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**Savitha BK**  
Department of Vegetable  
Science, Tamil Nadu  
Agricultural University,  
Coimbatore, Tamil Nadu, India

**G Ashok Kumar**  
Department of Vegetable  
Science, Tamil Nadu  
Agricultural University,  
Coimbatore, Tamil Nadu, India

**S Rameshkumar**  
Department of Vegetable  
Science, Tamil Nadu  
Agricultural University,  
Coimbatore, Tamil Nadu, India

**C Indu Rani**  
Department of Vegetable  
Science, Tamil Nadu  
Agricultural University,  
Coimbatore, Tamil Nadu, India

**Corresponding Author:**  
**Savitha BK**  
Department of Vegetable  
Science, Tamil Nadu  
Agricultural University,  
Coimbatore, Tamil Nadu, India

## Breeding potential of chilli genotypes using D<sup>2</sup> analysis

**Savitha BK, G Ashok Kumar, S Rameshkumar and C Indu Rani**

### Abstract

The present investigation was carried out at Dept. of Vegetable Science, HC & RI, TNAU, Coimbatore. All the genotypes were grouped into D<sup>2</sup> values, which exhibited no association between geographical and genetic divergence. At the intra cluster level, the maximum D<sup>2</sup> distance was noticed in cluster VII, followed by cluster I. At the inter cluster level, the maximum D<sup>2</sup> distance was observed between cluster V and VI, followed by that between cluster I and V. The least inter cluster distance was recorded between clusters III and IV. On the basis of mean performance cluster I had the highest mean value for number of fruits per plant, where as cluster II had highest mean value for fruit weight. The mean values of plant height and fruit length and fruit girth were higher in cluster III. Cluster V had the highest mean value for number of branches, fresh fruit yield per plant and dry fruit yield per plant. The mean value of number of thrips per three apical leaves, reaction to thrips in 9 grade score and percentage of damaged plants were higher in cluster IX.

**Keywords:** Chilli, D<sup>2</sup> analysis, genetic divergence

### Introduction

Chilli (*Capsicum annum* L.) is one of the important commercial crops of India. It is a widely cultivated vegetable cum spice crop and plays an important role as a constituent in many of the world food industries (Basland and Votava, 2000) [1].

It is a crop of tropical and sub-tropical regions and requires warm humid climate. The chillies are believed to be originated in the tropical America (Raju and Lukose, 1991) [5] and known from pre-historic times in Peru. Columbus carried chilli seed to Spain in 1493. The cultivation of chilli spread rapidly from Spain to Europe. The crop was introduced into India by the Portuguese in the 16<sup>th</sup> century AD and by the 19<sup>th</sup> century its cultivation spread throughout the country.

Wide diversity among genotypes of chilli was observed by Singh and Singh (1976a) [7]. The pattern of D<sup>2</sup> clusters obtained showed that the geographic distribution was not related to the genetic diversity. The 116 genotypes studied were grouped into 10 clusters depending on similarities of their D<sup>2</sup> values. An assessment of degree of divergence between populations by multivariate analysis helped to trace out the pattern of evolutionary process in many crop plants. An assessment of divergence is also useful in choosing desirable parents, which can be effectively used for achieving specific breeding objectives. It is well recognized by all the breeders that any breeding programme depends largely on the degree of genetic divergence of the parents involved in hybridization.

### Materials and Methods

The present investigation was carried out at the department of vegetable crops, Horticultural College and Research Institute, Coimbatore (T.N.). The experimental materials comprised of 116 genotypes of chilli collected from different parts of India. The experiment was laid out in a randomized block design with two replications. A spacing of 60 x 45 cm was maintained and all the recommended agronomic package of practices were followed. Eleven biometrical observations (plant height, number of branches per plant, number of fruits per plant, fruit length, fruit girth, fruit weight, red fruit yield per plant, dry fruit yield per plant, number of thrips per three apical leaves, reaction to thrips in nine grade score and percentage of damaged plants) were recorded in parents in order to check their divergence. Genetic diversity was studied based on D<sup>2</sup> analysis.

It is one of the potent techniques of measuring genetic diversity in plant breeding. The  $D^2$  analysis was done by using the GENRES statistical package. The quantitative measurement of genetic divergence among genotypes can be found out by  $D^2$  Mahalanobis statistics (Rao, 1952) [6].

### Results and Discussion

On the basis of  $D^2$  values, the 116 genotypes were grouped into ten highly divergent clusters (Table 1) when the tocher value was fixed at 28.90. The cluster divergence was proved

by the high intercluster and low intra-cluster  $D^2$  values. Cluster I consisted of 5 genotypes, Clusters II (46 genotypes), cluster III, IV, V, VI, IX (2 genotypes each), cluster VII (6 genotypes), cluster VIII (5 genotypes) and cluster X (44 genotypes). The cluster comprising of two genotypes (III, IV, V, VI, IX) with specific valuable traits and other genotypes falling in the highly divergent groups will help in broadening the existing genetic base and may produce new genotypes with hitherto unknown combinations.

**Table 1:** Distribution of 116 genotypes in different clusters

Cluster No.	No. of genotypes	Name of genotypes
I	5	CA 36, CA 97, CA 107, CA 64, CA 7
II	46	CA 67, CA 180, CA 188, CA 121, CA 58, CA 183, CA 112, CA 20, CA 72, CA 96, CA 126, CA 106, CA 92, CA 18, CA 176, CA 31, CA 174, CA 111, CA 172, CA 11, CA 1, CA 178, CA 4, CA 101, CA 163, CA 162, CA 104, CA 159, CA 17, CA 2, CA 139, CA 189, CA 175, CA 168, CA 160, CA 182, CA 28, CA 207, CA 119, CA 193, CA 45, CA 6, CA 197, CA 80, CA 82, CA 173
III	2	CA 27, Selection-1
IV	2	CA 52, CA 186
V	2	CA 190, Kashi Anmol
VI	2	CA 63, CA 171
VII	6	CA 192, CA 165, CA 25, CA 141, CA 179, CA 177
VIII	5	CA 166, CA 208, CA 29, CA 199, 09CHIVAR03
IX	2	CA 54, CA 161
X	44	CA 181, CA 10, CA 118, CA 185, CA 24, CA 201, CA 117, CA 88, CA 9, CA 247, CA 8, CA 110, CA 48, CA 75, CA 41, CA 15, CA 53, CA 164, CA 116, CA 108, CA 77, CA 71, CA 103, CA 66, CA 46, CA 30, CA 170, CA 169, CA 205, CA 158, CA 21, CA 167, CA 70, CA 60, CF 1, CF 2, CA 200, CA 191, CA 187, CA 184, CA 49, ACS 06-01, 09CHIHBY07, K-1

Average intra and inter cluster  $D^2$  distance values are presented in Table 2.

At the intra cluster level, the maximum  $D^2$  distance was noticed in cluster VII (4.717), followed by cluster I (4.033) indicated that genotypes included in this cluster are very diverse and was due to both natural and artificial selection forces among the genotypes. At the inter cluster level, the maximum  $D^2$  distance (6.110) was observed between cluster V and VI, followed by that between cluster I and V (5.770)

indicated that the genotypes included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregating population. The least inter cluster distance (2.583) was recorded between clusters III and IV indicated close relationship among the genotypes involved in these clusters. Similar results were revealed by Sreelathakumary and Rajamony (2004a) [8], Thul *et al.* (2009) [9] and Parthsinh *et al.*, (2021) [4].

**Table 2:** Estimates of average intra and inter cluster distance for the clusters constructed from 116 genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	4.033	4.172	3.956	4.572	5.770	4.488	4.581	3.778	4.284	4.051
II	4.172	3.777	3.233	3.718	5.123	4.274	4.371	4.138	3.261	3.659
III	3.956	3.233	0.637	2.583	4.822	3.547	4.081	3.825	3.054	3.012
IV	4.572	3.718	2.583	0.639	3.963	4.894	5.007	4.622	2.825	3.755
V	5.770	5.123	4.822	3.963	0.661	6.110	6.007	5.648	4.393	5.119
VI	4.488	4.274	3.547	4.894	6.110	0.866	4.757	3.701	4.279	3.885
VII	4.581	4.371	4.081	5.007	6.007	4.757	4.717	4.621	4.186	4.242
VIII	3.778	4.138	3.825	4.622	5.648	3.701	4.621	3.915	4.227	3.933
IX	4.284	3.261	3.054	2.825	4.393	4.279	4.186	4.227	1.324	3.369
X	4.051	3.659	3.012	3.755	5.119	3.885	4.242	3.933	3.369	3.512

The cluster mean of 116 genotypes (Table 3) showed that the mean value of clusters varied in magnitude for all the eleven characters. Genotypes in cluster I had the highest mean value

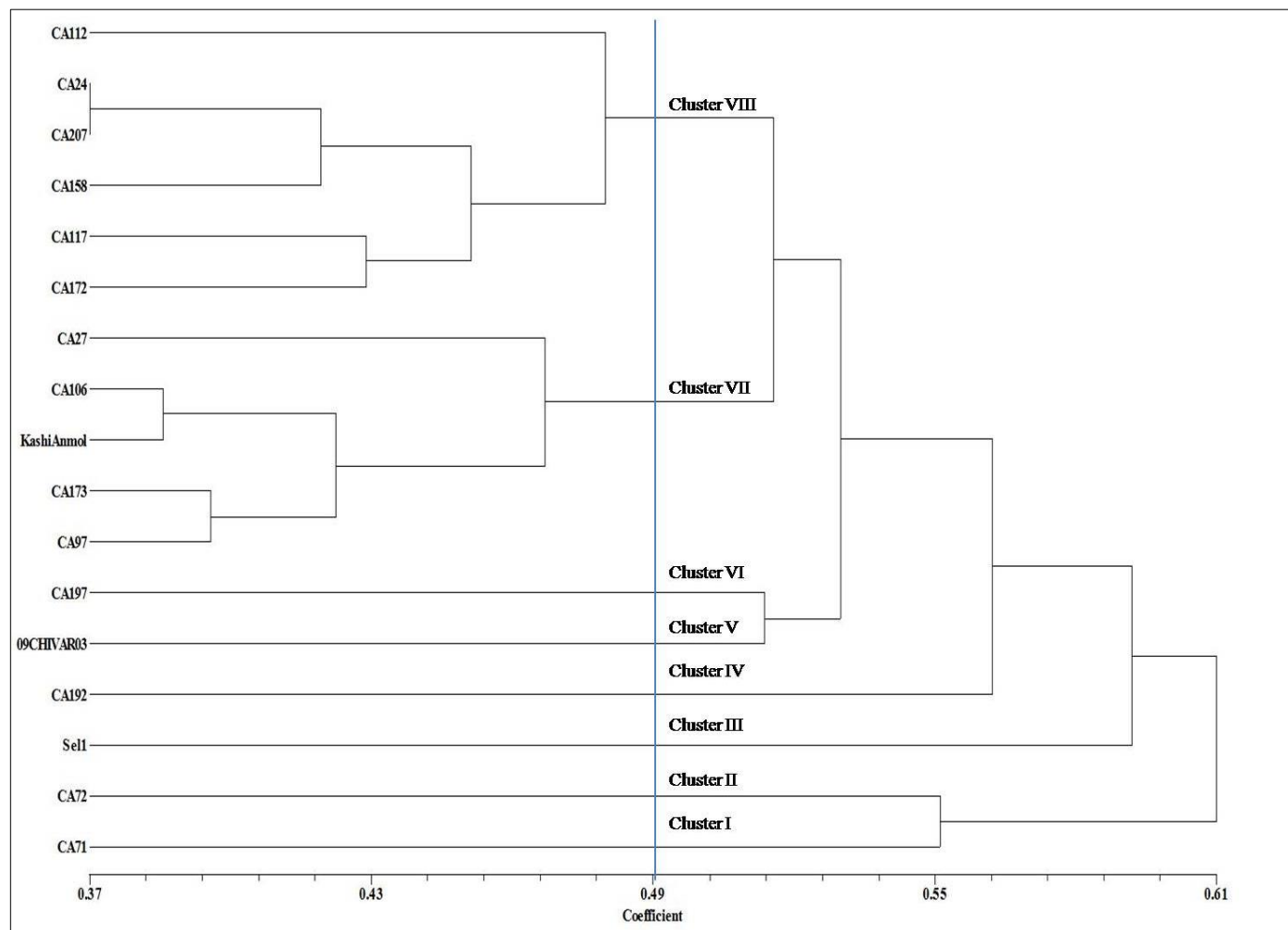
(62.44) for number of fruits per plant, where as cluster II had highest mean value for fruit weight (3.79).

**Table 3:** Mean value of different characters in various clusters

Characters	Clusters									
	I	II	III	IV	V	VI	VII	VIII	IX	X
Plant height (cm)	60.74	64.97	80.20	55.45	50.25	60.55	72.47	68.80	73.65	70.14
No.of branches	5.16	4.96	5.10	4.70	5.85	3.20	5.10	4.84	4.55	5.16
No. of fruits/plant	62.44	41.39	33.75	56.98	62.30	31.95	62.36	53.41	31.40	48.33
Fruit length (cm)	6.10	6.51	10.09	4.25	6.95	6.60	6.13	7.82	6.25	6.70
Fruit girth (cm)	3.47	3.15	4.25	2.74	3.17	3.42	2.87	2.91	3.57	3.14
Fruit weight (g)	3.45	3.79	3.21	3.48	3.70	2.68	3.77	3.75	3.62	3.77
Red fruit yield/plant (g)	134.31	146.46	102.39	161.04	223.56	76.73	190.06	195.98	106.32	164.71
Dry fruit yield/plant (g)	33.58	36.61	25.60	40.26	55.89	19.18	47.52	49.00	26.58	41.18
No.of thrips/3 apical leaves	3.56	3.70	3.20	4.70	3.85	4.10	5.07	4.52	5.40	4.67
Reaction to thrips in 9 grade score	3.52	4.25	4.15	4.40	4.30	4.40	5.80	4.48	5.80	5.10
Percentage of damaged plants	33.24	46.79	23.30	52.29	31.07	47.10	43.99	45.26	58.49	47.65

The mean values of plant height (80.20) and fruit length (10.09) and fruit girth (4.25) were higher in cluster III. Cluster V had the highest mean value for number of branches (5.85), fresh fruit yield per plant (223.56) and dry fruit yield per plant (55.89). The mean value of number of thrips per three apical leaves (5.40), reaction to thrips in 9 grade score (5.80) and percentage of damaged plants (58.49) were higher in cluster IX. Depending upon the aim of breeding, the potential lines to

be selected from different clusters as parents in a hybridization programme should be based on genetic distance. In accordance to the findings, Varalakshmi and Haribabu (1991)<sup>[10]</sup>, Mishra *et al.* (2004)<sup>[3]</sup> and Jogdhande Srinivas (2021)<sup>[2]</sup> the clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence.



**Fig 1:** Molecular diversity analysis of 17 Chilli genotypes using RAPD primes

**Conclusion**

For breeding programme aimed at higher yield, the genotypes from cluster V can be selected as parent showing highest mean yield per plant. To breed good varieties in small fruited group, selection from cluster IV will be highly useful and to

breed long fruited varieties, selection from cluster III will be useful. Thus, selection of divergent parents based on fruits per plant, yield per plant, fruit length, fruit girth and fruit weight should be involved in hybridization programme for getting desirable hybrids.

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