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ASSESSMENT OF GENETIC DIVERGENCE THROUGH CLUSTER ANALYSIS IN CHILLI (*CAPSICUM ANNUM* L.)

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ABSTRACT

Chilli crop development has so far been accomplished by utilising the existing sources of variability. Estimates of divergence across 36 chilli genotypes found that they differed significantly. The present experiment was conducted at Main Experiment Station of Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) during Rabi 2019- 20. Experimental material for the study consisted of 36 genotypes including one checks (KA-2). The clustering pattern of the thirty-six genotypes were grouped into ten different non- overlapping cluster. The Maximum inter cluster distance was observed between cluster X and IV which may be used for hybridization and desirable segregates in segregating generation. As a result, it may be assumed that selecting for these features will be useful to future chilli improvement efforts. Further, one or two promising genotypes from different clusters may be chosen for further genetic studies.

Keywords: Chilli, Cluster, Divergence

Introduction

Chilli (*Capsicum annum* L.) is a member of the Solanaceae family (2n=2x=24) (Nightshade). Because of the shape of the fruit, which neatly encloses seeds, the genus name Capsicum is derived from the Latin word 'capsa' meaning chest or box. Chilli is native to India but it is originated from 'South America" and these were brought to Asia by Portuguese at the end of 15th century. Chilli is one of the most important and the largest produced spice crop in Asia. Major chilli growing countries in world are India, China, Ethiopia, Myanmar, Mexico, Peru, Vietnam, Pakistan, Ghana, and Bangladesh. India tops among all of these in exporting chillies. *Capsicum annum* L., *Capsicum chinense* Jacq., *Capsicum frutescens* L., *Capsicum baccatum* L., and *Capsicum pubescens* L. are the only five domesticated and cultivated species in the genus Capsicum (Bosland and Votava, 2000). Red pepper is mainly used as vegetable, while green is used as spices when dried and processed. Its use in food, natural plant color, and as a pharmaceutical ingredient is extensive throughout the world. Chilli contains a range of essential nutrients and bioactive compounds which are known to exhibit antioxidant, antimicrobial, antiviral, anti-inflammatory and anticancer properties. It is an excellent source of Vitamin A, B, C, E and P (Quresh *et al.*, 2015). It is also a good source 'oleoresin', which permits better distribution of colour and flavour in foods (Chattopadhyay *et al.*, 2011).

Assessment of different desirable traits spread over diverse genotypes is important to rapid advance in yield improvement of any crop. The importance of genetic diversity in the improvement of a crop has been studied in both self & cross pollinated crop (Griffing and Lindstrom, 1954; Murthy and Anand, 1966; Gaur *et al.*, 1978). The plant breeders are always interested to know the genetic divergence among the varieties available due to reasons that crosses between genetically diverse parents are likely to produce high heterotic effect (Ramanujam *et al.*, 1974) and crosses

involving distantly related parents within the same species produce wide spectrum of variability. Genetic divergence analysis between genotypes is useful for identifying genetically varied parents that are likely to have strong heterotic effects in crossings as well as a wide range of variability during gene segregation and recombination at heterozygous polygenic blocks. The multivariate technique with D^2 statistics (Mahalanobis, 1928) is a useful tool for determining the degree of genotype divergence.

Materials and Methods

The present experiment was conducted at Main Experiment Station of Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) during Rabi 2019-20. Experimental material for the study consisted of 36 genotypes including one checks (KA-2). Each entry was transplanted in the plot size of 1.2 m x 3 m. in Randomized Complete Block Design in 3 replications with distance of 60 X 50 cm. All the recommended agronomic package of practices and plant protection measures were followed to grow a better crop. Observations were noted on 10 traits viz. days to 50% flowering, number of primary branches per plant, plant height (cm), and days to maturity (Mature Green Stage), fruit length (cm), days to maturity (Red Ripe Stage), average fruit weight (g), fruit diameter (mm), and fruit yield per plant. Throughout the growth season, the crop was visited on a regular basis, and interculture operations such as weeding and irrigation were performed as needed. Tochers method, as reported by Rao (1952), was used to arrange the genotypes into a number of clusters, and the most divergent ones were chosen using Mahalanobis (1928) D^2 statistics.

Result and Discussions

The studies of genetic divergence among the 36 genotypes of chilli were carried out by using Mahalanobis D^2 statistics. The clustering pattern of the thirty-six genotypes were grouped into ten different non- overlapping cluster (Table 1). Cluster I had highest number of genotypes (13) followed by cluster II (7), cluster III (6) whereas cluster IV, cluster V, cluster VI had presented two entries in each group and cluster VII, cluster VIII, cluster IX and cluster X had presented only one entry in each group. This indicated presence of considerable diversity in the genotype. The major clusters in the mentioned genetic divergence analysis contained frequently the genotypes of heterogenous origin. Although the genotypes of same origin or geographic region were also found to be grouped together in the same cluster. The instance of grouping of genotypes of different origin or geographic region in same cluster were frequently observed. This suggested that there is no parallelism between genetic and geographic diversity.

The estimates of intra and inter-cluster distance represented by D^2 values are given in table 2. The minimum intra cluster distance (0.00) was found for cluster VII, VIII, IX and X and maximum was found for cluster VI (54.33) followed by cluster II (46.95), cluster III (42.22), cluster I (35.48), cluster V (32.27) and cluster VI (25.91). The maximum inter-cluster distance was found between cluster IV to X (345.23) followed by cluster X to V (332.64), cluster IX to VI (287.45), cluster IX to IV (243.03), cluster VIII to IV (237.73), cluster VI to II (234.86), cluster VIII to VI (232.02), cluster VIII to V (207.13) were very high. The minimum inter- cluster D^2 value found in case of cluster VII to I (61.89) followed by cluster IV to III (63.61), cluster VII to V (66.29), cluster VI to III (71.40), cluster VI to IV (73.26). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. These results are in close conformation with the findings of Hasan *et al.* (2015), Janaki *et al.* (2016).

A perusal of table 3 showed that cluster means for the different traits indicated considerable differences between the clusters. The entire cluster from cluster I to cluster X had average mean performance for most of the characters. Cluster II showed maximum mean value for average fruit weight (4.49). Cluster IV showed maximum mean value for fruit diameter and primary branches per plant (11.91) while minimum mean value for fruits yield per plant (125.09). Cluster V showed maximum mean value for days to maturity (MGS) (73.40), days to maturity (RRS) (106.12) while minimum mean values for fruit diameter (3.45) and number of fruits per plant (49.54). Cluster VI showed maximum mean values for fruit length (8.86) while minimum mean values for average fruit weight (2.11). Cluster VII showed minimum mean values for fruit length (5.49) and maximum mean value for number of fruits per plant (74.38). Cluster VIII showed maximum mean value for days to 50% flowering (60.32). Cluster IX showed maximum mean values for plant height (63.78) and fruit yield per plant (316.41). Cluster X showed minimum mean values for days to 50% flowering (42.17), days to maturity (MGS) (67.05), days to maturity (RRS) (86.15), plant height (35.41) and primary branches per plant (5.52). These

results are in close conformation with the findings of Yadav *et al.* (2016) and Vanitha and Jansirani (2017).

Highest per cent contribution towards clustering of genotypes were observed in fruit yield per plant (29.75) followed by primary branches per plant (20.85), average fruit weight (17.93%), plant height (8.57%), fruit length (6.84%), number of fruit per plant (5.95%) and days to 50% flowering (5.36%) and the contribution for other three characters *viz.,* days to maturity (RRS) (1.64%), days to maturity (MGS) (1.59%) and fruit diameter (1.495) were very low for

the diversification of genotype in table 4. These results are in close conformation with the findings of Jogi *et al.* (2017), Singh *et al.* (2017) and Nahak *et al.* (2018).

The overall review of the results obtained by genetic diversity study in present investigation revealed that the crosses between the entries separated by the large inter-cluster distance and having high cluster mean values for one or other character will be helpful in the improvement of this important crop *i.e.,* chilli.

Table 1 : Clustering pattern of 36 genotypes of chilli on the basis of Mahalanobis' D^2 statistics

Cluster number	No. of genotypes	Genotypes
I	13	NDC-134, NDC-140, NDC-132, NDC-142, NDC-149, NDC- 147, NDC-143, NDC-131, NDC-145, NDC-155, NDC-144, NDC-141, NDC-150
II	7	NDC-138, NDC-139, KA-2, NDC-127, NDC-135, NDC-136, NDC-129
III	6	NDC-121, NDC-123, NDC-122, NDC-126, NDC-151, NDC-152
IV	2	NDC-124, NDC-125
V	2	NDC-133, NDC-154
VI	2	NDC-128, NDC-130
VII	1	NDC-148
VIII	1	NDC-146
IX	1	NDC-153
X	1	NDC-137

Table 2: Average an intra and inter-clusters D^2 values for ten clusters in chilli

Cluster numbers	I	II	III	IV	V	VI	VII	VIII	IX	X
I	35.48	101.12	82.77	169.86	93.09	160.79	61.89	82.47	100.74	85.64
II		46.95	126.79	190.54	128.08	234.86	112.45	127.01	73.02	102.18
III			42.22	63.61	101.54	71.40	86.54	124.23	163.14	215.22
IV				25.91	129.48	73.26	136.67	237.73	243.03	345.23
V					32.27	154.09	66.29	207.13	155.81	171.65
VI						54.33	192.72	232.02	287.45	332.64
VII							0.00	154.72	165.69	147.06
VIII								0.00	78.23	162.05
IX									0.00	88.81
X										0.00

Table 3: Intra-cluster group means for ten characters in chilli

Characters / Clusters	Days to 50% Flowering	Days to Maturity (MGS)	Days to Maturity (RRS)	Plant height	Fruit Length	Fruit Diameter	Number of fruits per plant	Average fruit weight	Primary branches per plant	Fruit yield perplant
I	49.71	71.39	96.17	46.30	6.88	3.71	70.72	3.05	6.72	221.70
II	48.94	67.97	95.43	48.75	6.53	3.78	64.47	4.49	9.80	281.08
III	50.54	69.92	102.55	54.63	7.58	3.48	66.06	2.87	10.24	174.25
IV	46.59	69.65	99.92	63.47	7.38	4.16	51.93	3.15	11.91	125.09
V	48.79	73.40	106.12	44.58	8.54	3.45	49.54	4.30	7.39	161.45
VI	53.41	71.58	97.42	45.10	8.86	3.74	56.36	2.11	11.27	129.67
VII	46.94	71.23	102.06	50.43	5.49	3.49	74.38	4.11	7.56	165.01
VIII	60.32	69.47	103.67	60.67	7.56	3.73	72.29	2.74	7.23	273.85
IX	47.27	70.67	92.97	63.78	7.71	3.63	52.14	3.82	7.02	316.41
X	42.17	67.05	86.15	35.41	5.98	3.79	71.08	3.58	5.52	315.77

Table 4 : Percent contribution of ten characters towards total genetic divergence inchilli.

S. No.	Characters	Percent Contribution
1	Days to 50% Flowering	5.36
2	Days to Maturity (MGS)	1.59
3	Days to Maturity (RRS)	1.64
4	Plant Height (cm)	8.57
5	Fruit length (cm)	6.84
6	Fruit Diameter	1.49
7	Number of fruits per plant	5.95
8	Average fruit weight	17.93
9	Primary Branches per plant	20.85
10	Fruit Yield per plant	29.75

Conclusion

Usually, the crosses are associated with the parents, which are included in the most distant clusters, are expected to give maximal heterosis and so create a wide variability in different and genetic architectures. The 36 genotypes of the most popular chilli species (*C. annuum* L.) under study were grouped into 10 clusters irrespective of their origin. Which exhibit high diversity among the genotypes. Distant parents were ready to exert high heterosis. Considering the group distance cluster IV showed maximal genetic distance with cluster X (345.23) followed by the genetic distance from cluster X and V (332.64) suggesting wide diversity, so inter-genotypic crosses between the members of cluster I and V and cluster I and III would exhibit high heterosis.

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