

GENETIC DIVERGENCE AND CLUSTER ANALYSIS FOR YIELD ATTRIBUTING TRAITS IN ELITE LINES OF CHILLI

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Abstract—The genetic diversity of thirty chilli elite lines was estimated using Mahalanobis D^2 and 12 yield attributing traits. ANOVA found that there was a significant degree of variation among elite lines. Because hybrids between lines of various clusters serve a vital role in choosing possible parents and assessing the degree of divergence in the chilli elite lines, genetic diversity knowledge is crucial in plant breeding. Fruit yield/plant (45.52) contributed the most (45.52 percent) to overall genetic difference, followed by fruit width (16.09). It also displayed lines that were divided into six groups. Clusters IV and V had the greatest inter-cluster distance, admitted lines from a diverse gene pool, and as per cluster mean analysis, these clusters contained high values for most of the yield attributing traits such as plant height, plant spread, fruit width, days of flower initiation, days of 50% flowering, and canopy temperature. The lines in these clusters act as superior segregants for yield traits and are 2020/CHIVAR-2, 2020/CHIVAR-3, K2, 2020/CHIVAR-5, 2020/CHIVAR-7, 2020/CHIVAR-8, 2020/CHIVAR-9, 2018 CHIHVYB 03, KASHI GAURAV, KASHI ANMOL.

INTRODUCTION

Chilli is the most important spice in everyday life, and the market's diversity of chili-related items raises the spice's manufacturing value. Fresh fruits, processed sauces, pickled foods, dried spices, and industrial extracts are all popular applications. Capsicum is also used in nutrition as a source of ascorbic acid (vitamin C), carotenoids (pro-vitamin A), tocopherols (vitamin E), flavonoids, and capsaicinoids, as well as in defence and ethnobotanical products. India is the world's leading pepper grower, exporter, and consumer. Due to the major issue of global warming and climate change, many agricultural and horticultural crops are losing economic productivity. Chili is the most commercially significant of these horticulture commodities, accounting for the majority of the value exported from India. India has the world's greatest market share, at 25%, followed by China, at 24%. Despite having a significant share of the world's hectares planted with chilies, India's production (1.74 t/ha) is low in comparison to other hot pepper-growing countries such as Korea and

Indonesia, where it ranges between 2-3 t/ha. Genetic diversity information from elite germplasm is critical for selecting prospective lines for the characteristic of interest. Exploiting transgressive segregation requires the selection of genetically different parents. A large genetic distance between parents is required to provide meaningful heterosis in children. Genetic divergence analysis is useful for determining the proportion contribution of characteristics and the genetic diversity prevalent among genotypes. Genetic variation may be an enthralling need for any breeding effort. Diversity analysis is important for parent selection in hybridization to generate high yield potential cultivars and achieve diverse plant breeding goals.

MATERIALS AND METHODS

During the Kharif season 2019-2022, the experiment was carried out at Maharajpur Farm under the Department of Horticulture, College of Agriculture, J.N.K.V.V., Jabalpur (M.P.). The thirty genotypes of capsicum were obtained from Indian Institute of Vegetable Research (IIVR), Varanasi, diverse

locations of Madhya Pradesh and South (Table 1). (Table 1). The genotypes were planted in a three-replication Randomized Complete Block Design (RCBD). On the basis of thirty-five qualitative features, phenotypic analyses of capsicum genotypes were performed (Table 2). During the Kharif season 2019-2020, a field experiment was conducted at Maharajpur Farm under the Department of Horticulture, College of Agriculture, J.N.K.V.V., Jabalpur (M.P.). In terms of geography and fertility, the experimental region was relatively homogeneous. The experimental material comprises of 30 chilli elite lines taken from several chilli-growing sites in Madhya Pradesh in order to determine genetic diversity. The genotypes were seeded in a Randomized Block Design (RBD) with plant spacing of 60 cm and row spacing of 45 cm. For typical chilli growth, regular agronomic methods were used. ruit yield/plant, fruit width, number of seed per fruit, days to maturity, days of flower initiation, fruit length, fruit length /breath ratio, plant spread, days of 50% flowering, plant height, number of branches /plant, and canopy temperature were all measured on randomly selected plants from each of the three replications. The data were examined using D^2 statistics according to the multivariate analysis of genetic divergence. The genotypes were classified into separate clusters using Tocher's approach (Rao *et al.*, 1952).

RESULTS AND DISCUSSION

The variance analysis found substantial discrepancies between the lines for all of the characters. The quantitative assessment of genetic divergence was examined on 30 genotypes across 12 yield attributing factors using Mahalanobis D^2 statistics. Cluster diagrams and clusters may offer a likeness of the genetic architecture of the plant population under study. Previous researchers researched genetic divergence and concluded that most of the factors analysed contributed differentially to genetic divergence and that there was no association between geographical origin and genetic variety (Singh *et al.*, 1999; Bharadwaj *et al.*, 2001; Sood., 2005)

As shown in Table 1, the character fruit yield/plant (45.52) contributed the most genetic divergence, followed by fruit width (16.09), number of seed per fruit (13.79), days to maturity (9.43), days of flower initiation (5.98), fruit length (3.22), fruit

Table 1. Contribution of different characters towards divergence in 67 rice genotypes

S. No.	Character	Times ranked 1st	Percentage of contribution towards divergence
1	Fruit Yield/ plant	198	45.52
2	Fruit Width	70	16.09
3	Number of seed per fruit	60	13.79
4	Days to maturity	41	9.43
5	Days of flower initiation	26	5.98
6	Fruit Length	14	3.22
7	Fruit length /breath ratio	14	3.22
8	Plant Spread	5	1.15
9	Days of 50% flowering	4	0.92
10	Plant Height	3	0.69
11	N. of Branches /Plant	0	0
12	Canopy Temperature	0	0

length /breath ratio (3.22), plant spread (1.15), days of 50% flowering (0.92), and plant height (0.69). Sreelathakumary and Rajamony (2004 and Hasan *et al.*, 2015 produced similar results for the characteristics fruit yield/plant and fruit width. Some traits viz. number of branches /plant and canopy temperature had no contribution towards divergence. This result supported by Pujar *et al.*, (2017).

Tocher's method was used to group 30 chilli elite varieties into six clusters based on divergence values. Clusters I and IV were poly-genotypic (each had seven genotypes), followed by VI (each had six genotypes), and V and II (each had three genotypes), as shown in Table 2. The presence of genetic variability was articulated by this group constellation. The genetic variety seen in different clusters from the same geographical area might be attributed to selection pressure, selection criteria, and environmental factors (Vivekanandan and Subramanian, 1993; Nayak *et al.*, 2004)

The average intra and inter-cluster values estimated as per the procedure given by Singh and Choudhary (1977). Cluster I showed maximum intracluster value ($D_2 = 253.93$), they can be selected as hybridization stock for the next-generation breeding program. Cluster II, II, III, IV, V and VI were solitary clusters with no intra-cluster distance. The result is represented in Table 3. The inter-cluster value was maximum between Cluster V and Cluster VI (960.76) followed by Cluster I and Cluster III (701.84) and Cluster IV and V (683.95), while it was minimum between clusters II and V (125.03) and Cluster II and III (113.5) as shown in Table 4. Inter-

Table 2. Distribution of rice genotypes in different clusters

S. No.	Cluster	Number of genotypes	Genotypes
1	I	7	MPKC-1, G 4, MPKC-2, 2019/CHIHBYB-06, MPC-1, MPC-2, MPKC-1
2	II	3	TEJA, CHAPATA, MPSC-1
3	III	4	2020/CHIVAR-1, RED TOP, KASHMIRI, GUNTUR
4	IV	7	2020/CHIVAR-2, 2020/CHIVAR-3, K2, 2020/CHIVAR-5, 2020/CHIVAR-7, 2020/CHIVAR-8, 2020/CHIVAR-9
5	V	3	2018/CHIHBYB-03, KASHI GAURAV, KASHI ANMOL
6	VI	6	2020/CHIVAR-4, 2020/CHIVAR-6, 2018/CHIHBYB-05, MPHIC-1, MPCTC-1, PUSA JWALA

crossing among the genotypes belonging to cluster III, IV and I was suggested to develop high yielding varieties with other desirable characters or may be used as potential donors for future hybridization programme to develop better chilli variety with good fruit yield (Kumar and Mallikarjunaiah, 2010.)

Cluster V (2018 CHIHBYB 03, KASHI GAURAV, KASHI ANMOL) genotypes had the greatest inter-cluster distance with cluster VI (2020/CHIVAR-4, 2020/CHIVAR-6, CHILI HYBRID 2018 - 5 AVT II, MPHIC-1, MPCTC-1, PUSA JWALA) genotypes, followed by cluster I (MPKC-1, G 4, MPKC-2, 2019 CHILLI HYBRID 06 AVT (2018 CHIHBYB 03, KASHI

GAURAV, KASHI ANMOL). These large inter-cluster distances indicate the most varied gene pool, which might be used as parents in a hybridization breeding effort. Crossings between divergent parents are widely recognised to create a stronger heterotic impact than crosses between closely related ones (Ranjith *et al.*, 2018). As a result, crossing prominent genotypes in distant clusters maximises heterosis and may result in the formation of prospective genotypes with a broader genetic base.

The cluster mean values for each of the 12 characteristics are shown in Table 5, which shows a large range of variance for all the traits tested. Most economic characteristics have a high cluster mean value in Cluster IV for three qualities: plant height (60.33), plant spread (59), and fruit width (1.53), and Cluster V for three traits: days of flower initiation (87.67), days of 50% blooming (101) and canopy temperature (25.43). The genotypes belonging to these clusters depict potential variability for the included traits such as genotype 2020/CHIVAR-2, 2020/CHIVAR-3, K2, 2020/CHIVAR-5, 2020/CHIVAR-7, 2020/CHIVAR-8, 2020/CHIVAR-9 of Cluster IV and 2018 CHIHBYB 03, KASHI GAURAV, KASHI ANMOL of Cluster V. Thus, lines of these clusters indulge potential variability for economic yield attributes and their cross can generate an ideotype with maximum yield attributing traits together. Also, these traits regarded as a beneficial source of gene for improvement of chilli yield.

Table 4. Inter cluster D2 values of chilli elite lines

Inter-cluster	Distance
Cluster V & VI	960.76
Cluster I & III	701.84
Cluster IV & V	683.95
Cluster I & VI	676.39
Cluster II & VI	558.33
Cluster I & II	514.82
Cluster I & IV	497.11
Cluster II & IV	493.17
Cluster I & V	490.26
Cluster III & VI	422.59
Cluster III & IV	341.75
Cluster III & V	280.63
Cluster IV & VI	266.6
Cluster II & V	125.03
Cluster II & III	113.5

Table 5. Average intra and inter cluster D² values of chilli elite lines

ClusterNo.	I	II	III	IV	V	VI
I	253.93	514.82	701.84	497.11	490.26	676.39
II		0	113.5	493.17	125.03	558.33
III			0	341.75	280.63	422.59
IV				0	683.95	266.6
V					0	960.76
VI						0

Table 5. Cluster means value of different characters

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days of flower initiation	56.77	87.33	76.33	44.33	87.67	54
Days of 50% flowering	66.33	98.33	95	56	101	76.67
Days to maturity	106.99	128	125.67	94.33	122	119
Plant height	49.21	56.67	42	60.33	34.67	54.33
Plant spread	40.94	34	42	59	34.67	44.33
N.of branches /plant	6.15	8	7.33	5.33	5.67	6.67
Fruit length	9.12	5.47	6.53	8.73	8.2	8.5
Fruit width	0.88	1.1	1.17	1.53	1.08	1.07
Fruit length /breath ratio	11.01	4.98	5.69	5.94	7.64	7.96
Number of seed per fruit	64.81	88	106	101.33	88	81
Canopy temperature	23.25	21.7	23.53	24.63	25.43	21.87
Fruit yield/ plant	331.01	400	522	570	144.67	941

CONCLUSION

Through results, it has been concluded that all 30 chilli elite lines contribute to genetic diversity with a total of 12 clusters. Amongst them, clusters I, has high value of intra-cluster distances could be adopted as donor parents in a crop improvement program to procure superior segregates in the future. The choice of parent belonging to clusters with maximum inter-cluster distance would help in the broadening of a genetic basis through the exploitation of hidden hybrid vigour. As, characters such as fruit yield/ plant and fruit width, committed the highest share in genetic diversity, so helpful in a selection based on these traits. The cluster means analysis revealed that the selection of genotypes of cluster IV and V, having a superior performance for a most of the trait could be used in the hybridization program for improvement of yield in chilli and also these clusters had maximum intercluster distance predicted heterosis on inter-crossing. Thus, future hybridization between 2020/CHIVAR-2, 2020/CHIVAR-3, K2, 2020/CHIVAR-5, 2020/CHIVAR-7, 2020/CHIVAR-8, 2020/CHIVAR-9 and 2018 CHIHVB 03, KASHI GAURAV, KASHI ANMOL could be fruitful. Hence, good genetic diversity which is present in this contrast breeding material may disclose the chances of genetic improvement in the research program.

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