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Assessment of genetic diversity in different Chilli (Capsicum annuum L.) genotypes

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Abstract

Fort five genotypes of chilli (*Capsicum annuum* L.) were investigated to understand the extent of genetic diversity through ten growth and yield attributing characters. Genetic diversity in chilli genotypes based on ten characters was estimated using Mahalanobis's D^2 statistics. The genotypes were grouped into six different clusters. Cluster I is the largest cluster having 29 genotypes, followed by cluster II with 12 genotypes, cluster III, V and VI cluster had one genotype each. The highest mean for Days to 50 per cent flowering was observed in the cluster VI (105) followed by cluster II (103.50), cluster I (102.64), cluster IV (101.00). The lowest mean was observed in the Cluster IV (95.00). The highest mean for Days to first picking was observed in the Cluster IV (152.00). The lowest mean was observed in the Cluster V (137.50). The highest mean for Yield per plant was observed in the Cluster VI (279.75) and lowest mean was observed in the Cluster I (2.38). The lowest mean was observed in the Cluster IV and Cluster IV (1.50).

Keywords: Chilli, genetic divergence and cluster analysis

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, 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) ^[10]. However, the high variability present in thecrop 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.*, In the hybridization programme, genetically diverse parents likely to produce high Hetrosis effect, and 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) [3, 9, 2]. Therefore, the present study was undertaken to assess the genetic diversity in 45genotypes of chilli to identify suitable genotypes.

Materials and Methods

The study was carried out at College of Horticulture, Bidar in a randomized block design with two replications to evaluate most promising genotypes with respect to the yield and quality parameters among the 45 genotypes of chilli.

Each genotype was raised with a spacing of 60 cm x 45 cm. The crop was grown with standard package of practices of University of Horticultural sciences, Bagalkot. The observations were recorded on nine economic traits from five randomly selected competitive plants from each genotypes and replication. Mahalanobis (1928) ^[13] generalized distance, D^2 – statistic was used for computing genetic divergence as described by Rao (1952) ^[11]. The original measurements were transformed to standardized uncorrelated variables by pivotal condensation (Rao, 1952) ^[11]. 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 (Vij). Following Tocher's method as described by Rao (1952)^[11], 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 intracluster distances were determined and represented.

Results and Discussion

Forty-five chilli genotypes were evaluated for ten traits to study the divergence and the obtained data was subjected to D^2 analysis. As many as six divergent clusters were grouped by using Trocher's method.

The relative contribution of different characters for genetic parameters for genetic divergence (D^2) is given in the Table 1. Yield per plant (30.40%) contributed maximum to the total divergence among the genotypes followed by Fruit width

(21.11%), Days to 50% flowering (12.93%), Test weight (11.82%), Fruit length (10.00%), Plant height (7.37%), Number of fruits per plant (4.34%) and Days to first picking (1.31%), Number of branches per plant (0.40%), and Incidence of leaf curl (0.30%). This is in agreement with the findings of other researchers (Mishra *et al.*, 2011; Hasan *et al.*, 2014; Janaki *et al.*, 2016) ^[7, 4, 5].

By adopting the method suggested by Trocher's (Rao, 1952) ^[11], Forty-five genotype were grouped into six clusters by treating estimated D^2 values as the squares of generalized distances. The distribution pattern of genotypes into various clusters is given in Table 2.

Cluster I is the largest cluster having 29 genotypes, followed by cluster II with 12 genotypes, cluster III, V and VI cluster had one genotype each. The highest mean for Days to 50 per cent flowering was observed in the cluster VI (105) followed by cluster II (103.50), cluster I (102.64), cluster IV (101.00). The lowest mean was observed in the Cluster V (95.00). The highest mean for Days to first picking was observed in the Cluster IV (152.00) followed by Cluster VI (151.00). The lowest mean was observed in the Cluster V (137.50). The highest mean for Yield per plant was observed in the Cluster VI (279.75) followed by Cluster II (234.15). The lowest mean was observed in the cluster I (259.33). The highest mean for Incidence of leaf curl was observed in the Cluster III (2.50) followed by cluster I (2.38). The lowest mean was observed in the Cluster IV and Cluster VI (1.50). Similar results were reported by Ullah et al., (2011)^[12], Chaudhary et al., (2013) ^[1] and Nahak *et al.*, 2018 ^[18].

Table 1: Rank and per cent contribution of quantitative traits towards total genetic diversity in chilli

Source	Times ranked 1 st	Contribution (%)		
Days to 50% flowering	128	12.93%		
Days to first picking	13	1.31%		
Plant height (cm)	73	7.37%		
Number of branches per plant	4	0.40%		
Number of fruits per plant	43	4.34%		
Fruit length (cm)	99	10.00%		
Fruit width (cm)	209	21.11%		
Test weight	117	11.82%		
Yield per plant	301	30.40%		
Incidence of leaf curl	3	0.30%		

Table 2: Clustering and distribution of 45 chilli genotypes based on yield parameters

Cluster No.	Number of accessions	Germplasm accessions				
	I 29	GPM-5, KA-2, GPM-41, BK Sel-1, GPM-31, KDL Deluxe, KCA-19-1, GPM-37, G-4, GPM-60, Pusa				
Ι		Jwala, Parekh, KCA-20-1, GPM-59, GPM-55, GPM-39, KCA-17-1, GPM-43, GPM-36, GPM-52, GPM-				
		45, GPM-34, GPM-38, GCA-2, GPM-51, GPM-54, KCA-21-1, BK Sel-2, GPM-40.				
п	II 12	GPM-42, KCA-18-1, KCA-2, GCA-1, HP-2, GPM-58, GPM-56, KCA-24-1, GPM-33, Pragna, BD Sel-1,				
11	12	Nalchatti				
III	1	GPM-34				
IV	1	Achari				
V	1	Bamra				
VI	1	Reshem Patto				

Table 3:	Cluster mean of	10 quantitative	traits in chilli	genotypes
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Traits Clusters	flowering	Days to first picking	Plant height (cm)	Number of branches per plant	Number of fruits per plant	Fruit length (cm)	Fruit width (cm)	Test weight	1	Incidence of leaf curl
Cluster I	102.64	148.60	33.62	8.02	10.55	6.30	8.35	4.51	109.91	2.38
Cluster II	103.50	150.79	38.65	7.50	17.50	6.79	9.85	4.52	234.15	1.71
Cluster III	96.00	142.50	30.00	13.00	17.50	3.90	9.38	3.33	112.75	2.50
Cluster IV	101.00	152.00	27.25	5.25	13.00	5.60	17.26	3.69	82.50	1.50
Cluster V	95.00	137.50	27.50	9.34	10.00	2.88	4.63	4.49	40.00	2.00
Cluster VI	105.00	151.00	43.50	7.38	9.00	6.27	24.07	5.55	279.75	1.50

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