Original Research Article

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

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A B S T R A C T

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Twenty nine chilli genotypes were evaluated on the basis of seven yield and yield contributing characters for genetic diversity studies as suggested by Mahalanobis D^2 statistics. The experiment was conducted at Chilli and Vegetable Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (MS) during kharif 2012-13. The 29 chilli genotypes were grouped in nine clusters. Maximum genotypes were grouped in cluster I followed by Cluster II and IV while six clusters found to be solitary having one genotypes in each cluster. The maximum intra cluster distance was in cluster IV followed by cluster II whereas maximum inter-cluster distance was exhibited between cluster IV and VI. An assessment of relative contribution of seven characters towards total genetic divergence revealed that fruit length had contributed highest by taking 108 times first ranking followed by plant spread E x W by 81 times and fruit girth by 61 times.

Introduction

Chilli (*Capsicum annuum* L.) is used as spices nit in India but also thorough the world on account of its pungency and pleasant flavours. The consumption of small amount enriches our diet and considered as good source of minerals, vitamins and other food components. Chilli is a crucial condiment in Indian cuisine and is cultivated as one of the important cash crop in India. Chilli is commercially important for two qualities, the red colour due to pigment capsanthin and the bitting taste due to the chemical constituent capsaicin. There are very few varieties available for cultivation and those are not widely adapted to different agro-climatic conditions. The lack of improved genotypes is the major constraints of low yield. It offers much scope for study of assessment of genetic diversity to select genetically diverse genotypes for future breeding programme. The plant breeders are always interested to know the genetic divergence among the varieties/genotypes available due to reasons that crosses between genetically diverse parents are likely to produce high heterotic effect. Genetic variation is essential for effective selection. In order to genetic variability, hybridization between genotypes of diverse origin is suggested to unlock new recombination. 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).

Therefore an effort was made to estimate the nature and magnitude of genetic diversity in a set of 29 genotypes of chilli.

Materials and Methods

The present experimental material comprised of 27 promising genotypes (Table 1) developed at chilli and Vegetable Research Unit, Dr. PDKV, Akola along with two varieties. The genotypes were evaluated through a field experiment conducted at Chilli and Vegetable Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (MS) in randomized block design with three replications during kharif 2012-13 spaced 60 cm between rows and 60 cm between plants. The fertilizer doses were as per the recommendations for commercial cultivation and cultural practices were followed as when required. Five plants were selected randomly for recording the observations on plant height (cm), fruit length (cm), fruit girth, plant spread E x W and plant spread N x S while fruit yield was recorded on plot basis and converted in qt./ha. by multiplying hectare factor. The data recorded was subjected to statistical analysis to estimate genetic divergence as suggested by Mahalanobis D^2 statistics (1936) and multivariate analysis named clustering analysis was performed. The data so generated is tabulated and discussed as under.

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 thereof the diversity analysis was carried out. The differences could be used in distinguishing genotypes on the basis of their morphology. Based on D^2 analysis all the genotypes were grouped into nine different clusters presented in Table 2, Cluster I and cluster II contained 11 and 7 genotypes followed by cluster IV which contains 5 genotypes while cluster III, V, VI, VII, VIII and IX were solitary with one genotype in each cluster. This indicated that there was a wide diversity among the genotypes for character studied. Similar results of solitary cluster were also reported by Farhad *et al.,* (2010) and Yatung *et al.,* (2014)

Since crosses among divergent parents are likely to yield desirable recombinants, a breeding programme may be initiated between the selected genotypes belonging to different clusters considering their cluster means presented in Table 3. Cluster means in Table 3 showed that maximum plant height and plant spread N x S exhibited by cluster IV followed by cluster III and cluster VIII. Highest cluster mean value for fruit length was recorded by cluster IX (8.80) followed by cluster I (8.68), cluster VIII (8.30) and cluster V (8.00) while lowest in cluster IV. Maximum fruit girth cluster mean value was observed in cluster VIII (1.20) followed by cluster VI (1.09), whereas cluster IX exhibited highest values for plant spread E x W followed by cluster VIII and IV. Cluster mean value for fruit yield per plot and quintal per hectare were recorded to be highest in cluster VII followed by cluster V, while clusters with the lowest values for this traits was cluster II. This indicated that none of the cluster contained genotypes with all the desirable characters which could be directly selected and utilized. The results so obtained are very much similar to the Karad, *et al.,* (2002) and Smitha and Basavaraja (2006) Also, most of the minimum and maximum mean values were distributed in relatively distant clusters. Therefore hybridization between genotypes falling in different clusters is necessary for development of desirable varieties.

Fig.1 Tree diagram of 29 genotypes of chilli for 7 studied characters using hierarchical cluster analysis
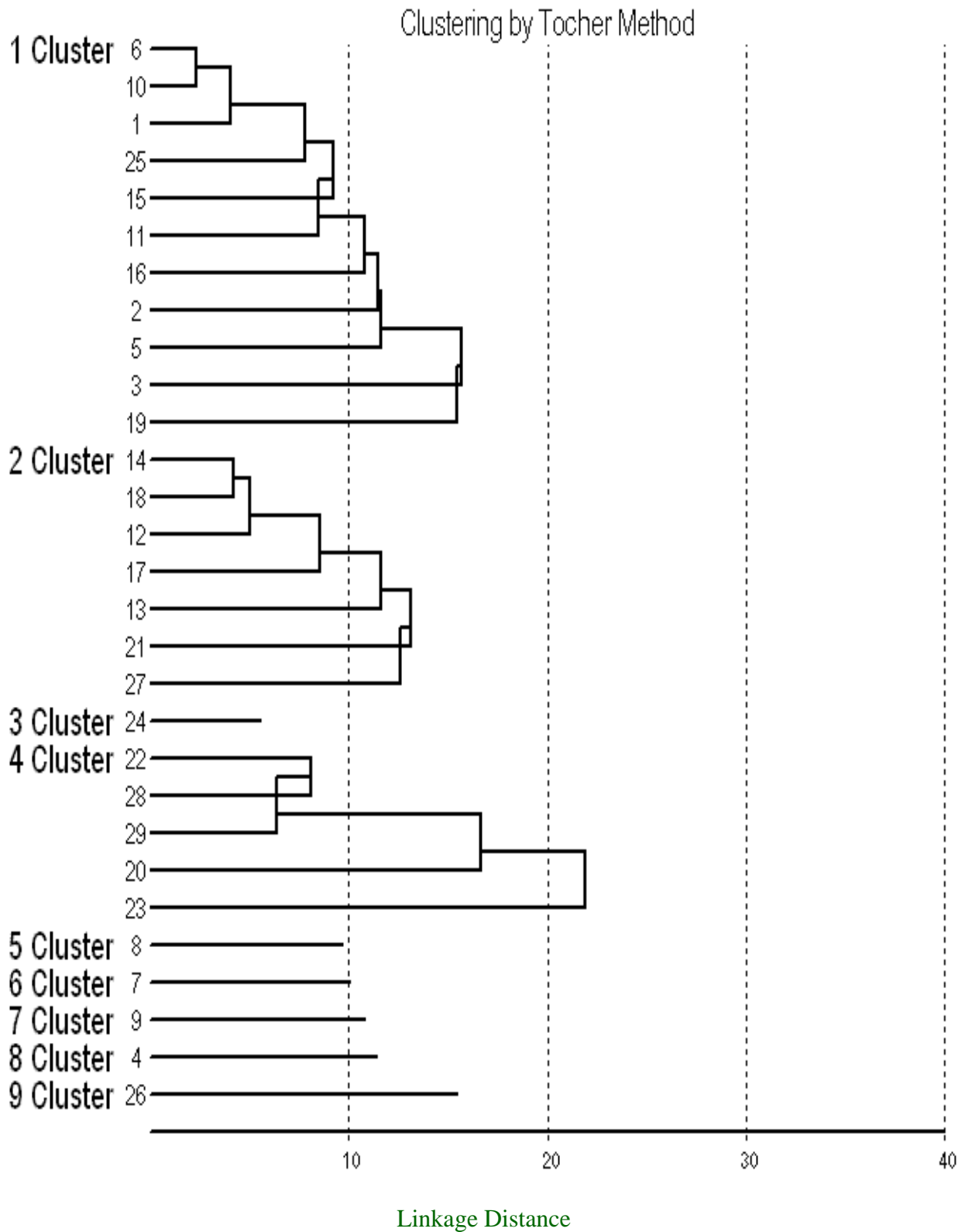

Linkage Distance

Table.1 The list of genotypes under study

Sr. No.	Genotypes / Varieties	Sr. No	Genotypes / Varieties
1	AKC-416	16	NCH-162-13-05-1
2	AKC-414	17	NCH-162-14-7-05
3	AKC-412	18	VS-685-05
4	AKC-411	19	NCH-162-05-14-7-3
5	AKC-423	20	Tej-F8-01-3-1-17-11-1-5-5
6	AKC-413	21	AKC-N-86-1
7	AKC-422	22	AKV-398
8	AKC-421	23	AKC-409
9	AKC-415	24	AKC-402
10	AKC-424	25	AKC-407
11	Jayanti	26	AKC-406
12	AKC-336	27	AKC-405
13	AKC-397	28	LCA-206
14	AKC-98-39	29	Pant- C-1
15	NCH-162-11-05		

Table.2 Clustering pattern of 29 chilli varieties by Tocher's Method

Cluster Group	Genotypes	Number of genotypes
Cluster I	AKC-416, AKC-414, AKC-412, AKC-423, AKC-413, AKC-424, Jayanti, NCH-162-11-05, NCH-162-13-05-1, NCH-162-05-14-7-3, AKC-407	11
Cluster II	AKC-336, AKC-397, AKC-98-39, NCH-162-14-7-05, VS-685-05, AKC-N-86-1 AKC-405	07
Cluster III	AKC-402	01
Cluster IV	Tej-F8-01-3-1-17-11-1-5-5, AKV-398. AKC-409, LCA-206, Pant- C-1	05
Cluster V	AKC-421	01
Cluster VI	AKC-422	01
Cluster VII	AKC-415	01
Cluster VIII	AKC-411	01
Cluster IX	AKC-406	01

Table.3 Cluster means for 7 characters of 29 chilli varieties

SN	Components	Clusters								
		I	II	III	IV	V	VI	VII	VIII	IX
1	Plant height	72.96	64.47	82.09	84.61	70.57	76.37	71.13	78.65	72.15
2	Fruit length	8.68	6.84	7.90	5.77	8.00	7.70	6.62	8.30	8.80
3	Fruit girth	0.98	0.81	0.86	0.78	1.00	1.09	1.00	1.20	0.75
4	Plant spread ExW	57.51	54.98	65.67	75.04	40.50	36.95	47.21	75.05	93.00
5	Plant spread NxS	57.26	49.67	68.33	66.30	42.30	26.74	58.63	60.45	60.35
6	Fruit yield per plot	4.14	3.41	4.44	3.88	5.03	4.83	5.20	4.87	4.50
7	Fruit yield qt. per ha.	35.92	29.62	38.53	33.69	43.69	41.95	45.14	42.24	39.09

Table.4 Average intra and inter cluster distance (D^2) for 29 chilli varieties

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	13.48	31.62	19.78	74.00	21.40	44.31	26.64	20.98	37.12
II		**13.26**	27.71	36.89	40.36	56.73	30.68	45.68	36.97
III			**0.00**	45.00	32.05	64.06	22.53	21.91	24.05
IV				**20.32**	91.86	111.67	50.75	68.87	51.91
V					**0.00**	10.01	15.87	37.84	73.35
VI						**0.00**	3549	62.01	109.02
VII							**0.00**	30.18	59.26
VIII								**0.00**	26.94
IX									**0.00**

Table.5 Percentage of ancillary characters towards total divergence

Sr. No.	Characters	Times ranked	Contribution (%)
1	Plant height (cm)	34	8.37
2	Fruit length (cm)	108	26.60
3	Fruit girth	61	15.02
4	Plant spread E X W	81	19.95
5	Plant spread N X S	60	14.78
6	Fruit yield per plot	53	13.05
7	Fruit yield qt/ per ha.	09	2.22

The average intra and inter cluster D^2 values were tabulated in Table no. 4 providing information that among the nine clusters, the intra cluster distance was maximum in cluster IV (20.32) followed by cluster II (13.26). The intra cluster distance of solitary cluster III, V, VI, VII, VIII and IX was zero. Further many reports Ajjappalavara, (2009), Dutonde, *et al.,* (2008) and Senapati, *et al.,* (2003) indicates the presence of intra cluster distance zero.

The cluster IV with only five genotypes namely Tej-F8-01-3-1-17-11-1-5-5, AKV-398, AKC-409, LCA-206 and Pant- C-1 exhibited maximum intra cluster distance. This cluster is most divergent group and genotypes falling in the cluster could be utilized as parents for hybridization. As far as inter cluster distance is concern, cluster IV and VI were found to be highly divergent from each other as indicated by maximum

D^2 value (111.67). This was followed by cluster VI and IX showing average inter cluster D^2 value of 109.02, cluster IV and V (D^2=91.88), cluster I and IV (D^2= 74.00) and cluster V and IX (D^2= 73.35). Parents selected from these individual groups showing maximum inter cluster distance are likely to produce superior recombinants. The minimum cluster distance was recorded between cluster V and VI (D^2 =10.01) and cluster V and VII (D^2 = 15.87) suggesting that genetic constitution of these genotypes in one cluster is in close proximity with the genotypes in other cluster.

An assessment of relative contribution of seven characters towards total genetic divergence (Table 5) revealed that fruit length had contributed highest (26.60 %) by taking 108 times first ranking followed by plant spread E x W (19.90 %) by 81 times, fruit girth (15.02 %) by 61 times, plant

spread N x S (14.78 %) by 60 times, fruit yield per plot (13.05 %) by 53 times, plant height (8.37 %) by 34 times and fruit yield quintal per hectare (2.22 %) by 9 times.

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