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ESTIMATION OF GENETIC DIVERGENCE IN SOME MID LATE AND LATE CAULIFLOWER (*Brassica oleracea var. botrytis* L.) GERMPLASM

SUBHRAJYOTI CHATTERJEE[1,2*], SHWETA SHARMA[1], DEBMALA MUKHERJEE[2] AND SUMIT PATIL[1]
[1]Department of Vegetable Science,
Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan - 173 230, Himachal Pradesh, INDIA
[2]Department of Vegetable Crops, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia - 741 252, West Bengal.
e-mail: subhrarahul@gmail.com

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***Corresponding author**

ABSTRACT
The present investigation was undertaken at the Experimental Farm of the Department of Vegetable Science, Dr. YS Parmar University of Horticulture and Forestry, Solan, Himachal Pradesh during Rabi season of 2016 to estimate genetic divergence in twenty mid late and late germplasm of cauliflower for ten quantitative characters. The genotypes were grouped into four clusters. Cluster II was found to have maximum (8) number of genotypes while both Cluster I and III contained minimum (3) genotypes each. The genetic stocks within a cluster had smaller D^2 values among themselves than those belonging to different clusters. Intra-cluster distance was maximum (2.091) in cluster IV whereas, it was minimum (1.086) in cluster I. Highest average inter-cluster distance (6.496) was recorded between cluster I and cluster IV. Cluster IV recorded highest mean value for most of the characters. Considering the diversity pattern and mean performances, the genotypes namely EC-683461 from cluster I, Sel-I from cluster II, Kt-25 from cluster III and Hermia, Sel-II, Pant Shubhra from cluster IV would be best choice as parents for future hybridization programme.

INTRODUCTION

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is an important member of the family Brassicaceae and most popular among all the 'cole' vegetables in India. It is characterized by forming a peculiar inflorescence consisting of thick, fleshy, strongly ramified flower stalks which make a compact, often nearly spherical 'curd'. Cauliflower is the only cole crop in which the intermediate stage of curding lies between vegetative and reproductive stage (Nieuwhof, 1969). It is mainly grown for its curds which are rich in vitamin-C (ascorbic acid) and protein. Cauliflower is low in fat but high in dietary fibre, foliate and water, possessing a high nutritional density. It contains a significant amount of glycoalkaloid. Sulforaphane, a compound released when cauliflower is chopped or chewed, may protect against cancer. (Kushwaha *et al*., 2013).

In India, cauliflower is cultivated in an area of 452.13 thousand ha of land having a production of 8498.85 thousand tonnes. The productivity is 18.79 t/ ha (Annonymous, 2017). But in terms of productivity, India is lagging far behind many countries viz., China, Spain and Italy. It is due to unavailability of high yielding improved cultivars and hybrids (Garg and Lal, 2006). Therefore, to narrow down the gap in productivity of this crop between India and other countries, it is important to develop improved hybrids through heterosis breeding among parents which having high genetic diversity.

Genetic diversity is one of the important tools to quantify genetic variability in both cross and self-pollinated crops (Naik and Prasad, 2015). The knowledge of genetic diversity, its nature and degree of variability would be useful for selecting desirable and diverse parents from available germplasm for a successful breeding programme (Ullah *et al*., 2015). Diverse parents are expected to produce high yielding hybrids through manifestation of heterosis, increase the probability to obtain transgressive segregants in F_2 and in subsequent generations. Multivariate analysis is a potent tool for measuring divergence among a set of populations based on multiple characters. D^2 statistic proposed by Mahalanobis (1936) has been generally used as an efficient tool in the quantitative estimation of genetic diversity for a rational choice of potential parent in a breeding programme (Kumar *et al*., 2016). Many researchers have adopted this D^2 technique for measuring divergence among genotypes of cauliflower previously viz., Sharma and Verma., 2001, Quamuruzzaman *et al*., 2007, Dey *et al*., 2010, Santhosha *et al*., 2011, Kumar *et al*., 2017.

In views of these facts, the present study was undertaken with the aim to analyze the genetic divergence of a number of mid-late and late cauliflower genotypes for selecting parents of diverse group for further breeding programme.

MATERIALS AND METHODS

The present study was conducted at the Experimental Farm of the Department of Vegetable Science, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan in Himachal Pradesh, India during Rabi season of 2016. The experiment was laid out with three replications in a Randomized Complete Block Design and experimental materials comprised of twenty genotypes of mid late and late type cauliflower, collected from different parts of country and abroad (**Table 1**). The seed

sowing of all the genotypes was carried out on September, 2016 in raised bed nursery. On 10th October, the healthy seedlings were transplanted at a spacing of 60 cm× 45 cm on individual plot size of 3 m× 2.25 m. Standard cultural practices recommended in the Package of Practices for Vegetable crops (Anonymous, 2013) were followed to ensure a healthy crop stand. Observations were recorded on ten randomly selected plants for ten quantitative characters viz., days to marketable maturity from date of transplanting, stalk length (cm), leaf number per plant, gross weight per plant (g), marketable yield per plant (g), curd depth (cm), plant height (cm), leaf size index (cm^2), curd size index (cm^2) and curd solidity (g/cm).

Genetic divergence was estimated by using D^2 statistics of Mahalanobis (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952). A dendrogram was generated using Wards method as a measure of similarity with the help of SPSS software version 16 and is presented in **Fig. 1**.

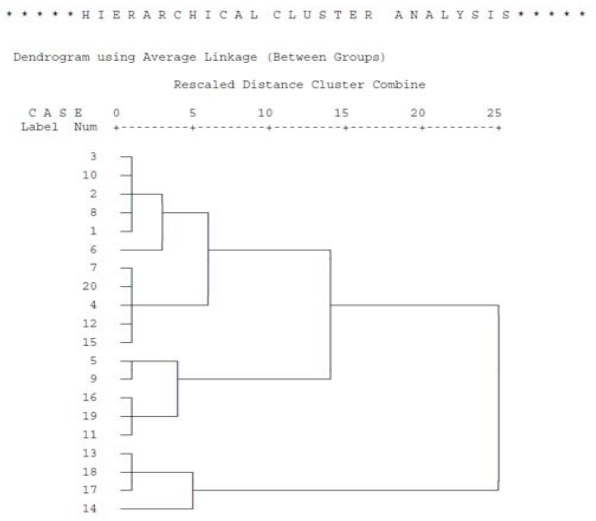

Figure 1: a Dendrogram of genotypes depicting cluster pattern

RESULTS AND DISCUSSION

Cluster composition

After estimating D^2 values for all the possible pairs, twenty genotypes were grouped into four clusters. It revealed that the genotypes of heterogeneous origin were frequently present in same cluster (Table 2). Although the genotypes originated in same place or geographic region were also found to be grouped together in same cluster. This indicated lack of any definite relationship or correlation between genetic diversity and geographic origin of the cauliflower genotypes evaluated in the present study. Therefore, the selection of parental material for hybridization programme simply based on geographic diversity may not be rewarding exercise. The choice of suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographical distances as suggested previously by Kumar *et al*., 2013, Langade *et al*., 2013, Pandey *et al*., 2013, and Singh *et al*., 2014. Maximum number of genotypes (8) were accommodated in cluster II followed by cluster IV (6 nos.) and both cluster I and III (3 nos. each).

Table 1: **List of cauliflower genotypes along with their sources**

Sr no	Genotype	Source
1.	UHF-C-2	Dr YSPUHF, Nauni, Solan
2.	Palam Uphar	CSKHPKV, Palampur
3.	King King	HRI, Wellesbourne, UK
4.	Pusa Himjyoti	IARI, Katrain
5.	EC-683466	NBPGR, New Delhi
6.	EC-683461	NBPGR, New Delhi
7.	EC-162587	NBPGR, New Delhi
8.	Hermia	HRI, Wellesbourne, UK
9.	Kt-18	IARI, Katrain
10.	Kt-25	IARI, Katrain
11.	Kt-19	IARI, Katrain
12.	Kt-20	IARI, Katrain
13.	Kt-22	IARI, Katrain
14.	Mukutamani	IARI, Katrain
15.	Sel-I	Dr YSPUHF, Nauni, Solan
16.	Sel-II	Dr YSPUHF, Nauni, Solan
17.	DC-76	IARI, New Delhi
18.	Pant Shubhra	GBPUAT, Pantnagar, Uttarakhand
19.	Snowball-16	IARI, Katrain
20.	PSBK-I (Check)	IARI, Katrain

Table 2: **Clustering pattern of twenty genotypes of cauliflower on the basis of genetic divergence**

Clusters	Number of genotypes	Genotypes
I	3	EC-683461, Kt-20, Mukutamani
II	8	UHF-C-2, Palam Uphar, King King, Pusa Himjyoti, PSBK-I, Kt-18, Sel-I, Snowball-16
III	3	Kt-25, DC-76, Kt-22
IV	6	EC-683466, Hermia, EC-162587, Kt-19, Sel-II, Pant Shubhra

Intra and Inter cluster differences

The analysis showed that the genetic stock within cluster had smaller D^2 values among themselves than those belonging to different clusters that confirm wider genetic diversity among genotypes of different clusters which was previously also suggested by Sharma and Verma., 2001, Quamuruzzaman *et al*., 2007 and Kumar *et al*., 2017 in cauliflower and Khan *et al*., 2009 in kale and Meena *et al*., 2013 in cabbage. Average intra and inter- cluster distance (D) values have been presented in the Table 3. Maximum intra-cluster distance (2.091) was recorded in cluster IV followed by cluster III (1.398), cluster II (1.291) and cluster I (1.086) with minimum distance suggesting that the genotypes of cluster IV are more heterogeneous while genotypes of cluster I are comparatively homogeneous. The inter-cluster distance was highest at 6.496 between cluster I and cluster IV. So, the members of these clusters were more divergent and there will be more chances of getting better segregants in F_2 and subsequent generations. It was lowest at 3.191 between cluster II and cluster IV, suggesting close proximity of genotypes of cluster II with those of cluster IV in respect of their genetic constitution and heterosis will not be pronounced in subsequent generations.

Cluster means

The cluster means for various horticultural traits have also

Table 3 : Intra and Inter cluster average D values

Clusters	I	II	III	IV
I	1.086			
II	4.151	1.291		
III	3.456	4.175	1.398	
IV	6.496	3.191	5.238	2.091

Table 4 : Cluster means for the characters among 20 genotypes of cauliflower

Characters	I	II	III	IV
Days to marketable maturity from date of transplanting	94.07	118.71	99.97	133.18
Stalk length (cm)	4.65	4.93	5.91	5.49
Leaf number per plant	13.03	14.41	19.92	17.35
Gross weight per plant (g)	945.33	1300.67	1082.67	1563.17
Marketable yield per plant (g)	510.18	581.33	740.66	848.33
Curd depth (cm)	7.88	9.09	9.03	11.20
Plant height (cm)	36.03	51.36	38.21	49.06
Leaf size index (cm^2)	1017.96	868.54	1012.33	656.33
Curd size index (cm^2)	100.64	143.04	114.83	196.17
Curd solidity (g/cm)	64.86	82.10	64.53	76.77

been presented in the Table 4. Among the four clusters, cluster I revealed highest mean performance for the trait leaf size index (1017.96 cm^2), while cluster II for curd solidity (82.10 g/cm) and plant height (51.36 cm). Cluster III recorded highest mean for the traits like leaf number per plant (19.92) and stalk length (5.91 cm). Cluster I showed recorded lowest mean for stalk length (4.65 cm). Cluster IV revealed highest mean performance for curd depth (11.20 cm), gross weight per plant (1563.17 g), marketable yield per plant (848.83 g), curd size index (196.17 cm^2) and days to marketable curd maturity from date of transplanting (133.18 days). Cluster I showed minimum mean performance for the trait days to marketable curd maturity from date of transplanting (94.07 days).

The above results clearly shows wide variation from one cluster to another in respect of cluster means for ten characters, which indicated that genotypes having distinctly different mean performance for various characters were separated into different clusters. The crossing between the entries belonging to cluster pairs having large inter-cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in cauliflower. Considering the mean performance for different characters of genotypes belonging to diverse clusters, the promising genotypes for exploitation as parents in hybridization programme were EC-683461 from cluster I, Sel-I from cluster II, Kt-25 from cluster III and Hermia, Sel-II, Pant Shubhra from cluster IV.

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