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Assessment of genetic diversity in chilli (*Capsicum annuum* L.) genotypes

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Abstract
Sixty three chilli genotypes were evaluated to understand the extent of genetic diversity through 16 yield and yield attributing characters. Genetic diversity among 63 genotypes based on 16 characters was worked out using Mahalanobis D^2 statistics. Based on genetic distance these genotypes were grouped into seven clusters. Cluster I was the largest having thirty-eight genotypes followed by cluster II with nineteen genotypes, cluster VI with two genotypes, cluster III, cluster V, cluster VI and cluster VII had one genotype each. The maximum intra cluster distance was in cluster II followed by cluster I whereas maximum inter cluster distance was between cluster IV and cluster V. The character red ripe fruit yield per plant contributed maximum towards genetic diversity followed by green fruit yield per plant. Hence, selection of parents differing in traits may be useful in heterosis breeding programme.

Keywords: Chilli, genetic diversity, inter cluster, intra cluster

Introduction
Chilli (*Capsicum annuum* L.) is one of the popular spice crops grown in India and many parts of the world. It belongs to the family Solanaceae having chromosome number 2n=24. The primary centre of origin of chilli is said to be Mexico with secondary centre in Guatemala and Bulgaria (Salvador, 2002) [12]. Chilli plays a pivotal role in Indian cuisine and it is cultivated one of the most important cash crops in India. It is rich source of vitamin A, B, C, E and P and it has commercially two important qualities, the pungency in chilli is due to chemical constituent capsanthin and red colour is due to pigment capsanthin. Since is often cross-pollinated crop exhibit wide range of variability and diversity with a tremendous scope for genetic studies and improvement by breeding. However, the high variability present in the crop has so far not been fully exploited in the crop improvement programmes.
The selection of parents for the purpose of hybridization depends on the existence of genetic diversity and productivity of chilli is low due to the unimproved genotypes. It offers much scope to study for assessing genetically divergent genotypes for future breeding programmes. Assessment of genetic diversity among the available germplasm is a prerequisite for plant breeders due to reason that crosses between highly divergent parents tend to produce high heterotic effect (Ramanujam *et al.*, 1974) [9] and crosses involving distantly related parents within the same species produce wide spectrum of variability. Genetic divergence has been used as an indirect parameter of moderate effectiveness in selecting parental lines to produce high yielding progenies. Success of the hybridization followed by selection depends largely on the selection of parents with high genetic diversity for traits of interest (Murthy and Arunachalam, 1966) [8]. This experiment was undertaken to study genetic diversity and selection of suitable genotypes for future hybridization programme.

Material and Methods
The present study was conducted at College of Horticulture, Mudigere which is located zone - 9 of Karnataka. The material for the present study comprised of 63 genotypes evaluated in Augmented Randomized Block Design (ARBD) with fifteen blocks during rabi 2019-20. Each block contains four genotypes with two checks. The seedlings were planted in a fashion accommodating 30 plants in each treatment at spacing of 45 cm line to line and 30 cm plant to plant. The package of practices and protection measures were taken according to the recommendations for raising the crop successfully. Five randomly selected plants from each genotype were observed for recording various quantitative characters for each genotype in

each block. The genetic divergence analysis was done by using Mahalanobis D^2 statistics and genotypes were grouped into clusters by the Tocher's method given by Rao (1952) [10].

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating considerable amount of genetic variability for all the characters and thereafter the diversity analysis was carried out. The multivariate analysis based on Mahalanobis D^2 statistics is used as powerful tool to measure genetic divergence among the genotypes. In the present investigation based on D^2 values all the genotypes were categorised into seven different clusters presented in Table 1. Cluster I was the largest having thirty-eight genotypes followed by cluster II with nineteen genotypes, cluster VI with two genotypes, cluster III, cluster V, cluster VI and cluster VII were solitary clusters. Genotypes obtained from different geographical locations were grouped into a single cluster. It indicates that genetic diversity and geographical diversity do not tally. This is in agreement with the findings of Misra *et al*. (2011) [7], Hasan *et al*. (2015) [5], Janaki *et al*. (2016) [6], Farhad *et al*. (2010) [2], Yatung *et al*. (2014) [11] and Gawande *et al*. (2018) [3]. Cluster II with nineteen genotypes showed maximum intra cluster distance. The distance between clusters IV and V was the highest and this was followed by the distance between clusters IV and VII. This indicates that the genotypes in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids and broad spectrum of variability in segregating generations. Similar results were recorded by Farhad *et al*. (2010) [2], Gogate *et al.* (2011) [4] and Yatung *et al.* (2014) [11]. Cluster I had the least inter-cluster (1136.84) with cluster III suggesting that genetic constitution of these genotypes in one cluster is in close proximity with the genotypes in another cluster.

Genetically distant parents are likely to yield superior recombinants a breeding programme may be initiated between the selected genotypes belonging to different clusters considering their cluster means presented in Table 3. The highest cluster mean was recorded in cluster V for days to first flowering (61.00) and days to 50 percent flowering (71.00). The highest cluster mean was recorded in cluster IV for days to first picking (92.50), number of green fruits per plant (124.73) and number of red ripe fruits per plant (107.40). The highest cluster mean for number of primary branches was observed in the cluster II (4.98) followed by cluster I (4.91) and the lowest cluster mean was observed in the cluster IV (3.33). The highest cluster mean was observed in cluster VI for number of secondary branches (17.99), green fruit diameter (2.50), green fruit weight (18.50), green fruit yield per plant (1810.78), red ripe fruit weight (17.55) and red ripe fruit yield per plant (1075.46). The highest cluster mean was noticed in cluster VII for plant height (80.35), green fruit length (13.25), red ripe fruit length (12.67) and red ripe fruit diameter (3.07). This indicated that none of the cluster contained genotypes with all the desirable characters which could be directly selected and utilized. The results are similar to Hasan *et al*. (2015) [5] Bijalawan *et al*. (2018) [1] and Gawande *et al*. (2018) [3].

Relative contribution of sixteen characters towards total genetic divergence (Table 4) revealed that red ripe fruit yield per plant (36.61%) contributed maximum to total divergence followed by green fruit yield per plant (32.97%), plant height (12.24%), number of green fruits per plant (5.79%), number of red ripe fruits per plant (4.25%), green fruit weight (3.69%), days to first flowering (1.69%), red ripe fruit weight (1.13%), green fruit length (0.97%), red ripe fruit length (0.46%), number of secondary branches (0.15%) and green fruit diameter (0.05%). However, traits like days to 50 percent flowering, days taken for first picking, number of primary branches and red ripe fruit diameter had no substantial contribution to total divergence.

Table 1: Classification of chilli genotypes into different clusters for various quantitative traits based on D^2 value.

Clusters	Number of genotypes	Genotypes included in the cluster
I	38	Green long chilli, IC-545649, IC-545661, IC-111593, IC-545727, Badami local, IC-545664, IC-119547, IC-119590, Gottikunte-1, Gottikunte-2, IC-545730, IC-119587, IC-545733, IC-545668, IC-545734, Hindupur, IC-545729, Srinivaspura, IC-119576, Balapuram, IC-545723, Pusa Jwala, IC-545720, IC-545658, IC-119585, LCA-353, LCA-620, G-4, IC-545725, IC-545653, G-3, IC-545660, Kolar, Chowdampalli-1, IC-545731, IC-545651, IC-119556
II	19	IC-545669, IC-545665, Byadagi, IC-545655, Piryapattana, Hosahudya local, LCA-235, IC-119563, LCA-625, Bagepalli, IC-119560, LCA-334, IC-545663, IC-545648, IC-545652, IC-545732, IC-545721, IC-545728, IC-119552
III	1	IC-545724
IV	2	IC-545667, IC-545735
V	1	Chowdampalli -2
VI	1	IC-545662
VII	1	IC-276117

Table 2: Average intra (diagonal) and inter cluster distance (D^2) for sixteen characters formed by sixty three genotypes of chilli.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	590.63	2649.89	1136.84	6627.72	1164.47	1814.4	1205.6
Cluster II		692.59	2195.21	1662.62	5709.34	1616.63	3442.04
Cluster III			0	5047.93	2379.26	2187.37	3083.36
Cluster IV				413.05	11578.00	3697.7	7887.45
Cluster V					0	4134.66	1792.64
Cluster VI						0	1551.63
Cluster VII							0

Table 3: Cluster mean values of sixteen characters for seven clusters in chilli genotypes.

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16
Cluster I	54.92	66.71	90.58	52.04	4.91	9.25	9.28	2.41	65.55	9.45	600.15	8.39	2.25	55.68	8.30	451.23
Cluster II	53.32	65.47	91.26	54.86	4.98	9.03	10.43	1.32	95.98	5.34	510.85	9.05	1.53	88.24	4.45	380.31
Cluster III	50.00	62.00	84.00	28.95	4.50	10.00	9.55	1.35	78.70	5.50	432.85	6.90	1.07	59.70	4.30	256.71
Cluster IV	52.00	66.50	92.50	50.10	3.33	7.77	8.95	1.30	124.73	4.93	610.18	7.07	1.22	107.40	4.56	481.51
Cluster V	61.00	71.00	92.00	50.00	4.15	10.00	9.00	1.00	45.20	6.23	326.81	9.20	1.10	36.43	4.40	160.29
Cluster VI	55.00	64.00	89.00	65.45	4.26	17.99	12.95	2.50	97.88	18.50	1810.78	9.33	2.03	61.28	17.55	1075.46
Cluster VII	56.00	61.00	90.00	80.35	3.90	8.00	13.25	2.25	66.80	11.33	756.51	12.67	3.07	49.67	10.29	511.07

Table 4: Percent contribution of different quantitative characters to the total divergence in chilli genotypes.

Source	Contribution%	Times ranked 1st
Days to first flowering	1.69	33
Days to 50 percent flowering	0.00	0.00
Days taken for first picking	0.00	0.00
Plant height (cm)	12.24	239
Number of primary branches	0	0
Number of secondary branches	0.15	3
Green fruit length (cm)	0.97	19
Green fruit diameter (cm)	0.05	1
Number of green fruits per plant	5.79	113
Green fruit weight (g)	3.69	72
Green fruit yield per plant (kg)	32.97	644
Red ripe fruit length (cm)	0.46	9
Red ripe fruit diameter (cm)	0	0
Number of red ripe fruits per plant	4.25	83
Red ripe fruit weight (g)	1.13	22
Red ripe fruit yield per plant (kg)	36.61	715

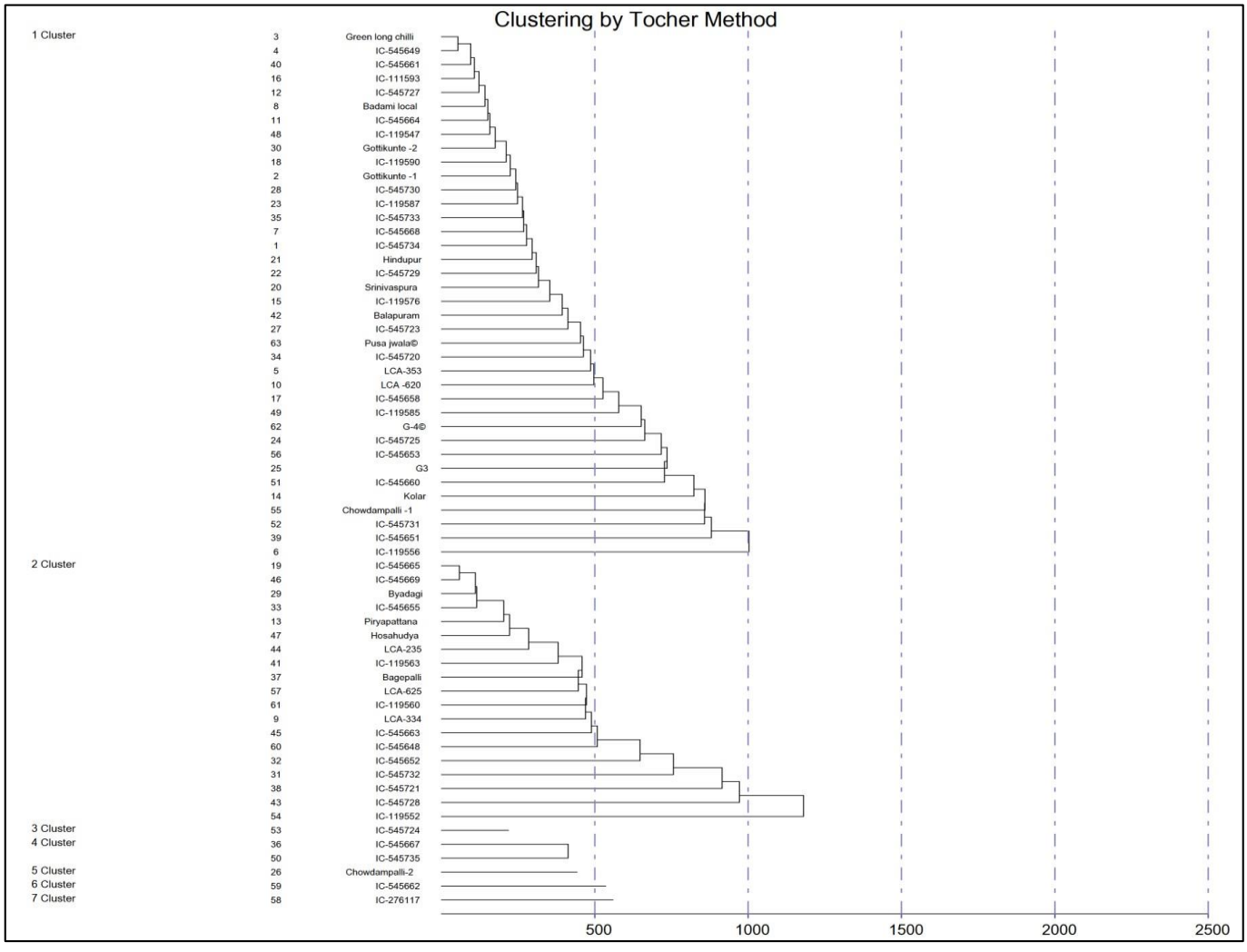

Fig 1: Dendrogram showing the genetic diversity among 63 genotypes of chilli

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