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Study of genetic divergence for earliness and yield attributing traits in tropical cauliflower (*Brassica oleracea* var. *botrytis* L)

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Abstract
An experiment conducted during session 2015-2016 at two different season to study the genetic diversity among the different lines taken. All the genotypes were divided into four different clusters. Cluster I was the largest and cluster III and IV were the smallest cluster classified. The highest inter cluster distance (580.42) was observed in between cluster I and cluster IV followed by cluster I and III (438.36), cluster I and II (180.79) and cluster II and cluster IV (185.76). In the present investigation, cluster IV contains genotype with early curd initiation (73.25 days) and curd maturity (84.75 days). The cluster with highest net curd weight was found to be in cluster IV (304.08 g), while the lowest curd weight was in cluster I (212.38 g). It is may be concluded that crossing between genotypes of cluster IV and I are likely to be exploited for high heterosis for net curd weight, marketable curd weight in cauliflower.

Keywords: cauliflower, tropical, yield attributing traits, genetic

Introduction
Cauliflower is the most important crop among the Cole crop in India. The tropical and Indian cauliflower was developed under the natural crossing between Cornish and other European types followed by the selection for the heat tolerant variety. Not only adapted to high temperature, tropical cauliflower was suitable for early crop sowing, high rainfall as well as early harvest Chittora and Singh (2015) [1]. Cultivation of F_1 hybrid now a day's becomes very famous in cauliflower as it gives uniform maturity as well as high yield or earlier (Dey *et al.* 2017) [8]. To get high yielding hybrid, available of diverse line is utmost important (Sharma and Verma 2001). For the quantitative measure of genotypic divergence among the parents Mahalanobis's (1936) [4] D^2· statistics has been extensively used as a breeding tools. Hence, an attempt had been taken to study the genetic diversity among the twenty one lines.

Materials and Methods
A group of twenty one lines including two national variety *i.e* Sabour agrim and Pusa kartik sankar had been taken in this study. They were evaluated in a randomized complete block design at University Farm, Bihar Agricultural University, Sabour, Bhagalpur (Bihar) during 2015-16 and 2016-17. In the present investigation the following characters were recorded like days to 50 per cent curd initiation (D50%CI), days to 50% curd maturity (D50%CM), number of leaves per plant (NL), curd equatorial diameter (cm), curd polar diameter (cm), plant canopy diameter (cm), net curd weight (g), marketable curd weight (g), harvest index (%), curd compactness and biological weight of plant (g). The curd compactness was determined according to Pearson (1931).

$$Z = \frac{\text{Net curd weight}}{\frac{1}{2} \times (\text{Curd equatorial diameter} + \text{Curd polar diameter})} \times 100$$

Z = curd compactness
Data analysis was carried out following Panse and Sukhatme (1978). The genetic divergence among the cauliflower lines was estimated by using D^2 statistics (Mahalanobis, 1936) [4]. All genotypes were clustered into different groups accomplished by Tocher's method (Rao, 1952) [7]. The average distance between the cluster and within the cluster was calculated by the statistical procedure given by Singh and Choudhary (1985).

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Results and Discussion

Clustering pattern on genotypes was different in the individual experiment when compared with the pooled analysis. Pooled data analysis for morphological diversity revealed that all the 21 genotypes were grouped into four groups or clusters (Table 1). Cluster I includes 14 lines, cluster II includes 5 lines, cluster III and cluster IV include single genotype in each cluster. The highest inter cluster distance (580.42) was observed in between cluster I and cluster IV followed by cluster I and III (438.36), cluster I and II (180.79) and cluster II and cluster IV (185.76) showed in table 2.

Table 1: Clustering pattern of diverse cauliflower lines

Clusters	Number of Genotypes	Name of genotypes
I	14	Hzp 108, Sel 35-2, IIVR-52-1, Sel 39, Hzp 114, Sel 16, Sel 31-1, Brmcf 125, Hzp 112, Sel 31-3, Hzp 106, Sel 332, Hzp 111, IIVR 312
II	5	S-A-1, Hzp 110, Pusa kartik sankar, Sel-3, Sel 38-1
III	1	Hzp 101
IV	1	Sabour Agrim

Table 2: Pooled Mean intra (bold) and inter cluster D^2 for the 21 genotypes of cauliflower obtained on the basis of 11 quantitative traits

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	60.17	180.79	438.36	580.42
Cluster 2	180.79	61.49	137.61	185.76
Cluster 3	438.36	137.61	0.00	106.85
Cluster 4	580.42	185.76	106.85	0.00

Pooled cluster mean for all the characters were presented in table (3). Data analysis revealed that number of leaf, curd polar and equatorial diameter, curd compactness and harvest index exhibited moderate variation. In the present investigation, cluster IV contains genotype with early curd initiation (73.25 days) and curd maturity (84.75 days). All the clusters had plant canopy width in the range of 49.56 - 56.19. The cluster with highest net curd weight was found to be in cluster IV (304.08 g), while the lowest curd weight was in cluster I (212.38 g). The genotypes under Cluster IV showed compact curd (26.58 g/ cm^3) in comparison to cluster I (19.30 g/ cm^3). Marketable curd weight (379.08 g) and biological weight (893.16 g) were highest in cluster IV while it was calculated lowest under cluster I (288.65 g) and (522.82), respectively. This result was found to be in similar trend as in net curd weight.

Table 3: Pooled Cluster mean for 11 quantitative characters of cauliflower

	D50%CI	D50%CM	NL	CED	CPD	PCW	NCW	CC	HI	MCW	BW
Cluster 1	83.96	95.41	16.77	12.08	8.58	49.56	212.38	19.30	37.11	288.65	572.82
Cluster 2	83.20	95.10	16.77	12.29	8.77	54.50	240.96	20.68	33.36	319.06	722.50
Cluster 3	98.50	111.75	17.38	12.15	8.88	51.65	302.01	26.46	33.86	375.76	888.33
Cluster 4	73.25	84.75	18.17	12.96	8.88	56.19	304.08	26.58	33.93	379.08	893.16

The exploration of genetic diversity in the available germplasm is a pre-requisite in a breeding programme for effective selection of superior genotypes. A plant breeder, therefore, sets hopes of improvement on the extent of genetic variation and degree of improvement possible on the beneficial genetic variability (Quamruzzaman *et al.,* 2007) [6]. The high D^2 value indicated a high degree of genetic diversity among the genotypes. The similar finding was also obtained by Quamruzzaman *et al.* (2007) [6]. According to Arunachalam *et al*. (1984), the optimum level of genetic divergence between the parents gave the best heterosis and better segregants. Genotypes belonging to the clusters with maximum inter cluster distance are genetically more diverse. Selection of parents for hybridization should be done from two clusters having wider inter cluster distance to get more variability (Dey *et al.*, 2011) [2].

The study of cluster mean value of pooled mean for 11 quantitative characters of cauliflower depict differences in cluster means existed for almost all characters. The highest mean value for biological weight, marketable curd weight, net curd weight, plant canopy width, number of leaf, curd equatorial diameter and curd polar diameter was observed in cluster IV. The less cluster mean for days to 50 % curd initiation and days to 50 % curd maturity was also observed in cluster IV. The cluster I ranked lowest in biological weight, marketable curd weight, curd compactness, net curd weight, plant canopy width, curd equatorial diameter, curd polar diameter and number of leaf, which might be due to small size of the marketable curd weight. It is observed from table 2 that crossing between genotypes of cluster IV and I are likely to be exploited for high heterosis for net curd weight, marketable curd weight in cauliflower.

References

1. Chittora A, Singh DK. Genetic variability studies in early cauliflower (*Brassica oleracea* var. *botrytis* L.) Electronic Journal of Plant Breeding. 2015; 6(3):842-847.
2. Dey SS, Sharma SR, Prakash C, Barnwal RN, Bhatia R. Genetic divergence in snowball cauliflower (*Brassica oleracea* var *botrytis* L.) Indian J Plant Genet. Resour. 2011; 24(1):48-51.
3. Sharma KC, Verma S. Genetic divergence in cauliflower (*Brassica oleracea* var botrytis sub var cauliflora) Indian Journal of Agricultural Sciences. 2001; 71(8):529-30.
4. Mahalanobis PC. On generalized distance in statistics. Proceedings of National Institute of Science, India. 1936; 2:49-55.
5. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers. ICAR, New Delhi, India, 1984.
6. Quamruzzaman AKM, Rahman MM, Uddin MN, Siddiky MA, prodhan MDH. Genetic diversity in cauliflower (*Brassica oleracea* L. var. botrytis). Indian J Hort. 2007; 64(1):50-52.

7. Rao CR. The concept of distance and the problem of group constellation. In: Advance Statistical Methods in Biometrical Research. John Willey and Sons. Inc. New York. USA. 1952; 351.

8. Dey SS, Bhatia R, Bhardwaj I, Mishra V, Sharma K, Parkash C, Kumar S, Sharma VK, Kumar R. Molecular-agronomic characterization and genetic study reveals usefulness of refined Ogura cytoplasm based CMS lines in hybrid breeding of cauliflower (*Brassica oleracea* var. *botrytis* L.) Scientia Horticulturae. 2017; 224:27-36.

9. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India. 1985, 318.