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Assessment of Genetic Diversity in Different Chilli (*Capsicum annuum* L.) Genotypes

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A B S T R A C T

Eleven genotypes of chilli (*Capsicum annuum* L.) were investigated to understand the extent of genetic diversity through 16 growth and yield attributing characters. Genetic diversity in chilli genotypes based on sixteen characters was estimated using Mahalanobis's D^2 statistics. The genotypes were grouped into four different clusters by non-hierarchical clustering. The cluster I had the maximum number (7) of genotypes while cluster III and IV each contained only one genotype. Cluster II and III had highest inter cluster distance (249.759) followed by cluster III and IV (239.433). It was also observed that the contribution of fruit yield per plant to genetic divergence of genotypes in chilli was the maximum followed by leaf curl/plot and fruit weight. So, selection of parents differing in these quantitative traits may be proved useful for heterosis breeding programme in chilli.

Introduction

Chilli (*Capsicum annum* L.) is a member of the Solanaceae family, originated from South and Central America. It is one of the most important spice crop worldwide, with a global production 30.71 lakh tonnes and 20.378 lakh ha area harvested, in 2010-11. In India chilli ranked first in spice crops in terms of production (12.23 lakh tonnes) and area harvested (7.92 lakh ha), in the year 2010-11 (FAOSTAT, 2012). The primary centre of origin of chilli is said to be Mexico with secondary centre in Guatemala and Bulgaria (Salvador, 2002). It was introduced in Europe by Columbus in the 15th century and spread to rest of the world along the spice trading routes to Africa, India, China and Japan. Chilli was introduced in southern India by the Portuguese from Brazil in the middle of 17th century and cultivation spread throughout India by the end of the 19th century. Due to long history of cultivation, selection and popularity of crops, sufficient genetic variability has been generated. Rich variability in morphological traits in hot pepper occurs throughout India, particularly in south peninsular region, North Eastern foot hills of Himalayas and Gangetic plains (Pradheep and Veeraragavatham, 2006). However, the high variability present in the crop has so far not been fully exploited in the crop improvement programmes.

Genetic diversity is the basic requirement for any successful breeding programme. Assessment of genetic diversity among germplasms is a prerequisite for plant breeders in choosing potential parental lines because of two reasons: i.e., (i) In the hybridization programme, genetically diverse parents likely to produce high heterotic effect, and (ii) Genetically distant parents could produce a wide spectrum of variability in the segregating generation. Therefore, a clear characterization of germplasms is the first step to facilitate successful breeding efforts.

The degree of genetic divergence can be quantified using Mohalanobis's D^2 statistic of multivariate analysis which is recognized as a powerful tool for assessing the relative contribution of different characters to the total divergence in self-pollinated crops (Golakia and Makne 1992; Natarajan *et al.,* 1988; Das and Gupta 1984; Shidhu *et al.,* 1989). Therefore, the present study was undertaken to assess the genetic diversity in 13 genotypes of chilli to identify suitable genotypes.

Materials and Methods

The study was carried out at All India Coordinated Research Project on Vegetable Crops, O.U.A.T, Bhubaneswar during rabi season of 2016 in a randomized block design with three replications to evaluate most promising genotypes with respect to the quality parameters among the 11 genotypes of chilli. Each genotype was raised in 8.1 m2 area with a spacing of 50 cm x 30 cm accommodating 54 plants per plot. The crop was grown with standard package of practices. The observations were recorded on sixteen economic traits from five randomly selected competitive plants from each genotypes and replication. Mahalanobis (1928) generalized distance, D^2 – statistic was used for computing genetic divergence as described by Rao (1952). The original measurements were transformed to standardized uncorrelated variables by pivotal condensation (Rao, 1952). The divergence between any two varieties was obtained as the sum of squares of the difference in the values of the corresponding transformed values of the corresponding transformed values (V_{ij}). Following Tocher's method as described by Rao (1952), the genotypes were grouped into clusters. The criterion of grouping was that any two genotypes belonging to the same cluster should have a smaller D^2 value than those between genotypes belonging to different clusters. Inter and intra-cluster distances were determined and represented.

Results and Discussion

The data of varietal trial on chilli (Mean performance of the varieties are present in Table 1) were subjected to further analysis of genetic divergence. The multivariate analysis based on Mahalanobis' D^2 statistics is being employed as a powerful tool for measuring genetic divergence among the tested genotypes. Ramanujan *et al.,* (1974) have categorically suggested the merits of D^2statistics for genetic grouping of germplasm. In the present investigation, the grouping by multivariate technique has shown good results. Being a numerical estimate, the multivariate technique has the added advantage over other criteria of permitting precise comparison among all possible pairs of population in any given group. Since, the estimates are obtained from study of potential parents themselves, the required information is available before deciding parents for future recombination breeding, thus, can be used with advantage. It is well established that hybrid derivatives from divergent parents are found to be promising, probably because of complementary interaction of divergent genes in the parents taken for cross in the parents. A perusal of Table 2 shows that the 11 genotypes of chilli could be grouped into 4 clusters on the basis of intra and inter cluster distances. The first cluster I comprised of 7 genotypes, cluster II consisted of 2 genotypes, while cluster III and IV consisted of 1 genotype each. Cluster II and III had highest inter cluster distance followed by cluster III and IV.

Cluster I had the highest mean value for plant height. Cluster III recorded the highest mean values for fruit length, fruit girth, fruit weight, leaf area, initial flowering, 50% flowering, fruit borer (no. of fruits/ plant), leaf curl (no. of plants/plot) and wilting(no. of plants/plot). Cluster IV had the highest mean values for branches/plant, plant spread (E-W), plant spread (N-S), no. of fruits/plant, anthracnose (no. of fruits/plant), fruit yield/plant.

Relative contribution of fruit yield per plant to genetic divergence of genotypes in chilli was the maximum, followed by leaf curl/plot and fruit weight. In the present study, Cluster II and III had highest inter cluster distance followed by cluster III and IV. So, promising hybrid derivatives can be obtained by crossing the parents selected from these two divergent groups (Table 3–5).

Table.1 Mean performance of different genotypes in chilli (Pooled)

Genotypes	PH	BP	PSEW	PSNS	LA	DIF	DFF	FW	FL	FG	NFP	FYP	YQH
2014/CHIVAR-2	91.47	14.00	57.10	48.07	22.28	43.83	53.50	5.31	9.29	3.61	54.75	146.14	76.26
2014/CHIVAR-3	79.72	12.83	55.05	52.35	22.99	37.00	55.17	4.57	9.16	3.37	63.29	150.99	91.93
2014/CHIVAR-4	79.01	12.00	51.50	45.83	22.20	26.33	42.17	7.18	9.00	3.78	31.04	149.12	70.09
2014/CHIVAR-5	83.40	13.00	54.20	52.14	21.32	42.17	52.17	4.50	8.62	3.27	37.91	53.13	36.16
2014/CHIVAR-6	71.20	13.00	49.83	43.31	25.58	52.83	61.17	6.21	8.79	4.12	45.60	126.51	73.30
2014/CHIVAR-7	81.37	13.67	55.00	44.91	23.41	32.33	47.00	8.23	10.01	3.75	52.06	161.74	103.41
2014/CHIVAR-8	89.80	11.00	60.13	60.13	23.82	35.83	51.83	3.78	6.53	3.30	76.55	94.82	56.76
2014/CHIVAR-9	78.48	12.67	45.90	42.71	25.44	43.17	57.17	15.14	13.75	3.89	22.64	101.45	50.22
2014/CHIVAR-10	64.73	12.83	67.47	62.08	23.54	38.50	50.50	3.95	7.17	3.42	94.85	152.12	86.26
KA-2(C)	52.97	10.00	63.62	57.80	22.25	49.50	57.33	3.18	7.64	3.33	44.21	83.19	50.35
LCA-334(C)	92.90	12.00	63.07	54.07	18.99	34.33	44.83	3.52	7.75	3.64	65.73	48.54	55.41
SEm(±)	3.41	0.76	2.68	1.95	0.94	2.18	1.58	0.11	0.41	0.13	4.41	17.11	0.94
CD at 5%	7.12	1.58	5.58	4.06	1.96	4.56	3.30	0.24	0.86	0.27	9.19	50.47	2.78

PH-Plant Height (cm), BP- Branches/Plant, FL- Fruit Length (cm), FG- Fruit Girth (cm), FW- Fruit weight (g), LA-Leaf Area (cm^2), PSEW - Plant Spread (E-W) (cm), PSNS - Plant Spread (N-S) (cm), DIF- Days Initial Flowering (DAP), DFF- Days 50% Flowering (DAP), NFP- No. of Fruits/Plant, FYP- Fruit Yield/Plant (g), YQH-Yield (q/ha).

Table.2 Clustering pattern of 11 genotypes in chilli

Cluster No.	Number of chilli genotypes	Name of genotypes
I.	7	2014/CHIVAR-2, 2014/CHIVAR-3,2014/CHIVAR-4, 2014/CHIVAR-5, 2014/CHIVAR-6, 2014/CHIVAR-7, 2014/CHIVAR-8
II.	2	KA-2(C), LCA-334(C)
III.	1	2014/CHIVAR-9
IV.	1	2014/CHIVAR-10

Table.3 Intra and inter cluster average (D^2) and corresponding D values in (parenthesis) among genotypes

	I.	II.	III.	IV.
I.	3488.810 (59.066)	3500.333 (59.164)	43387.320 (208.296)	4144.512 (64.378)
II.		778.567 (27.903)	62379.641 (249.759)	2104.354 (45.873)
III.			0.000 (0.000)	57328.309 (239.433)
IV.				0.000 (0.000)

Table.4 Cluster wise mean values of 16 characters of genotypes in chilli

	PH	BP	FL	FG	FW	LA	PSEW	PS-NS	DIF	DFF	NFP	FBP	AP	LP	WP	FYP
I.	82.281	12.786	8.770	3.601	56.816	23.083	54.688	49.535	38.619	51.857	50.345	4.906	1.663	10.667	5.452	276.253
II.	72.933	11.000	7.695	3.485	33.520	20.618	63.343	55.933	41.917	51.083	54.970	5.275	1.528	3.917	5.333	187.038
III.	78.483	12.667	13.750	3.887	151.383	25.443	45.900	42.713	43.167	57.167	22.643	13.417	3.580	29.500	13.833	334.420
IV.	64.733	12.833	7.173	3.417	39.530	23.537	67.467	62.080	38.500	50.500	94.847	6.337	2.570	4.333	5.667	379.043

PH-Plant Height (cm), BP- Branches/Plant, FL- Fruit Length (cm), FG- Fruit Girth(cm), FW- Fruit weight (g), LA- Leaf Area (cm^2), PSEW - Plant Spread(E-W) (cm), PSNS - Plant Spread (N-S) (cm), DIF- Days Initial Flowering (DAP), DFF- Days 50% Flowering (DAP), NFP- No. of Fruits/Plant, FBP- Fruit Borer (no. of fruits/ plant), AP- Anthracnose (no. of fruits/plant), LP- Leaf Curl (no. of plants/plot), WP- Wilting (no. of plants/plot), FYP- Fruit Yield/Plant(g).

Table.5 Relative contribution of different characters to genetic divergence of genotypes in chilli

Name of Characters	No of 1st rank	Percent contribution
Plant height(cm)	0	0.0000
Branches/plant	0	0.0000
Fruit length(cm)	0	0.0000
Fruit girth(cm)	0	0.0000
Fruit weight (g)	4	7.2727
Leaf area(cm^2)	0	0.0000
Plant spread(E-W)(cm)	0	0.0000
Plant spread(N-S)(cm)	0	0.0000
Days initial flowering	1	1.8182
Days 50% flowering	0	0.0000
No. of fruits/plant	2	3.6364
Fruit borer (no. of fruits/ plant)	1	1.8182
Anthracnose (no. of fruits/plant)	0	0.0000
Leaf curl(no. of plants/plot)	13	23.6364
Wilting(no. of plants/plot)	2	3.6364
Fruit yield/plant(g)	32	58.1818
Total	55	100

In the present study, genotypes obtained from different geographical locations were grouped into a single cluster (Cluster I). Therefore, it is apparent that genetic diversity and geographical diversity do not tally. This is in agreement with the findings of other researchers (Mishra *et al.*, 2011; Hasan *et al.*, 2014; Janaki *et al.*, 2016).

It was also observed that the contribution of fruit yield per plant to genetic divergence of genotypes in chilli was the maximum as was also reported by Hasan *et al.*, (2014). It was followed by leaf curl/plot and fruit weight. So, selection of parents differing in these quantitative traits may be proved useful for heterosis breeding programme in chilli.

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