm) (91.60), Days to first flower Initiation (94.10), Days to 50% percent flowering (92.30), Number of Fruits per plant (96.60), Fruit length (cm) (94.40), Fruit Diameter (cm) (80.50), Fruit Weight (g) (96.30), Number of Seeds per fruit (99.70), Fruits yield per plant (g) (98.60), Fruit yield per plot (kg) (98.60), Total Soluble Solids (0Brix) (97.80), Ascorbic Acid (mg) (99.70) and Fruit yield (t ha-1) (98.60). The range of genetic advance (GA) among different character varied from 0.48% for fruit diameter to 93.17% for fruits yield per plant. The GA as % of mean varied from 16.76% for ascorbic acid to 93.04% for fruits yield per plant and fruit yield (t ha^{-1}) suggesting predominance of additive gene action and lower influence of environmental factors in the expression of these traits with possibility for improvement through selection.

The (Table 3) revealed that cluster II followed by cluster I and III was the largest comprising six, four and three genotypes respectively. The result showed that geographical diversity was not necessarily a direct cause of genetic diversity. The geographical diversity has been disapproved to be an index of genetic diversity in several crops. Frequent exchange of breeding materials from one place to another and further selection may also be responsible for distribution of gene complex over distant locations. Thus, it is more appropriate to select genotypes for hybridization based on genetic diversity rather than geographical diversity. The intra cluster distance ranged from 0 to 237.44 and inter cluster distance (D) ranged from 701.36 to 6399.24 (Table 4). Maximum inter cluster D-value was observed between cluster-II and cluster V (6399.24) followed by cluster-IV and cluster V (3446.51). The average cluster means of 14 traits are presented in Table 3. Perusal of the table reveals that cluster V had the highest mean value for yield plant 1 (205.64). It was found that ascorbic acid (31%) contributed maximum to total divergence followed by number of Seeds per fruit (26%) and fruit weight (13.3%) (Table 5). Fruit diameter (cm), plant height (cm) and days to first flower initiation followed by other traits had least contribution to the total divergence. So, from the present study, the diverse clusters (I and II) hold good promise for various hybridization based breeding programmes, genotypes from these clusters can be used for obtaining high heterotic response.

Table 1: Analysis of variance for 16 quantitative and qualitative characters in chilli

S. No.	Characters	Mean sum of squares		
		Replication (df = 2)	Treatment (df = 14)	Error (df= 28)
1.	Plant height (cm)	0.354	1113.301**	0.18
2.	Number of Branches per plant	2.455	8.945**	0.717
3.	Plant Spread E-W (cm)	15.875	113.074**	3.385
4.	Plant Spread N-S (cm)	1.902	117.282**	3.485
5.	Days to first flower Initiation	0.484	77.367**	1.588
6.	Days to 5% percent flowering	1.514	82.168**	2.226
7.	Number of Fruits per plant	0.783	138.257**	1.605
8.	Fruit length (cm)	0.287	13.026**	0.253
9.	Fruit Diameter (cm)	0.008	0.214**	0.016
10.	Fruit Weight (g)	0.034	1.373**	0.017
11.	Number of Seeds per fruit	0.554	903.154**	0.761
12.	Fruits yield per plant	12.28	6254.817**	29.874
13.	Fruit yield per plot	0.003	1.228**	0.006
14.	Total Soluble Solids (0Brix)	0.002	4.995**	0.038
15.	Ascorbic Acid	0.538	443.433**	0.445
16.	Fruit yield (t ha-1)	1.504	766.222**	3.659

* and ** significant at 5% and 1% level of significance respectively

Table 2: Estimation of Genetic variability parameters for growth parameters and yield attributes of Chilli

S. No.	Characters	GCV	PCV	Heritability H2 (Broad sense)	GA	GAM (%)
1.	Plant height (cm)	9.03	9.05	99.50	12.26	18.55
2.	Number of Branches per plant	16.28	18.29	79.30	3.04	29.86
3.	Plant Spread E-W (cm)	17.10	17.88	91.50	11.92	33.70
4.	Plant Spread N-S (cm)	17.14	17.91	91.60	12.14	33.80
5.	Days to first flower Initiation	12.52	12.90	94.10	10.04	25.01
6.	Days to 50% percent flowering	10.60	11.04	92.30	10.22	20.98
7.	Number of Fruits per plant	19.81	20.15	96.60	13.67	40.11
8.	Fruit length (cm)	28.57	29.40	94.40	4.13	57.17
9.	Fruit Diameter (cm)	14.52	16.18	80.50	0.48	26.84
10.	Fruit Weight (g)	23.81	24.26	96.30	1.36	48.14
11.	Number of Seeds per fruit	43.56	43.61	99.70	35.6	89.62
12.	Fruits yield per plant (g)	45.94	45.81	98.60	93.17	93.04
13.	Fruit yield per plot (kg)	45.52	45.86	98.60	1.31	93.10
14.	Total Soluble Solids (0Brix)	23.54	23.80	97.80	2.62	47.94
15.	Ascorbic Acid (mg)	8.15	8.16	99.70	25.00	16.76
16.	Fruit yield (t ha-1)	45.49	45.81	98.60	32.61	93.04

GCV-genotypic coefficients of variation, PCV-phenotypic coefficients of variation, GAM (%)-genetic advance mean percentage

Table 3: Number and name of genotypes in different clusters

Clusters	No. of genotypes	Name of genotype
Cluster-I	4	D1 Local variety D2 Local variety GAA Ganga G1 Farmer variety
Cluster-II	6	G_3 Farmer Variety G_5 Farmer Variety G_4 Farmer Variety G_8 Farmer Variety G_6 Farmer Variety G_7 Farmer Variety
Cluster-III	3	Arka Meghana Arka Sweta Arka Shupal
Cluster–IV	1	G_2 Farmer Variety
Cluster –V	1	Arka Kyathi

Table 4: Average Intra (Bold) and Inter Cluster Distance (D)

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	207.89	2207.65	1418.64	811.54	2552.06
Cluster 2		237.44	3334.86	701.36	6399.24
Cluster 3			197.22	1438.62	723.93
Cluster 4				0	3446.51
Cluster 5					0

Table 5: Percent contribution of each character toward genetic divergence of Chilli

Source	Contribution
Plant height (cm)	5.7
Number of Branches per plant	0
Plant Spread E-W (cm)	0
Plant Spread N-S (cm)	0
Days to first flower Initiation	3.8
Days to 50 percent flowering	0
Number of Fruits per plant	0.95
Fruit length (cm)	1.9
Fruit Diameter (cm)	8.55
Fruit Weight (g)	13.3
Number of Seeds per fruit	26
Fruits yield per plant (g)	0.95
Fruit yield per plot (kg)	2.85
Total Soluble Solids (Brix)	2.85
Ascorbic Acid	31
Fruit yield (t ha-1)	0.95

Conclusion

Genetic variability in chilli was studied during Rabi season involving 15 genotypes showing wider variation for all traits. Result revealed that high PCV and GCV was observed for characters like fruit length (cm), fruit weight (g), number of seeds per fruit, fruit yield per plant (g), fruit yield per plot (kg), total soluble solids (^{0}Brix) and fruit yield (t/ ha). High heritability coupled with genetic advance as percent mean were observed for characters like number of seeds per fruit, fruit yield per plant (g), ascorbic acid (mg) and fruit yield (t/ha) suggesting predominance of additive gene action and lower influence of environmental factors in the expression of these traits with possibility for improvement through selection. These characters were governed by additive genes where selection will be rewarding for improvement of such traits. 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 highest contribution in manifestation of genetic divergence was exhibited by ascorbic acid (31%) followed by number of Seeds per fruit (26%) and fruit weight (13.3%).

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