Genetic Divergence in Chilli (*Capsicum annuum* L.)

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ABSTRACT

Fifty seven indigenously developed genotypes selected from the exotic open pollinated hybrids of chilli (*Capsicum annuum* L.) were evaluated to study the variability and genetic divergence. Genetic diversity analysis revealed good amount of variation among the genotypes studied. D^2 values ranged between 26.15 to 508.60. Fifty seven genotypes were grouped into eighteen clusters. The cluster I was the largest containing 22 genotypes, followed by cluster X (9), cluster II (8) and cluster VII (4). The remaining clusters (III, IV, V, VI, VIII, IX, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII) are monogenotypic. The first five principal components with eigen value more than one contributed 84.17 per cent of the total variability amongst 57 genotypes evaluated for 15 quantitative and qualitative traits. Through cluster analysis, the fifty seven genotypes were grouped into eight clusters and among all the clusters, cluster VI was the largest with 15 genotypes followed by cluster I with 11 genotypes and cluster III with 8 genotypes.

Key words : Chilli, Cluster Analysis, D^2 analysis, Genetic Divergence, Principal Component Analysis

· Chilli (*Capsicum annuum* L.) is one of the most important spice cum vegetable crops grown in India with great export potential. At present apart from developing traditional varieties, yield heterosis is exploited in chilli through hybrid breeding programme. For hybridization, existence of variability and relative divergence among the genotypes is a must. In the present investigation attempts are made to assess variability and genetic diversity in 57 chilli genotypes through Mahalanobis' D^2 analysis, cluster analysis and principal component analysis.

MATERIAL AND METHODS

The studies were carried out at Regional Agricultural Research Station, Lam, Guntur during 2007-08 with 57 diverse chilli genotypes laid in three replications in randomized complete block design. Six weeks old seedlings were transplanted at inter- and intra-row spacing of 60 x 30 cm. Each treatment was considered as a plot and was consisting of three rows of thirteen plants per row. Ten randomly selected plants were tagged in each genotype in each replication. Data were recorded on plant or plot basis for fifteen characters *viz.,* plant height (cm), plant spread (cm), days to 50 % flowering, days to maturity, number of branches per plant, number of fruits per plant, 100-dry fruit weight (g), fruit length (cm), fruit girth (cm), number of seeds per fruit, 1000-seed weight (g), oleoresin (%), capsanthin (EOA colour value), capsaicin content (%) and dry fruit yield per plant (g). For divergence studies, mean of each entry was computed and calculated as per D^2 statistics proposed by Mahalanobis (1928), hierarchical cluster analysis by Anderberg (1993), PCA technique as applied in cotton by Brown (1991) and Jackson (1991).

RESULTS AND DISCUSSIONS

Differences between the genotypes were highly significant for all the characters studied, indicating appreciable amount of diversity among the genotypes. The results of Mahalanobis' D^2 analysis revealed that 57 genotypes were grouped into eighteen clusters and are presented in Table 1. The cluster I had 22 genotypes, followed by cluster X (9), cluster II (8), cluster VII (4) and remaining ones (III, IV, V, VI, VIII, IX, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII) are solitary or monogenotypic. The cluster I included genotypes of early and late flowering, early and late maturity, medium to tall height, medium to maximum spread, high fruit length and number of seeds per fruit and low to high number of fruits per plant (Sundaram *et al.,* 1980).

In the present study, relatively maximum contribution was put forth by oleoresin content (29.57 %), followed by capsaicin content (26.00 %), capsanthin (EOA colour value) (23.75 %), dry fruit yield per plant (7.14), 100-dry fruit weight (4.14 %), fruit girth (3.07 %), number of seeds per fruit (2.44 %) and plant spread (2.13 %). The existence of ample amount of divergence in genotypes with respect to the traits suggests that the selection of best genotypes for such traits would be helpful in utilizing the maximum heterosis in future breeding

Table 1 Clustering of 57 chilli (*Capsicum annuum* L.) genotypes by Tocher's method

Cluster No.	No. of genotypes	Name of the genotype(s)
I	22	LCA-810, LCA-812, LCA-840, LCA-853, LCA-830, LCA-811, LCA-832, LCA-849, LCA-831, LCA-801, LCA-848, LCA-844, LCA-833, LCA-806, LCA-845, LCA-834, LCA-839, LCA-353, LCA-827, LCA-823, LCA-814, LCA-817
II	8	LCA-807, LCA-808, LCA-804, LCA-803, LCA-835, LCA-828, LCA-838, LCA-824
III	1	LCA-842
IV	1	LCA-851
V	1	LCA-821
VI	1	LCA-836
VII	4	LCA-819, LCA-829, LCA-816, LCA-805
VIII	1	LCA-846
IX	1	LCA-825
X	9	LCA-822, LCA-852, LCA-818, LCA-850, LCA-847, LCA-815, LCA-334, LCA-843, LCA-813
XI	1	LCA-854
XII	1	LCA-802
XIII	1	LCA-841
XIV	1	LCA-820
XV	1	LCA-837
XVI	1	LCA-855
XVII	1	LCA-809
XVIII	1	LCA-826

programmes. Other characters *viz.,* fruit length (0.56 %), number of fruits per plant (0.44 %), days to 50% flowering (0.44 %), number of branches per plant (0.19 %) and days to maturity (0.13 %) contributed less to divergence indicating that these traits will not help in yield improvement through hybridization until new variability is created for these traits (Table 3).

Intra- and inter-cluster D^2 values were worked out from divergence analysis. The highest intra-cluster distance was observed for cluster X (112.49), followed by cluster VII (86.98), cluster II (65.39) and cluster I (62.70). The cluster III, IV, V, VI, VIII, IX, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII showed no intra-cluster distance. The high intra-cluster distance in cluster X indicates the presence of wide genetic diversity among the genotypes present in this cluster (Table 2).

The maximum inter-cluster distance was observed between cluster IX and XVII (508.608), followed by cluster IV and XVII (404.706) and cluster VIII and XVII (401.030). The minimum inter-cluster distance was observed between cluster III and IV (26.15), followed by cluster III and VI (30.674), cluster

IV and VI (31.323) and between cluster VIII and IX (31.357). Inter-cluster distance ranged from 26.45 between (III & IV) to 508.60 between clusters (IX & XVII) indicating the genotypes belonging to these groups were genetically more diverse from each other. In this regard genotypes belonging to more diverse groups irrespective of geographical origin should be chosen for breeding programme. From inter-cluster distance, cluster IX showed the highest divergence from cluster XVII, followed by cluster XVII and IV. This suggested that the genotypes belonging to cluster IX and cluster XVII may be undertaken in a hybridizing programme for evolving good hybrids or segregants. Roy and Sharma (1996) suggested intercrossing among genotypes with outstanding mean performance for crop improvement in chilli.

Based on the mean performance of the clusters for 15 characters (Table 4) the cluster V recorded least yield because the genotype was found to have appreciably less number of fruits per plant and minimum fruit girth. It was observed that the cluster XIV and XV recorded maximum yield (833.33 g) and was characterized by maximum plant height,

Table 3. The per cent contribution of each character towards genetic divergence in 57 genotypes of chilli (*Capsicum annuum* L.).

Source	Times ranked first	Contribution (%)	Rank
Plant height	0	0.00	13
Plant spread	34	2.13	8
Days to 50% flowering	7	0.44	10
Days to maturity	2	0.13	12
No. of branches plant^{-1}	3	0.19	11
No. of fruits plant^{-1}	7	0.44	10
100 dry fruit weight	66	4.14	5
Fruit length	9	0.56	9
Fruit girth	49	3.07	6
Number of seeds pod^{-1}	39	2.44	7
1000-seed weight	0	0.00	13
Oleoresin (%)	472	29.57	1
Capsanthin (EOA colour value)	379	23.75	3
Capsaicin (%)	415	26.00	2
Dry fruit yield plant^{-1}	114	7.14	4

Fig 1 Two dimensional graph showing relative position of chilli (*Capsicum annuum* L.) genotypes based on PCA scores
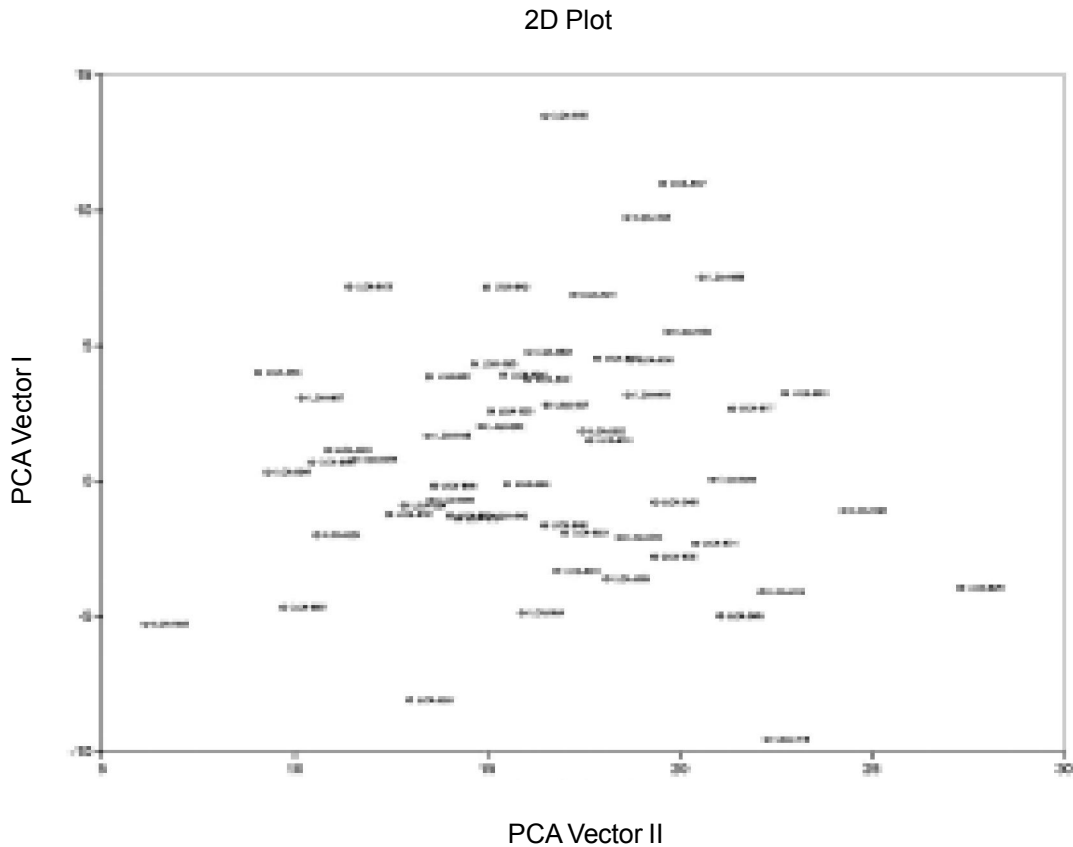
2D Plot

Table 4. Mean values of eighteen clusters (obtained by Tocher's method) estimated from 57 chilli (*Capsicum annuum* L.) genotypes.

Cluster	Plant height (cm)	Plant spread (cm)	Days to 50% flowering	Days to maturity	No. of branches/ plant	No. of fruits/ plant	100-dry fruit weight (g)	Fruit length (cm)
I	109.3	72.5	58.3	125.0	2.2	175.3	82.4	7.8
II	112.2	95.7	57.7	123.3	2.0	160.2	82.6	7.1
III	103.0	66.1	60.6	130.3	1.6	196.1	68.9	7.2
IV	104.3	56.2	58.6	126.3	1.9	150.3	71.1	6.4
V	110.6	85.4	56.6	121.3	2.6	181.7	65.7	7.6
VI	111.8	72.1	56.3	120.6	2.0	154.8	94.2	5.8
VII	116.4	76.8	57.6	123.7	2.6	155.0	99.0	8.2
VIII	114.5	58.4	60.3	129.3	1.8	158.4	91.6	7.8
IX	102.4	75.5	58.3	124.6	2.8	187.1	83.5	7.9
X	113.6	65.8	59.9	127.2	2.0	158.6	79.5	8.0
XI	122.2	71.0	57.0	122.3	2.2	161.4	97.2	3.4
XII	106.8	91.7	62.3	133.6	2.3	147.4	165.4	7.4
XIII	113.8	67.8	63.6	135.6	1.9	158.0	160.0	6.8
XIV	108.0	61.2	55.6	119.3	2.3	215.0	82.2	7.3
XV	138.2	75.4	56.3	120.6	1.9	214.0	94.2	9.3
XVI	119.4	85.3	58.3	125.6	1.7	122.7	62.6	5.8
XVII	100.7	73.4	56.3	120.6	2.4	154.8	89.5	7.8
XVIII	104.0	59.6	56.6	121.3	2.4	149.7	209.5	8.0

Cluster	Fruit girth (cm)	No. of seeds/ fruit	1000-seed weight (g)	Oleo-resin (%)	Capsanthin (EOA colour value)	Cap-saicin (%)	Dry fruit yield/ plant (g)
I	3.4	55.8	6.2	8.9	39276.4	0.2	440.1
II	3.4	48.5	6.7	6.4	43209.9	0.2	418.7
III	3.0	65.9	5.8	9.1	20841.6	0.3	616.6
IV	3.3	70.3	5.9	10.1	16185.3	0.3	350.0
V	3.2	42.5	5.3	8.2	29788.3	0.4	366.6
VI	4.6	60.0	6.6	8.6	15778.6	0.3	433.3
VII	3.8	55.6	7.0	12.0	50912.6	0.3	383.3
VIII	3.6	55.3	6.6	11.7	20577.3	0.2	416.6
IX	3.3	51.1	6.5	13.5	23485.0	0.2	400.0
X	3.5	54.0	5.9	8.0	36611.6	0.4	444.4
XI	5.1	54.5	8.0	9.3	36681.3	0.1	550.0
XII	5.8	61.7	7.1	7.1	48676.3	0.2	600.0
XIII	3.7	36.8	8.1	8.5	18015.3	0.3	266.6
XIV	6.2	49.8	6.5	8.7	45994.0	0.3	833.3
XV	4.6	51.2	6.8	8.5	21106.0	0.2	833.3
XVI	2.8	41.8	4.6	9.0	27633.0	0.2	683.3
XVII	7.3	60.3	7.5	6.2	57767.0	0.2	700.0
XVIII	3.4	55.3	8.1	8.1	46055.0	0.1	300.0

Table 5. Eigen values, proportion of the total variability represented by first five principal components, cumulative per cent variability and component loading of different characters in chilli (*Capsicum annuum* L.).

	Principal components				
	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector
Eigen value (Root)	1138.722	989.786	570.847	294.103	218.641
Expression of variance (%)	29.842	25.939	14.960	7.707	5.730
Expression of Cumulative Variance	29.842	55.780	70.740	78.447	84.177
Plant height (cm)	0.014	0.017	0.026	0.113	0.066
Plant spread (cm)	-0.018	-0.081	-0.117	0.165	-0.263
Days to 50% flowering	0.075	0.046	-0.074	-0.006	0.040
Days to maturity	-0.037	0.016	0.020	0.001	0.077
No. of branches/plant	-0.056	0.033	0.040	-0.080	-0.010
No. of fruits/ plant	-0.001	0.008	0.062	0.035	0.111
100-dry fruit weight (g)	-0.226	-0.021	0.051	-0.231	0.649
Fruit length (cm)	-0.001	0.003	0.169	0.191	0.090
Fruit girth (cm)	-0.122	-0.105	0.060	-0.017	0.526
Number of seeds/ fruit	-0.074	0.100	0.082	0.189	0.208
1000 -seed weight (g)	-0.083	-0.005	-0.011	-0.152	0.190
Oleoresin (%)	-0.365	0.850	0.240	0.195	-0.069
Capsanthin (EOA colour value)	-0.458	-0.429	0.719	-0.011	-0.246
Capsaicin %	0.753	0.143	0.597	-0.030	0.119
Dry fruit yield/ plant (g)	0.038	-0.204	-0.047	0.874	0.203

plant spread and maximum fruit girth, fruit length, number of fruits per plant and number of seeds per fruit. All these characters played an important role in determining the yield of this cluster. Similar results were obtained by Gill *et al.* (1982).

In the principal component analysis, the first five principal components with eigen values more than one contributed 84.17 per cent towards the total variability (Table 5). The first principal component (PC_1) contributed maximum towards variability (29.84 %) are presented in Table 5. The PCA scores for 57 chilli genotypes in the first three principal components were computed. Principal component I, II and III were considered as three axes X, Y and Z and squared distance of each genotype from these three axes were calculated and presented in Table 6. The PCA scores for 57 chilli genotypes were plotted in graph to get 2 D scatter diagrams. The graph showed wide divergence between the genotypes (LCA-809, LCA-838 and LCA-824) from (LCA-825, LCA-846 and LCA-851) signifying their usefulness in chilli breeding (Fig 1).

Through cluster analysis, the fifty seven genotypes were grouped into eight clusters (Table 7) and among all the clusters, cluster VI was the largest with 15 genotypes followed by cluster I with 11 genotypes and cluster III with 8 genotypes (Table 7). Out of the 8 clusters formed, maximum intra-cluster Euclidean[2] distance was recorded in cluster VII (279.43) followed by cluster V (275.14) and cluster IV (203.24).The maximum inter-cluster distance was observed between cluster IV (LCA-815, LCA-847, LCA-334, LCA-850) and cluster V (LCA-802, LCA-835, LCA-809, LCA-826) followed by cluster II (LCA-819, LCA-829, LCA-816) and IV (LCA-815, LCA-847, LCA-334, LCA-850) and cluster II (LCA-819, LCA-829, LCA-816) and V (LCA-802, LCA-835, LCA-809, LCA-826) and are presented in Table 8. This suggested that there is wide genetic diversity between these clusters. Hence, crosses can be made between the genotypes of these clusters to obtain better and desirable segregants.

Based on the agglomerative cluster analysis, principal component analysis and D[2] statistic, the genotypes LCA-816, LCA-815 and LCA-809 were from diverse groups and can be utilized in future hybridization programmes to produce superior segregants in chilli.

Table 6. PCA scores of 57 chilli (*Capsicum annuum* L.) genotypes.

	Vector I	Vector II	Vector III
Genotype	X Vector	Y Vector	Z Vector
LCA-801	-3.335	16.823	16.425
LCA-802	-4.663	9.708	18.701
LCA-803	1.132	10.882	15.167
LCA-804	-0.907	12.850	16.694
LCA-805	-2.798	19.349	19.489
LCA-806	-0.125	15.513	21.248
LCA-807	3.070	10.182	15.223
LCA-808	0.693	10.458	15.558
LCA-809	-5.292	6.138	20.391
LCA-810	-1.385	14.251	21.558
LCA-811	1.489	17.669	19.107
LCA-812	-1.230	12.465	20.351
LCA-813	7.172	11.421	25.908
LCA-814	4.530	17.847	16.116
LCA-815	13.492	16.520	20.722
LCA-816	-9.548	22.277	25.305
LCA-817	2.680	21.362	18.442
LCA-818	1.677	13.462	23.498
LCA-819	-4.108	22.154	24.387
LCA-820	-0.697	13.560	22.130
LCA-821	6.877	17.262	19.784
LCA-822	3.749	16.060	25.376
LCA-823	2.005	14.860	16.654
LCA-824	0.322	9.307	20.225
LCA-825	-3.945	27.314	16.057
LCA-826	-8.099	12.999	18.283
LCA-827	3.848	13.492	16.331
LCA-828	0.790	11.557	15.149
LCA-829	0.049	20.872	25.852
LCA-830	-1.278	14.047	16.173
LCA-831	-2.309	20.414	17.354
LCA-832	-2.091	18.450	18.826
LCA-833	-3.618	18.114	21.679
LCA-834	3.917	15.422	16.925
LCA-835	-1.999	10.588	19.184
LCA-836	4.464	18.727	15.380
LCA-837	2.802	16.557	15.005
LCA-838	3.997	9.047	20.217
LCA-839	2.574	15.098	20.739
LCA-840	-1.302	14.971	19.348
LCA-841	3.176	18.655	14.944
LCA-842	5.506	19.717	16.350
LCA-843	7.157	14.985	19.873
LCA-844	-0.188	13.630	20.381
LCA-845	-4.985	21.065	19.832
LCA-846	-1.103	24.270	15.022
LCA-847	10.977	19.567	20.127
LCA-848	-1.635	16.492	20.234
LCA-849	-0.790	19.374	19.371
LCA-850	7.527	20.575	23.666
LCA-851	3.236	22.739	15.427
LCA-852	4.757	16.098	25.454
LCA-853	-1.919	17.020	18.253
LCA-854	-4.881	15.907	15.487
LCA-855	1.831	17.484	14.046
LCA-334	9.736	18.645	17.528
LCA-353	4.321	14.661	19.931

Table 7 Clustering of 57 chilli (*Capsicum annuum* L.) genotypes by Ward's minimum variance method.

Cluster No.	No. of genotypes	Name of genotype(s)
I	11	LCA -801, LCA-854, LCA-831, LCA-845, LCA-832, LCA-849, LCA-853, LCA-811, LCA-805, LCA-825, LCA-846
II	3	LCA-819, LCA-829, LCA-816
III	8	LCA-814, LCA-842, LCA-836, LCA-817 LCA-851, LCA-841, LCA-837, LCA-855
IV	4	LCA-815, LCA-847, LCA-334, LCA-850
V	4	LCA-802, LCA-835, LCA-809, LCA-826
VI	15	LCA-807, LCA-808, LCA-804, LCA-803, LCA-810, LCA-812, LCA-824, LCA-838, LCA-828, LCA-830, LCA-823, LCA-821, LCA-353, LCA-827, LCA-834
VII	5	LCA-813, LCA-843, LCA-822, LCA-852, LCA-818
VIII	7	LCA-820, LCA-839, LCA-833, LCA-848, LCA-840, LCA-844, LCA-806

Table 8. Intra- and inter- cluster Euclidean^2 distance between eight clusters formed by Ward's minimum variance method in 57 chilli (*Capsicum annuum* L.) genotypes.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**191.3**	348.9	295.3	700.1	551.6	392.5	577.7	278.5
Cluster II		**183.4**	641.1	908.0	728.2	700.0	626.3	410.3
Cluster III			**168.1**	397.1	706.9	344.7	467.3	337.8
Cluster IV				**203.2**	1176.4	555.2	406.7	619.5
Cluster V					**275.1**	429.4	665.3	395.7
Cluster VI						**202.0**	389.5	278.5
Cluster VII							**279.4**	327.5
Cluster VIII								**128.7**

Bold figures in the diagonal indicate intra-cluster distance.

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