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Original Research Article

Genetic Variability and Genetic Divergence Study in Early Cauliflower (*Brassica oleracea* L. var *botrytis*)

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A B S T R A C T

Fifteen genotypes of cauliflower were evaluated to study the magnitude of genetic variability, heritability, genetic advance and genetic divergence. The genotypes were evaluated for fourteen quantitative characters *viz.*, Plant height (cm), Plant spread (cm), No. of leaves, leaf length(cm) leaf blade width (cm), days to 1st curd initiation, days to 50% curd initiation, net curd weight(g), gross curd weight, curd length, curd width, harvest duration, harvest index (%), total yield (q/ha). The present study showed that PCV was higher than GCV for all the traits indicated the presence of environmental effect for traits expression. High heritability coupled with high genetic advance was observed for number of leaves, leaf blade width, net curd weight, gross curd weight, curd width harvest index and total yield which are governed by additive gene and could be effectively improved through selection. The genotypes were grouped into 4 clusters. A majority of genotypes grouped together in cluster 1 (with 12 genotypes) and other clusters were having 1 genotype each. Intra-cluster value was maximum in cluster 1. Maximum intercluster distance was observed between cluster 4 and 2 followed by that between cluster 3 and 2 and between cluster 4 and 1. Hence, genotypes Sabour Agrim of cluster 4 and genotypesRCEF4 of cluster 2 present the best choice for hybridization. Highest mean value of plant spread (cm), leaf length (cm) leaf blade width (cm), days to 50% curd initiation, net curd weight(g), gross curd weight, curd length, curd width, harvest duration, total yield (q/ha) was observed in cluster 3.Therefore cluster3 and cluster 2 also used for heterosis for improvement of traits.

Keywords

Genetic variability, Genetic divergence, Cauliflower, Heritability, Genetic advance

Introduction

Cauliflower (*Brassica oleracea* L var *botrytis*) has wide adaptability from temperate regions to the tropical and cultivated throughout India (Singh *et al.*, 2005; Varalakshmi, 2009). It is believed that it has been originated in the island of Cyprus (Verma *et al.*, 2011) from where it moved to other areas like Syria, Turkey, Egypt, Italy, Spain and North Western Europe. It is originated from wild cabbage "cole wart" (*Brassica oleracia* var *sylvastris*) through mutation, human selection and adoption. Dr. Jemson at Saharanpur introduced it to India in 1822 during the period of east India company (Swarup and Chatterjee, 1972). It is herbaceous annual vegetable grown for its tender curd and biennial for seed production (Pratima *et al.*, 2013). It has small, thick stem, bearing whorls of leaves and branched tap root system. The main growing point develops into shortened shoot system whose apices make up the convex surface of curd. It

is monogenomic species belonging to 'C' genome and possessed the chromosome number n = 9 *Brassica oleraceae* is a triple tetrasomic with the genomic formula ABBCCDEEF with 6 basic genomes & some secondary paring. India is the second largest producer of cauliflower in the world after China. It is rich source of minerals like phosphorus, potassium, calcium, sodium and iron and has medicinal values. Cauliflower is high in glucosinolates & isothiocyanates, two groups of antioxidants that have been shown to slow the growth of cancer cells.

Genetic variability in a population is of immense importance for biodiversity because variability not only helps in crop improvement but also provides crop adaptability to environmental changes & therefore, makes it less prone to extinction. Hence study of genetic variability along with heritability and genetic advance is required for formulating breeding method.

Information on genetic divergence of plant is vital to a plant breeder for efficient choice of parents for hybridization. Parent identification on the basis of divergence analysis is expected to be more promising in hybridization for both self and cross pollinated crops. Present investigation was carried out to estimate genetic variability and genetic divergence in cauliflower.

Materials and Methods

Present investigation was carried out at Vegetable Research Farm, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar during ravi season in 2019-2020. Research was conducted using 15 genotypes of cauliflower in Randomized Block Design (RBD) in 3 replications. The materials were collected from different districts of Bihar. The genotypes were evaluated for fourteen quantitative characters *viz.*, Plant height (cm), Plant spread (cm), No. of leaves, leaf length (cm) leaf blade width (cm), days to 1st curd initiation, days to 50% curd initiation, net curd weight(g), gross curd weight, curd length, curd width, harvest duration, harvest index (%), total yield (q/ha).

Data analysis was carried out by Panse and Sukhatme (1978). Phenotypic and Genotypic coefficients of variation were calculated by the method suggested by Burton (1952). Heritability in broad sense is the ratio of genotypic variance to the total variance and genetic advance as percent of mean were obtained by the formula given by Lush (1949) and Johnson *et al.,* (1955). To access genetic diversity among the 15 genotypes of early cauliflower, Mahalanobis (D^2) statistic (Mahalanobis, 1936) was used, following the procedure given by Rao, 1952. Grouping of genotypes into clusters was done using Tocher's method as described by Rao, 1952.

Results and Discussion

Analysis of Variance clearly depicted that significant genetic variation was observed for all the characters under study (Table 1). The 15 genotypes included in the study were genetically diverse and considerable amount of variability were present among the genotypes. Hence there are relevant prospects for isolating promising genotypes for high yield and other desirable parameters.

Information on genetic variability of yield and its component traits is of paramount importance in crop improvement programme. The extent of genotypic variability indicates the amenability of given characters for its improvement as reported by Burton, 1952. The estimate of Genetic parameters of fourteen characters of cauliflower is presented in Table 2. Phenotypic Coefficient of Variation (PCV) was higher than Genotypic Coefficient of Variation (GCV)

for all the characters indicated that the characters were influenced by environment (Singh *et al.,* 2010). Low GCV was recorded for the characters days to first curd initiation (7.25%), days to 50% curd initiation (9.75%) and for harvest duration (8.59%). None of the characters show low PCV.

Moderate GCV were recorded for traits like plant height (14.03%), plant spread (12.13%), number of leaves (13.33%), leaf length (10.37%) and leaf blade width (12.99%), Curd length (10.94) and curd width (14.83) while moderate PCV were recorded for all characters except net curd weight, gross curd weight, harvest index and total yield.

High PCV and GCV were recorded for the traits, net curd weight (39.72%, 38.74%), gross curd weight (32.65%, 31.42%), harvest index (33.17%, 31.83%) and total yield similar result was found by Singh, 2013 and Kumar *et al.,* 2017. The result shows that these traits were improved through selection in cauliflower.

In this experiment high heritability was recorded for number of leaves (61.91%), leaf blade width (68.37%), net curd weight (95.15%), gross curd weight (92.64%), curd length (64.489%), curd width (76.01%), harvest index (92.05%) and total yield (85.58%). Characters including plant height (59.77%), plant spread (55.51%), leaf length (59.82%), days to first curd initiation (40.04%), days to 50% curd initiation (52.17%) and harvest duration (52.91%) were found to record moderate heritability.

High genetic advance as percent of mean were recorded in plant height (22.35%), number of leaves (21.60%), leaf blade width (22.13%), net curd weight (77.85%), gross curd weight (62.30%), curd width (26.62%), harvest index (62.90%) and total yield (61.49%). Low genetic advance was recorded in one character *i.e.* days to first curd initiation (9.45%). High heritability alone is not enough to make efficient selection in segregating generation unless the information is accompanied for substantial amount of genetic advance (Singh *et al.,* 2006; Burton, 1952 and Panse, 1957).

High heritability coupled with high genetic advance was observed for number of leaves (61.91%, 4.92%), leaf blade width (68.37%, 3.63%), net curd weight (95.15%, 239.87%), gross curd weight (92.64%, 502.54%)curd width (76.01% 3.05%), harvest index (92.05%, 24.39%) and total yield which are governed by additive gene and could be effectively improved through selection.

On the basis of relative magnitude of D^2 value, the 15 genotypes of early cauliflower were grouped into 4 clusters (Fig. 1) with an assumption that those within a cluster had smaller differences in D^2 value among themselves than those of other clusters.

Depending upon the genetic divergence, cluster 1 had maximum number of genotypes indicating less variation existed among the genotypes for character study. Inter cluster distance were higher than intra-cluster distance indicating the presence of wider genetic diversity among genotypes included in these cluster (Table 3 and 4).

These results are in accordance to the findings of Quamruzzaman *et al.,* (2007) and Santhosa *et al.,* (2011). Occurrence of wider genetic diversity contributes to heterosis.

Intra-cluster value was maximum in cluster 1. Maximum intercluster distance was observed between cluster 4 and 2 followed by that between cluster 3 and 2 and between cluster 4 and 1. Hence, genotypes Sabour Agrim of cluster 4 and genotypesRCEF4 of cluster 2 present the best choice for hybridization.

Table.1 Analysis of Variance for fourteen characters in cauliflower

Sl No	Traits	Source of variation	Mean squares			
			Replicate	Treatment	Error	CV
		df	2	14	28	
1	Plant height(cm)		0.07	18.89**	3.46	11.51
2	Plant spread(cm)		18.65	213.94**	45.10	10.86
3	No.of leaves		1.09	33.26**	5.66	10.46
4	leaf length(cm)		5.65	56.15**	10.27	8.50
5	leaf blade width (cm)		0.09	15.73**	2.10	8.84
6	Days to 1st curd initiation		18.60	48.28**	16.08	8.87
7	Days to 50% curd initiation		0.62	102.84**	24.07	9.34
8	Net curd weight(g)		912.23	43473.75**	725.95	8.74
9	Gross curd weight (g)		12810.06	197814.25**	5101.72	8.86
10	Curd length (cm)		0.86	6.55**	1.02	8.12
11	Curd width (cm)		0.02	9.55**	0.91	8.33
12	Harvest Duration (days)		1.87	133.06**	30.44	8.11
13	Harvest index(%)		2.69	470.14**	13.16	9.35
14	total yield (q/ha)		324.77	6982.85**	371.27	13.24

** Significant at 1% level

Table.2 Genetic parameters of fourteen characters in cauliflower

Sl. no.	**Characters**	**σ 2 g**	**σ 2 p**	**GCV (%)**	**PCV (%)**	**h 2**	**GA**	**GA % mean**
1	Plant height(cm)	5.14	8.60	14.03	18.15	59.77	3.61	22.35
2	Plant spread(cm)	56.28	101.38	12.13	16.28	55.51	11.51	18.62
3	No. of leaves	9.20	14.86	13.33	16.94	61.91	4.92	21.60
4	leaf length(cm)	15.29	25.57	10.37	13.41	59.82	6.23	16.53
5	leaf blade width (cm)	4.54	6.65	12.99	15.71	68.37	3.63	22.13
6	Days to 1st curd initiation	10.73	26.81	7.25	11.46	40.04	4.27	9.45
7	Days to 50% curd initiation	26.26	50.33	9.75	13.50	52.17	7.62	14.51
8	Net curd weight(g)	14249.27	14975.22	38.74	39.72	95.15	239.87	77.85
9	Gross curd weight (g)	64237.51	69339.23	31.42	32.65	92.64	502.54	62.30
10	curd length (cm)	1.84	2.86	10.94	13.62	64.49	2.25	18.09
11	curd width (cm)	2.88	3.79	14.83	17.00	76.01	3.05	26.62
12	Harvest Duration (days)	34.21	64.64	8.59	11.81	52.91	8.76	12.88
13	Harvest index (%)	152.33	165.48	31.83	33.17	92.05	24.39	62.90
14	total yield (q/ha)	2203.86	2575.13	32.27	34.88	85.58	89.46	61.49

Where, σ 2 g= Genotypic variance, σ 2 p= Phenotypic variance, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h 2 = Heritability and GA= Genetic advance

Table.3 Clustering pattern of fifteen genotypes of cauliflower on the basis of D2 statistics

Cluster	**Genotypes**											
I	RCEF1	RCEF2	RCEF3	RCEF5	RCEF6	RCEF7	RCEF8	RCEF9	RCEF10	RCEF12	RCEF13	RCEF14
II	RCEF4											
II	RCEF11											
IV	Sabour Agrim											

Table.4 Cluster mean of fourteen characters in cauliflowers

Cluster	Plant height(cm)	Plant spread(cm)	No.of leaves	leaf length(cm)	leaf blade width (cm)	Days to 1st curd initiation	Days to 50% curd initiation	Net curd weight(g)	Gross curd Weight (g)	curd length (cm)	curd width (cm)	Harvest Duration (days)	Harvest index (%)	total yield (q/ha)
I	16.09	59.28	22.14	36.98	16.11	44.17	51.06	269.71	728.82	12.07	10.96	67.17	36.91	130.50
II	15.48	67.40	26.67	43.80	19.40	52.00	61.00	300.00	1316.66	13.80	12.20	75.00	22.78	140.74
III	16.60	79.40	26.33	44.60	20.40	51.00	61.00	610.00	1386.67	14.40	15.20	75.00	42.95	266.22
IV	17.20	69.60	22.67	33.40	13.00	45.00	53.67	475.00	650.00	13.20	12.80	65.00	73.07	209.53

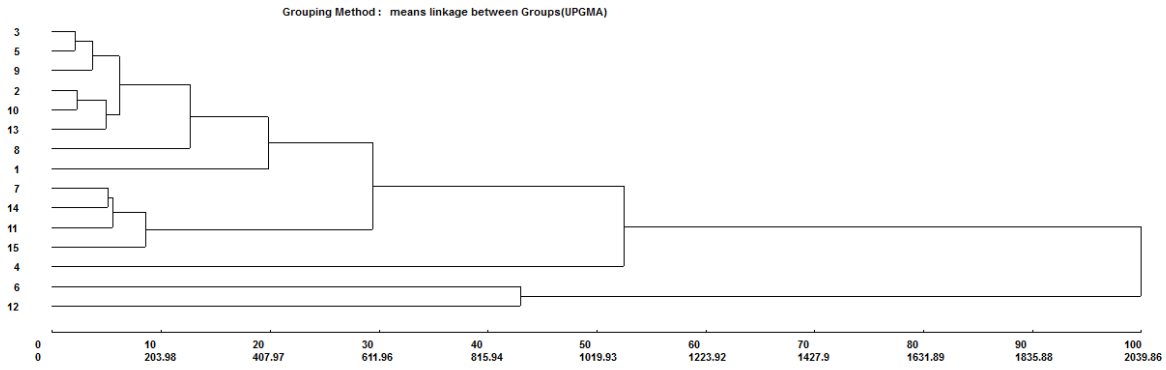
Table.5 Mean intra and inter cluster distance (D^2) among four clusters in cauliflower

Clusters	**I**	**II**	**III**	**IV**
I	**394.407**	1071.212	1448.233	2314.367
II		0	2695.897	5189.51
III			0	876.582
IV				0

Table.6 Contribution percentage of fourteen characters towards genetic divergence in cauliflower

Sl No	Source	Contribution (%)
1	Plant height(cm)	1.46
2	Plant spread(cm)	1.79
3	No. of leaves	2.65
4	leaf length(cm)	0.97
5	leaf blade width (cm)	1.58
6	Days to 1st curd initiation	0.56
7	Days to 50% curd initiation	0.69
8	Net curd weight(g)	49.57
9	Gross curd weight (g)	11.05
10	curd length (cm)	1.96
11	curd width (cm)	0
12	Harvest Duration (days)	0.36
13	Harvest index (%)	16.57
14	total yield (q/ha)	10.75

Fig.1 Clustering pattern of 15 cauliflower genotypes on the basis of D^2 statistic by Tocher's method



Highest mean value of plant spread (79.40 cm), leaf length (44.60 cm) leaf blade width (20.40 cm), days to 50% curd initiation (61), net curd weight(610 g), gross curd weight (1386.67g), curd length (14.40 cm), curd width (15.20 cm), harvest duration (75), total yield (266.22 q/ha) was also observed in cluster 3 (Table 5 and 6).

For heterosis breeding, cluster 4 and 2 were

selected, whereas for improvement of traits, cluster 3 was selected because it had highest number of characters with maximum cluster means.

The present findings have adequate genetic variability in the germplasm and there is need for evaluation of improvement of economic traits. High PCV has been recorded for respective GCV. Therefore, selection has been made on the basis of GCV. High heritable characters and genetic advance were recorded for number of leaves, leaf blade width, net curd weight, gross curd weight curd width, harvest index and total yield. On the basis of relative magnitude of D^2 value, the 15 genotypes of early cauliflower were grouped into 4 clusters with an assumption that those within a cluster had smaller differences in D^2 value among themselves. Cluster 4 and 2 were selected for heterosis breeding because they have maximum inter-cluster distance.

References

Burton, G.W., 1952. Quantitative inheritance in grasses. *Pro VI IntGrassl Cong, 1952*, pp.277-283.

Johnson, H.W., Robinson, H.F. and Comstock, R.E., 1955. Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal*, *47*(7), pp.314-318.

Kumar, V., Singh, D. K., Panchbhaiya, A. and Singh, N. 2017. Correlation and path coefficient analysis studies in mid-season cauliflower (Brassica oleracea var. botrytis L.). *Journal of Pharmacognosy and Phytochemistry*. 6(4): 1130-1137.

Lush, J.L., 1949. Heritability of quantitative characters in farm animals. *Heritability of quantitative characters in farm animals.*

Mahalanobis, P.C., 1936. On the generalized distance in statistics. National Institute of Science of India.

Panse, V.C. and Sukhatme, P.V., 1978. Statistical methods for Agricultural workers. III Rev. *Ed. ICAR, New Delhi*.

Panse, V.G. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics*. 17:318-328

Panse, V.G. and Sukhatme, P.V., 1954. Statistical methods for agricultural workers. *Statistical methods for agricultural workers.*

Pratima, S., Sanjay, K., Sutanij, M. and Abhishek, S., 2013. Genetic variability, heritability and genetic advance in cauliflower (Brassica oleracea var. botrytis L.). *International Journal of Plant Sciences (Muzaffarnagar)*, *8*(1), pp.179-182.

Quamruzzaman, A.K.M., Rahman, M.M., Uddin, M.N., Siddiky, M.A. and Prodhan, M.D.H., 2007. Genetic diversity in cauliflower (Brassica oleracea L. var. botrytis). *Indian Journal of Horticulture*, *64*(1), pp.50-52.

Rao, C.R., 1952. Advanced statistical methods in biometric research.

Santhosha, H.M., Varalakshmi, B. and Gowda, N.N., 2011. Genetic diversity in early cauliflower (*Brassica oleracea var. botrytis* L.) germplasm. *Journal of Horticultural Sciences*, *6*(1), pp.21-24.

Singh G, Singh DK, Bhardwaj SB. Variability studies in November maturity group of cauliflower (*Brassica oleracea* var. *botrytis*). Pantnagar J Res. 2010; 8(2):202-205.

Singh, B., Mishra, A.K., Sanwal, S.K., Singh, P.K. and Mathura, R., 2013. Genetic variability and character association analysis in cabbage hybrids. *Indian*

Journal of Horticulture, *70*(2), pp.296-299.

Singh, B., Pandey, A.K., Verma, A. and Rai, M. 2006. Genetic Variability in Aghani Group of Indian Cauliflower (*Brassica oleracea*var. *botrytis* L.). *Indian Journal of Plant Genetic Resources*. 19(1): 113-117.

Singh, D., Varalaksmi, B. and Reddy, NMA. (2005). Combining ability studies in early cauliflower *(Brassica oleracea* var. *botrytis* L*). Indian J. Hortic.,* 62:27-32.

Swarup, V. and Chatterjee, S. S. (1972). Origin and genetic improvement of Indian cauliflower. *Econ. Bot*.,26(4):381-393.

Varalaksmi, B. (2009). Heterosis and combining ability for yields and its components in cauliflower. *Indian J.Hortic.,* 66:198-203.

Verma, I.C., Saxena, R. and Kohli, S., 2011. Past, present & future scenario of thalassaemic care & control in India. *The Indian journal of medical research*, *134*(4), p.507.