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Parent selection for hybridization in chilli (*Capsicum annuum* L.) using multivariate analysis and K-means clustering

Farhana Sharmeen[1], Mohammad Mehfuz Hasan Saikat[1], Jalal Uddin Ahmed[2], Md Tofazzal Islam[3], A K M Aminul Islam*[1]

[1]Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur 1706, Bangladesh
[2]Department of Crop Botany, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur 1706, Bangladesh
[3]Institute of Biotechnology and Genetic Engineering, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur 1706, Bangladesh

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anwargpb@bau.edu.bd

**Corresponding Author*
A K M Aminul Islam
aminulgpb@bsmrau.edu.bd

ABSTRACT

The study was conducted to elucidate the phenotypic variability and extent of genetic diversity of 28 chilli (*Capsicum annuum* L.) genotypes. The selected chilli genotypes were grown at the Field Laboratory of the Department of Genetics and Plant Breeding of Bangbandhu Sheikh Mujibur Rahman Agricultural University, Bangladesh with recommended agronomic practices. The experiment was laid out in a randomized complete block design with tree replications. The analysis of variance revealed considerable variability among the genotypes for the character studied. Genetic diversity in chilli genotypes were estimated based on 16 growth and yield contributing characters using Mahalanobis's D^2 statistics and K-means clustering. The genotypes were grouped into four different clusters by non-hierarchical clustering. Cluster II had the maximum number (13) of genotypes followed by cluster IV, III and I with 7, 5 and 3 genotypes, respectively. The highest inter-cluster genetic divergence (9.87) was recorded between clusters I and III, whereas the highest intra-cluster distance was recorded in cluster I (4.37). Cluster I was observed to be the most important with maximum cluster means for most of the valuable traits including number of fruits per plant and number of fruit yield per plant. The characters fruit yield/plant, days to 100% fruiting, days to first flowering and individual fruit weight contributed maximum towards divergence. Considering diversity pattern and other horticultural performance Genotype 7 from cluster II, Genotype 20 from cluster III, and Genotype 8, Genotype 10 and Genotype 24 from cluster IV may be taken into consideration as better parents for an efficient hybridization program of chilli.

Keywords: Chilli, genetic variability, D^2 statistics, clustering, genetic divergence

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1 Introduction

Chilli (*Capsicum annuum* L.) is grown worldwide both as a spice and as a vegetable crop and world's second most important solanaceous vegetable after tomato. Chilli grown for its fruits, which are used in green as well as ripe dried form for its pungency. Chilli belongs to the genus Capsicum, family Solanaceae. It has originated from south and Central America (Bahurupe et al., 2013) spp. viz. *C. annuum*, *C. baccatum*, *C. chinense*, *C. frutescens*, and *C. pubescens*.

Among these, *C. annuum* L. is the most widely cultivated species all over the world for its pungent (chilli syn. Hot pepper) and non-pungent (sweet pepper) fruits (Bosland, P.W. and Votava, E.J., 2012). It is self-pollinated crop but 2% to 96% out crossing was observed under open pollination (Berker, 2000). Chilli is widely cultivated throughout the year in Bangladesh. A rich diversity of chilli exists due to varied geo-climatic regions of Bangladesh. In Bangladesh, the production of chilli was 0.492 million mt in 0.1 million ha of land with an average yield of 405 kg/ha during 2021-22 (BBS, 2022). Despite having a rich diversity, the production of chilli is decreasing day by day. The lack of improved genotypes is the prime cause of low production. Assurance of production of chilli in a large scale is feasible only by means of breeding programs.

A number of chilli cultivars are grown in Bangladesh differing in habit, size, shape, color, pungency and yield which indicating their wide range of variability (Afroz et al., 2017). The chilli landraces of different district in Bangladesh are heterogeneous and a wide variability in respect of fruit morphology, pungency, bearing habit and crop duration is found throughout country (Deepo et al., 2020). Bangladeshi chilli varieties have been developed traditionally by selection, hybridization and back crossing with locally adapted cultivars (Sharmin et al., 2018). An important source for the introduction of new traits is the existence of a genetically diverse pool of chilli germplasm available in the country but they are mostly lying unexplored. Genetic resources play a pivotal role in its economical utilization and desirable traits improvements. Genetic divergence existing in the population helps in the selection of suitable parents for chilli breeding (Herath et al., 2020; Karim et al., 2021). The variability among local and exotic genotypes in genetic attributes which can be combined through hybridization to develop varieties with higher yield and nutritional qualities (Wang and Bosland, 2006). The genus capsicum is often-cross pollinated crop and hence exhibits wide variability for different quantitative and qualitative traits (Sharma et al., 2010). Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, N., 1991).

Genetic diversity is the basic requirement for any successful breeding program (Mishra et al., 2022). Assessment of genetic diversity among germplasm is a prerequisite for plant breeders in choosing potential parental lines because of two reasons: i.e., (i) In the hybridization program, genetically diverse parents likely to produce high heterotic effect, and (ii) Genetically distant parents could produce a wide spectrum of variability in the segregating generation. Jinks and Hayman (1953) and Griffing (1956) have described analysis of diallel crosses which provide rapid overall evaluation of certain genetic relationship such combining ability among the parents and their crosses entering diallel crosses. Therefore, a clear characterization of germplasm is the first step to facilitate successful breeding efforts. Selection of genotypes from divergent clusters and components having more than one positive trait for hybridization program may lead to improvement in yield (Singh et al., 2017). 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 (Jakhar et al., 2016; Sutariya et al., 2016; Bhandari et al., 2017). Therefore, the present study was undertaken to assess the genetic diversity in 28 genotypes of chilli to identify suitable parents for hybridization program.

2 Materials and Methods

2.1 Study location

The field experiment was conducted at the experimental farm of Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur during the period from November 2016 to September 2017. The location of experimental site was at the center of Madhupur Tract (24.05° N latitude and 90.25° E longitude) with an elevation of 8.4 m from the sea level. The soil of experimental field belongs to the Shallow Red Brown Terrace type under Salna Series of Madhupur Tract of Agro-ecological Zone (AEZ) 28 which is characterized by silty clay with pH value of 5.5. The climate of the experimental site is subtropical in nature characterized by heavy rainfall during the months from June to September and scanty in water with gradual fall of temperature from the month of September.

2.2 Materials and experimental design

Twenty eight genotypes of chilli were used to study the genetic diversity among the germplasm. The genotypes were grown in the field Laboratory of the Department of Genetics and Plant Breeding of Bangbandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh. The experiment was laid out in a randomized complete block design with three replications. The experimental area was divided into three blocks. Each block consisted of 28 unit plots (4 m $\times$ 2.5 m). Plants of the same genotype were planted with a spacing of 0.5 m $\times$ 0.5 m. Thus, the total number of plots was 84. The blocks and plants were spaced at 1 m. The seeds of different chilli genotypes were sown in earthen tub. The seedlings at the age of 4 to 5 leaves were suitable for transplanting and this took 35-45 days after sowing. The transplantation of seedlings was done on December 28, 2018.

Raised beds were prepared for transplanting. The experimental plots were fertilized with, urea, TSP, MoP and gypsum @ 210, 330, 200 and 110 kg/ha , respectively (Haque et al., 2020). The total amount of cowdung, TSP, gypsum and one third of MoP were applied during land preparation. The rest of MoP and urea were applied at three equal splits after 20, 50 and 70 days of transplanting. At the time of transplanting, Dursbarn 20 EC and Ridomil MZ 68 WP were used at the rate of 5 mL/L and 3 g/L, respectively for soil treatment. Irrigation was given as and when necessary. Weeding was done after every 20 days of transplanting.

2.3 Data recording

Ten plants from each plot were randomly selected and tagged with labels. Data were collected from these plants. Data were recorded on the growth and yield contributing traits viz., days to flowering, days to fruit setting, plant height, days to green fruit maturity, number of fruits per plant, fruit length, fruit diameter, individual fruit weight, fruit yield per plant, number of seeds per fruit.

2.4 Data analyses

The 'R' statistical package (version 4.0.2) was used to perform all statistical analyses (R Core Team, 2021). One way ANOVA followed by Tukey's post hoc test were conducted for comparing the means of studied traits among the chilli genotypes. The R packages 'ggplot2', 'ggfortify', 'usethis', 'devtools', 'plyr', 'scales', and 'grid' were used to perform principal component analysis (PCA). 'Metan' package was used to calculate the intra- and inter-cluster differences of the chilli genotypes. The 'ggplot2' package was used to plot the PCA biplot and other figures.

3 Results and Discussion

The analysis of variance (Table 1) exhibited significant differences among the genotypes for all the traits under study, except for 50% days to flowering (DFTF) which indicated considerable amount of genetic variability and subjected for further analysis. The mean performance with their standard error for 16 growth and yield contributing characters of 28 chilli genotypes are presented in Table 2. It can be seen from Table 2 that there are considerable variations in these characters among the studied genotype. The length of chilli fruits varied from 1.2 $\pm$ 0.26 cm (genotype 22) to 15.08 $\pm$ 1.89 cm (genotype 22). The highest individual fruit weight (5.5 $\pm$ 0.53 g) was recorded in genotype 18 while the lowest (0.73 $\pm$ 0.06 g) was recorded in genotype 14. Genotype 17 produced the maximum fruit yield (0.97 $\pm$ 0.11 kg/plant) and the lowest yield (0.02 kg/plant) was recorded genotype 28.

Genetic diversity of germplasm determines their potential for improved efficiency and thereby utilizing diverse genetic material in breeding program which may eventually result in enhanced crop production (Mishra et al., 2022). Amongst the various tools to assess genetic diversity, D^2 statistic is a powerful tool for estimating genetic diversity and to identify the parents for hybridization to obtain desirable recombinants since diverse parents lead to high heterosis (Khodadadi et al., 2011). Inclusion of diverse parents in hybridization program provides an opportunity to combine desirable genes and hence, resulted in isolation of superior lines with requisite traits (Gaiero et al., 2018; Nahak et al., 2018; Taylor and Larson, 2019).

Cluster analysis is the most suitable approach in identifying variability in germplasm, lessen the number of breeding lines by eliminating duplicates from large germplasm and thereby, suggests appropriate parents to be involved in conventional breeding (Mustafa et al., 2015; Jarwar et al., 2019). With Euclidean cluster analysis, 28 genotypes of chilli were grouped into four clusters (Fig. 1). All four clusters were polygenotypic. Cluster I and II, III and IV were composed of 3, 13, 5 and 7 genotypes, respectively (Table 3). Cluster II comprised of maximum 13 genotypes. However, other researchers (Dutonde et al., 2008; Datta and Jana, 2010; Pujar, 2017; Negi and Sharma, 2019) found maximum genotypes in cluster-I. Different clustering patterns in chilli were also reported by earlier workers (Janaki et al., 2015; Bijalwan et al., 2018) in their respective studies.

The intra-cluster distance varies from 0 to 4.37 with the highest in cluster I followed by 4.01 in cluster IV and 3.77 in cluster II while cluster III had intra-cluster distance with zero value (Fig. 2). The inter-cluster distance ranged from 0 to 9.87 (Fig. 2). The highest inter-cluster genetic divergence (9.87) was recorded between clusters I and III followed by III and IV, and I and II. The clustering pattern of different genotypes did not follow their geographical distribution and was fairly at random. This suggests that falling of materials of same origin into different clusters was an indication of broad genetic base of the genotypes belonging to the origin. It also indicates that the genotypes included in the clusters with high inter-cluster distance showed sufficient genetic diversity and selection of parents from these diverse clusters would be useful in hybridization program for improving yield and other desirable horticultural traits. The crosses involving the diverse genotypes would be expected to manifest maximum heterosis and are more likely to evolve desirable recombinants in segregating generations.

Table 1. Analysis of variance (ANOVA) for growth and yield contributing characters of 28 chilli genotypes

Traits	Sources of variation (mean squares)			CV (%)
	Genotype (27)	Replication (2)	Error (54)	
DFRF	143.46 ***	0.44 ns	3.23	1.71
DFTF	157.57 ns	106.75 ns	119.95	9.55
DHDF	106.23 ***	1.94 ns	2.1	1.15
DFFS	300.59 ***	0.33 ns	2.63	1.65
DFTS	107.36 ***	3.25 ns	3.016	1.38
DHFS	88.92 ***	1.48 ns	1.66	0.96
DFFM	130.54 ***	1.11 ns	1.65	0.84
DFTM	127.14 ***	1.58 ns	1.42	0.74
DHFM	94.05 ***	8.37 ns	3.75	1.15
FRLN	24.30 ***	0.91 ns	0.52	11.14
FRDM	10.70 ***	2.90 ns	1.53	12.1
FRPP	5123.08 ***	1223.38 ns	679.97	19.32
IFRW	6.64 ***	0.05 ns	0.06	10.15
NSPF	792.19 ***	42.82 ns	93.11	13.48
YLPL	0.15 ***	0.01 ns	0.01	24.4
PLHT	482.90 ***	168.48 **	26.72	9.77

DFRF: days to first flowering, DFTF: days to 50% flowering, DHDF: days to 100% flowering, DFFS: days to first fruiting, DFTS: days to 50% fruiting, DHFS: days to 100% fruiting, DFFM: days to first green fruit maturity, DFTM: days to 50% green fruit maturity, DHFM: days to 100% green fruit maturity, FRLN: fruit length (cm), FRDM: fruit diameter (mm), FRPP: number of fruits/plant, IFRW: individual fruit weight (g), NSPF: numbers of seeds/fruit, YLPL: green chilli yield/plant (kg), PLHT: plant height (cm). Values in the parenthesis with sources of variation column are degrees of freedom (df); *** = significant at 01% level of significance, ns = not significant

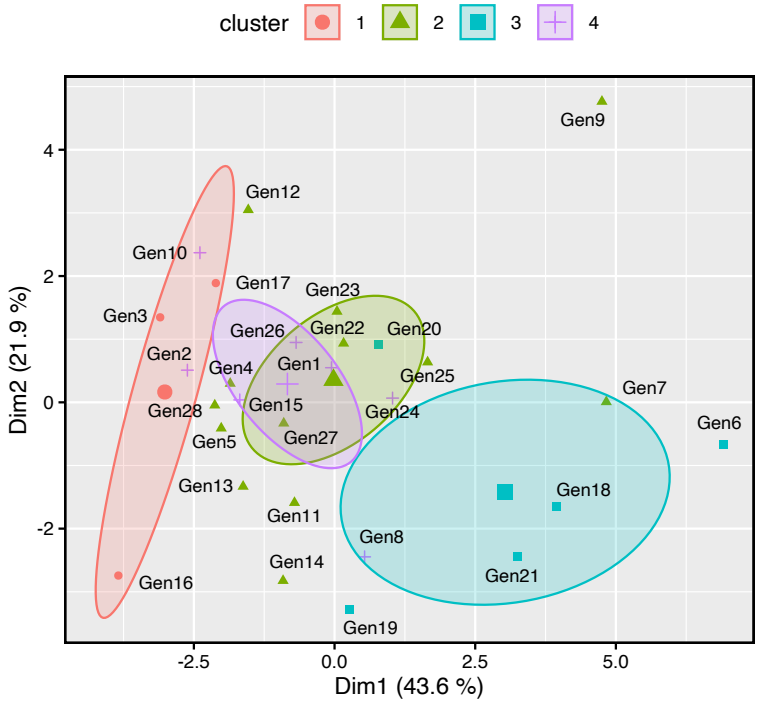

Figure 1. K-means clusters of 28 chilli genotypes based on their performance of 16 plant characters, yield contributing characters and yield

Table 2. Performance of 28 chilli genotypes for growth and yield contributing characters

Genotype	DFRF	DFTF	DHDF	DFFS	DFTS	DHFS	DFFM	DFTM
Gen1	107 ± 2.08	115 ± 2	122 ± 2.08	117 ± 0.58	127 ± 1	128 ± 1.15	151 ± 0.58	160 ± 0.58
Gen2	110 ± 0.58	120 ± 1.53	127 ± 1.53	119 ± 1.53	129 ± 1.53	136 ± 1.73	150 ± 1	161 ± 0.58
Gen3	104 ± 2.08	113 ± 2	124 ± 1.15	114 ± 1.15	125 ± 1.53	134 ± 1	146 ± 1.53	156 ± 2.08
Gen4	103 ± 3	114 ± 2.65	120 ± 1	114 ± 3	127 ± 1	130 ± 0.58	153 ± 2.08	161 ± 1
Gen5	103 ± 1	114 ± 1.53	118 ± 1.53	94 ± 1.15	127 ± 1	129 ± 1	152 ± 1.73	161 ± 1.53
Gen6	102 ± 1.53	113 ± 1	123 ± 1.15	94 ± 1.53	124 ± 1.53	131 ± 1.73	147 ± 1.15	158 ± 1.15
Gen7	110 ± 0.58	120 ± 1	124 ± 2.08	100 ± 1	130 ± 1.53	133 ± 1.53	154 ± 1.53	163 ± 1.73
Gen8	107 ± 0.58	118 ± 0.58	122 ± 1.15	98 ± 1	130 ± 1.15	132 ± 1	159 ± 0.58	167 ± 0.58
Gen9	112 ± 2	123 ± 2.31	131 ± 1.15	102 ± 1	127 ± 1	138 ± 1.53	159 ± 1	168 ± 1.53
Gen10	113 ± 1.73	123 ± 2.65	130 ± 0.58	103 ± 1	130 ± 1.15	139 ± 1	159 ± 1.15	169 ± 1
Gen11	112 ± 1.53	122 ± 1.53	128 ± 1.53	100 ± 1	131 ± 0.58	138 ± 2	161 ± 2.08	169 ± 1.53
Gen12	109 ± 1	119 ± 1.15	131 ± 1.53	99 ± 1	127 ± 1.53	138 ± 1	156 ± 1.15	167 ± 1.53
Gen13	107 ± 1.73	117 ± 2	131 ± 0.58	98 ± 2	125 ± 1	140 ± 1	157 ± 0.58	167 ± 0.58
Gen14	92 ± 1.53	103 ± 2.52	110 ± 1.53	84 ± 1.53	112 ± 1.53	121 ± 1	139 ± 1	147 ± 1.15
Gen15	92 ± 1	106 ± 0.58	115 ± 1	82 ± 1	115 ± 1	127 ± 0.58	140 ± 0.58	150 ± 1
Gen16	103 ± 0.58	114 ± 1	128 ± 2.31	93 ± 1.53	126 ± 1.15	135 ± 1.15	152 ± 1.53	161 ± 1
Gen17	93 ± 1.15	103 ± 2.52	114 ± 1	82 ± 1.15	115 ± 1.53	120 ± 1.53	139 ± 1.15	150 ± 1.15
Gen18	111 ± 0.58	122 ± 2.08	131 ± 1.15	101 ± 1	130 ± 1.15	137 ± 1.15	160 ± 0.58	169 ± 0.58
Gen19	108 ± 1.53	118 ± 2.08	131 ± 2.52	97 ± 1.53	129 ± 2.52	136 ± 0.58	152 ± 1	161 ± 1.53
Gen20	106 ± 1.15	116 ± 1	133 ± 1.53	96 ± 2.08	129 ± 0.58	138 ± 1	157 ± 1.53	166 ± 1
Gen21	103 ± 1	123 ± 0.58	131 ± 1.73	94 ± 1.53	130 ± 1	140 ± 1	150 ± 0.58	158 ± 0.58
Gen22	107 ± 1	118 ± 1.15	129 ± 1.15	96 ± 0.58	128 ± 1.53	139 ± 1	156 ± 1.15	165 ± 1
Gen23	96 ± 56.89	120 ± 1	133 ± 2	111 ± 0.58	137 ± 2.65	142 ± 0.58	161 ± 1.15	170 ± 1
Gen24	114 ± 3.51	124 ± 4.04	126 ± 1.53	104 ± 3.61	131 ± 4	136 ± 1.53	152 ± 1.15	164 ± 1.15
Gen25	96 ± 2.52	106 ± 1.53	122 ± 1.15	86 ± 1.53	115 ± 2	131 ± 1.53	141 ± 1.73	150 ± 1.53
Gen26	105 ± 1.73	115 ± 1.53	129 ± 0.58	95 ± 0.58	123 ± 2.52	137 ± 1	154 ± 1.73	161 ± 1
Gen27	100 ± 4.04	111 ± 3.79	127 ± 0.58	91 ± 3.21	120 ± 2.52	134 ± 1.15	155 ± 0.58	165 ± 1
Gen28	96 ± 1.53	107 ± 2.52	126 ± 1.15	87 ± 1	117 ± 2.65	131 ± 2.65	145 ± 1.73	156 ± 1.53

	DHFM	FRLN	FRDM	FRPP	IFRW	NSPF	YLPL	PLHT
Gen1	170 ± 1.53	10.7 ± 2.34	8.83 ± 0.32	120 ± 16.98	1.9 ± 0.2	75.1 ± 6.1	0.23 ± 0.04	61.73 ± 5.85
Gen2	171 ± 2.08	15.08 ± 1.89	10.77 ± 2.27	144 ± 20.7	4.33 ± 0.45	83.2 ± 6.17	0.63 ± 0.15	64.1 ± 15.1
Gen3	169 ± 1.15	7.73 ± 0.55	9.67 ± 0.85	134 ± 18.46	2.83 ± 0.12	75.87 ± 12.58	0.38 ± 0.04	72.77 ± 14.15
Gen4	166 ± 1	2.8 ± 0.26	12.77 ± 0.85	172 ± 10.76	2.83 ± 0.21	83.73 ± 17.45	0.49 ± 0.04	56.1 ± 5.28
Gen5	167 ± 1.73	7.17 ± 0.8	10.07 ± 1.07	106 ± 20.07	2.5 ± 0.2	66.07 ± 10.45	0.27 ± 0.07	55.2 ± 4.65
Gen6	164 ± 1	8.7 ± 0.3	9.3 ± 5.2	142 ± 32.59	2.33 ± 0.35	91.63 ± 10.97	0.34 ± 0.11	43 ± 2.61
Gen7	167 ± 1.15	7.7 ± 0.72	11.63 ± 0.96	102 ± 2.6	3.77 ± 0.23	68.3 ± 10.93	0.39 ± 0.03	54.77 ± 5.41
Gen8	166 ± 4.93	6.23 ± 0.42	9.37 ± 0.93	156 ± 32.06	1.83 ± 0.15	63.4 ± 7.56	0.29 ± 0.08	63.2 ± 7.37
Gen9	172 ± 0.58	8.53 ± 0.59	8.53 ± 0.87	138 ± 63.35	2.93 ± 0.31	72.77 ± 6.43	0.4 ± 0.17	42.27 ± 1.75
Gen10	173 ± 0.58	4.87 ± 0.32	13.23 ± 0.61	94 ± 7.54	3.67 ± 0.24	70.33 ± 10.06	0.34 ± 0.01	56.07 ± 5.56
Gen11	172 ± 2.52	5.63 ± 0.25	9.7 ± 0.36	191 ± 31.51	3.63 ± 0.31	72.5 ± 7.73	0.69 ± 0.13	75.47 ± 5.25
Gen12	170 ± 0.58	7.13 ± 0.32	10.5 ± 0.96	156 ± 32.25	2.57 ± 0.29	70.27 ± 4.75	0.39 ± 0.05	68.03 ± 2.46
Gen13	175 ± 1.53	9.87 ± 0.83	7.8 ± 0.56	164 ± 41.14	2.43 ± 0.32	56.03 ± 4.76	0.41 ± 0.16	64.9 ± 6.16
Gen14	151 ± 1	7.5 ± 0.44	11.07 ± 0.21	94 ± 12.27	0.73 ± 0.06	68.07 ± 2.9	0.07 ± 0	35.17 ± 5.1
Gen15	157 ± 1	7.03 ± 0.15	8.57 ± 0.61	184 ± 24.03	1.57 ± 0.12	75.73 ± 5.05	0.29 ± 0.02	54.8 ± 5.46
Gen16	168 ± 0.58	4.87 ± 0.15	10.2 ± 0.75	115 ± 22.01	0.87 ± 0.06	43.63 ± 4.16	0.1 ± 0.03	34.27 ± 1.25
Gen17	164 ± 1.15	9.03 ± 0.72	12.7 ± 0.4	159 ± 22.25	6.1 ± 0.26	102.73 ± 2.97	0.97 ± 0.11	52.83 ± 3.45
Gen18	175 ± 1	7.83 ± 0.87	14.53 ± 0.6	98 ± 6.38	5.5 ± 0.53	90.77 ± 2.47	0.54 ± 0.04	39.27 ± 1.53
Gen19	172 ± 1	5.2 ± 0.46	9.17 ± 0.42	167 ± 15.42	0.77 ± 0.06	76.67 ± 6.87	0.13 ± 0.02	33.37 ± 3.2
Gen20	174 ± 4.73	4.53 ± 0.42	11.5 ± 0.6	165 ± 21.75	0.87 ± 0.06	67.57 ± 2.89	0.14 ± 0.01	55.17 ± 4.75
Gen21	174 ± 2.65	2.8 ± 0.3	8.6 ± 0.62	151 ± 30.2	0.87 ± 0.06	43.73 ± 6.09	0.13 ± 0.03	41.1 ± 2.4
Gen22	175 ± 1.15	1.2 ± 0.26	11 ± 0.1	123 ± 51.13	2.63 ± 0.21	95.17 ± 8.81	0.33 ± 0.15	58.8 ± 4.97
Gen23	174 ± 0.58	2.97 ± 0.21	7.2 ± 0.17	220 ± 4.95	0.8 ± 0.1	41.73 ± 7.43	0.18 ± 0.02	72.9 ± 3.3
Gen24	171 ± 1.15	6.53 ± 0.42	10.13 ± 0.87	194 ± 37.92	3.3 ± 0.36	91.87 ± 10.29	0.64 ± 0.12	62.9 ± 4.03
Gen25	163 ± 2.52	4.97 ± 0.25	8.07 ± 0.21	92 ± 20.62	1.33 ± 0.15	67.03 ± 22.63	0.12 ± 0.04	44.67 ± 1.5
Gen26	169 ± 1.53	3.23 ± 0.21	7.47 ± 0.06	59 ± 3.76	0.8 ± 0.1	47.3 ± 6.24	0.05 ± 0.01	38.03 ± 2
Gen27	169 ± 0.58	6.5 ± 0.44	13.37 ± 0.71	80 ± 13.48	3.77 ± 0.32	88.97 ± 20.16	0.31 ± 0.07	42.17 ± 3.01
Gen28	164 ± 3.79	5.4 ± 0.52	10.43 ± 1.1	58 ± 6.73	0.33 ± 0.06	53.67 ± 3.12	0.02 ± 0	38.63 ± 2.14

Values are mean ± standard deviation; DFRF: days to first flowering, DFTF: days to 50% flowering, DHDF: days to 100% flowering, DFFS: days to first fruiting, DFTS: days to 50% fruiting, DHFS: days to 100% fruiting, DFFM: days to first green fruit maturity, DFTM: days to 50% green fruit maturity, DHFM: days to 100% green fruit maturity, FRLN: fruit length (cm), FRDM: fruit diameter (mm), FRPP: number of fruits/plant, IFRW: individual fruit weight (g), NSPF: numbers of seeds/fruit, YLPL: green chilli yield/plant (kg), PLHT: plant height (cm)

Table 3. Distribution of 28 chilli genotypes among different clusters on the basis of Mahalanobis D^2-analysis

cluster	Genotypes
Cluster I	Gen3, Gen16, Geen17
Cluster II	Gen4, Gen5, Gen7, Gen9, Gen11, Gen12, Gen13, Gen14, Gen22, Gen23, Gen25, Gen27, Gen28
Cluster III	Gen6, Gen18, Gen19, Gen20, Gen21
Cluster IV	Gen1, Gen2, Gen8, Gen10, Gen15, Gen24, Gen26

Table 4. Mean values of 16 traits for each of the four clusters identified in 28 chilli genotypes. The number of genotypes included in each cluster is given in the respective parenthesis

Traits	Cluster I (n = 3)	Cluster II (n = 13)	Cluster III (n = 5)	Cluster IV (n = 7)
DFRF	**115.11**	104.23	97.8	107.71
DFTF	114.11	115.56	108.33	**117.95**
DHDF	**129.22**	125.59	122.87	126.14
DFFS	**104.89**	99.08	88.6	100.67
DFTS	**132.89**	125.54	117.33	128.52
DHFS	**138.67**	133.77	130.8	134.19
DFFM	**158.11**	151.31	146.87	154.76
DFTM	**167.89**	160.77	155.73	164.14
DHFM	**172.44**	168.82	163.07	170.76
FRLN	5.04	**7.28**	5.52	6.33
FRDM	9.01	9.94	10.08	**11.36**
FRPP	**201.44**	156.31	76.64	108.51
IFRW	2.58	2.48	1.39	**2.98**
NSPF	68.7	**74.1**	65.01	72.77
YLPL	**0.5**	0.38	0.11	0.31
PLHT	70.42	54.74	39.73	51.44

DFRF: days to first flowering, DFTF: days to 50% flowering, DHDF: days to 100% flowering, DFFS: days to first fruiting, DFTS: days to 50% fruiting, DHFS: days to 100% fruiting, DFFM: days to first green fruit maturity, DFTM: days to 50% green fruit maturity, DHFM: days to 100% green fruit maturity, FRLN: fruit length (cm), FRDM: fruit diameter (mm), FRPP: number of fruits/plant, IFRW: individual fruit weight (g), NSPF: numbers of seeds/fruit, YLPL: green chilli yield/plant (kg), PLHT: plant height (cm); the boldface numbers are the highest values among all cluster for the respective traits

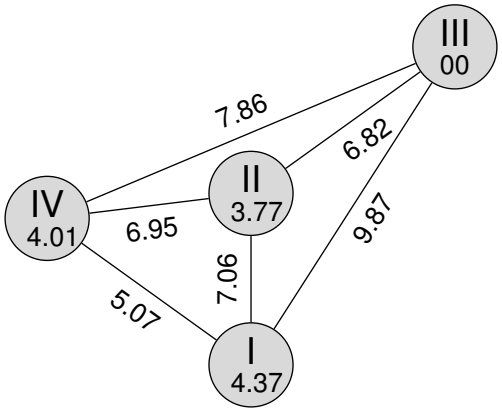

Figure 2. Average intra and inter cluster distance (D^2) for 28 chilli genotypes

The minimum inter-cluster distance (4.37) was observed between genotypes of cluster II and III (Fig. 2) which can be used for backcross breeding program. The genotypes of cluster I and II also showed minimum inter-cluster distance. The low inter-cluster distance between these cluster pairs suggested close proximity of genotypes grouped in these clusters with respect to their genetic constitution. The genotypes grouped into the same cluster presumably diverge very little from one another and crossing of genotypes belonging to the same cluster is not expected to yield desirable segregants. Based on inter- cluster distance, the earlier workers (Mishra et al., 2001; Janaki et al., 2015; Srinivas et al., 2015) have also suggested selection of parents from diverse clusters for utilization in hybridization program to obtain desirable transgressive segregants.

The composition of cluster means of chilli genotypes for different characters showed considerable differences among the clusters for each trait (Table 4). Cluster I was observed to be the most important with maximum cluster means for most of the valuable traits including number of fruits/plant and number of fruit yield/plant. On the other hand, the highest values for fruit diameter, days to 50% flowering and individual fruit weight were estimated in cluster I. The highest values of fruit length and number of seeds/fruit were recorded from cluster II. It has been well established that more the genetically diverse parents used in hybridization program, greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in segregating generations. Hence, different clusters of genotypes on the basis of means revealed divergence for different characters and can be utilized as indicators for selecting diverse parents for specific trait in hybridization program (Kumar and Mallikarjunaiah, 2010; Janaki et al., 2015; Bijalwan et al., 2018; Sindhusha and Rawat, 2020).

4 Conclusion

According to the results of the study, it can be concluded that Genotype 7 from cluster II, Genotype 20 from cluster III, and Genotype 8, Genotype 10 and Genotype 24 from cluster IV are better parents for an efficient hybridization program of chilli.

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Conflict of Interest

The authors declare that there is no conflict of interests regarding the publication of this paper.

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