Himachal Journal of Agricultural Research 44(1&2) : 50-53 (2018)

Genetic divergence studies in cauliflower (*Brassica oleracea* L. var. *botrytis*) under mid hill conditions of Himachal Pradesh

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Manuscript Received: 15.07.2018; Accepted: 30.11.2018

Abstract

The extent of genetic diversity plays an important role in varietal improvement programme of a particular crop. An experiment was conducted to study genetic divergence in 25 genotypes of cauliflower and data was recorded for 17 quantitative characters. On the basis of D^2 statistics, the genotypes were grouped into three clusters. Based on inter and intra-cluster distances, maximum intra-cluster distance was observed in Cluster I, indicating that the genotypes included in this cluster were genetically diverse. Further, inter-cluster distances revealed maximum values between Clusters I and II, followed by Clusters I and III and, clusters II and III. On the basis of cluster means, Cluster I was observed to be important for earliness and yield characters suggesting the scope of improvement for these traits through the use of genotypes included in this cluster. On the other hand, for morphological and quality characters, Cluster II was observed to be important. Hence, genotypes from diverse clusters with high mean values for different characters present the best choice for further exploitation in cauliflower improvement programme.

Key words: Cauliflower, genetic diversity, genotypes, improvement, yield traits.

Cauliflower (*Brassica oleracea* L. var. *botrytis*) is one of the most popular *Brassica* vegetables cultivated worldwide in different climatic conditions. The name cauliflower has originated from the Latin words 'caulis' and 'floris' which means cabbage and flower, respectively. Another distinctive name given to cauliflower is queen of winter vegetable (Elahi *et al.* 2015). It has been rightly described as "Aristocrat of cole crops" and is grown throughout the world for tender white curds (Nimkar and Korla, 2014). It is believed that it has been originated in the island of Cyprus from where it moved to other areas like Syria, Turkey, Egypt, Italy, Spain and North Western Europe (Kumar *et al.* 2017). Human nutrition from vegetables can be improved by higher per capita consumption, intake of vegetables rich in phytochemicals, their high bioavailability and understanding of bioactivity (Ray *et al.* 2007). Cauliflower is a low-calorie food with good dietary fiber, abundant in vitamins (C, B, A, K) and minerals like phosphorus, potassium, calcium, sodium, iron, manganese, magnesium and molybdenum. It also contains fair amount of glucosinolates and isothiocyanates, those having antioxidant and anti-inflammatory properties. A high intake of cauliflower has been associated with reduced risk of aggressive prostate cancer (Kushwaha *et al.* 2013).

In Himachal Pradesh, it is being cultivated in an area of 5,191 ha with a production of 1,17,012 metric tonnes and productivity of 22.54 metric tonnes/ha (Anonymous, 2015). In the state, it is grown commercially as an off-season crop during summer-rainy (March to November) season in Shimla, Mandi, Solan, Kullu and Kangra districts, bringing lucrative returns to the farmers. The major constraints in increasing and stabilizing production and productivity are the lack of genotypes with high yielding and quality traits. To overcome such constraints, exploring natural biodiversity as a source of novel alleles, is of prime importance in twenty-first century breeding programmes (Fernie *et al.* 2006; Dey *et al.* 2014). The knowledge of nature and degree of divergence in

existing germplasm is prerequisite to formulate such breeding programmes. Successful breeding programme depends on selection of suitable and genetically diverse parents, which can be achieved by using multivariate analysis (Sharma *et al.* 2010). D^2 statistics has been extensively used as quantitative measure of genotypic divergence among parents by earlier workers in their studies under different environments and location of studies. Keeping this in view, the present investigation was undertaken to study the genetic variability and divergence among 25 genotypes of cauliflower under mid hill conditions of Himachal Pradesh.

Materials and Methods

The present investigation was carried out in 2014-15 at the Experimental Farm of the Department of Vegetable Science and Floriculture, CSK HPKV, Palampur. The experimental farm is situated at 32º 6' North latitude, 76 º 3' East longitudes at an elevation of 1290.8 m above mean sea level. The place is characterized by severe winter and mild summer with high rainfall. Agro-climatically, the location represents mid hill zone of Himachal Pradesh and is characterized by humid sub temperate climate with an annual rainfall of 2500 mm of which 80 per cent is received during June to September. The soil is acidic in nature with pH ranging from 5.0 to 5.6 and soil texture is silty clay loam. The experiment material comprising of 25 genotypes along with one standard check namely, cauliflower hybrid Madhuri was laid out in randomized complete block design (RBD) with three replications. Each genotype was transplanted at spacing of 45 cm each within rows and 45 cm between plants. The standard cultural practices to raise the crop were followed as per the recommendations of package of practices for vegetable crops by CSKHPKV, Palampur.

Data were recorded on days to curd initiation from transplanting, days to marketable curd maturity from date of transplanting, gross weight per plant, marketable yield per plant, curd depth, curd diameter, curd size index, per cent marketable curds, curd compactness, curd solidity, stalk length, number of leaves per plant, plant height, dry matter content, ascorbic acid content, total soluble solids and harvest index. Mean values were subjected to Mahalanobis's generalized distance (D^2) to determine the degree of divergence and the group constellations were arrived by Tocher's method as described by Rao (1952).

Results and Discussion

Information on nature and magnitude of variability present in a population is an important pre-requisite for starting any systematic breeding programme. In the present study, the analysis of variance revealed highly significant differences for all the characters indicating existence of sufficient variability and validated further genetic analysis. Cluster analysis based on D^2 statistics is highly useful in grouping of genotypes based on phenotypic diversity. On the basis of D^2 statistics, 25 genotypes were grouped into three clusters (Table 1). Majority of the genotypes were grouped together in Cluster III (12), followed by Cluster II (7) and Cluster I (6). Different genotypes were grouped into different clusters by Dey *et al.* (2015). Heterogeneous geographic origin of genotypes was revealed through the cluster composition indicating that the genotypes were distributed amongst different clusters randomly irrespective of their geographic origin (Sharma *et al.* 2010). Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. Similar findings were also reported by Sharma and Verma (2001).

Table 1. Grouping of 25 cauliflower genotypes based on non-hierarchical cluster analysis

Clusters	Number of genotypes	Genotype (s)
I	6	H 1, H 2, H 6, H 11, H 12, H 15
II	7	H 7, H 9, H 16, H 17, H 20, H 21, H 25 (Madhuri)
III	12	H 3, H 4, H 5, H 8, H 10, H 13, H 14, H18, H 19, H 22, H 23, H 24

Intra-cluster value was maximum in Cluster I (3.454) and minimum in Cluster II (3.314) (Table 2). Maximum inter-cluster distance was observed between Clusters I and II, followed by Clusters I and III and clusters II and III. Hence, genotypes from diverse clusters viz., cluster I and cluster II present the best choice for hybridization for obtaining useful segregants for further exploitation in cauliflower improvement programme. Selection of genotypes based on genetic divergence will be helpful in identifying parental lines for developing heterotic hybrids and hybridization based programme. Minimum inter-cluster distance between clusters II and III displayed the lowest degree of divergence suggesting close genetic makeup of the included genotypes. Different inter and intra cluster distances were also reported by Santosha *et al.* (2011). Homogeneous nature of strains within clusters and heterogeneous strains between the clusters was indicated by lesser magnitude of intra-cluster distance than inter-cluster ones (Sharma *et al.* 2010).

On the basis of cluster means, Cluster I was observed to be important for earliness and yield characters like days to initiation, days to marketable curds, gross weight, marketable yield, curd size index, curd diameter, curd compactness and number of leaves per plant (Table 3). It indicates the importance of genotypes residing in Cluster I for hybridization programme for earliness and yield contributing characters. Whereas, for morphological characters like, stalk length, plant height and quality trait, ascorbic acid, Cluster II was observed to be important. Cluster III showed maximum mean values for curd depth, curd solidity, % marketable curds, dry matter, TSS and harvest index indicating its significance for these traits. Different cluster means for various characters have also been reported by earlier research workers (Santosha *et al.* 2011).

Table 2. Average inter and intra cluster distances in different clusters

Cluster	I	II	III
Cluster I	**3.454**	5.138	3.708
Cluster II		**3.314**	3.515
Cluster III			**3.342**

Bold values indicate intra-cluster distances

Table 3. Cluster means based on genetic divergence

Characters	Cluster I	Cluster II	Cluster III	Maximum	Minimum	Mean
Days to initiation	96.22	105.24	103.97	105.24	96.22	101.81
Days to marketable curds	113.39	119.62	121.75	121.75	113.39	118.25
Gross weight	1278.16	1097.49	1154.62	1278.16	1097.49	1176.76
Marketable yield	834.21	619.48	741.39	834.21	619.48	731.69
Curd size index	98.13	75.29	83.97	98.13	75.29	85.80
Curd depth	7.25	7.47	7.79	7.79	7.25	7.50
Curd diameter	12.74	11.73	11.99	12.74	11.73	12.15
Curd compactness	113.55	108.94	113.12	113.55	108.94	111.87
Curd solidity	95.01	70.46	95.82	95.82	70.46	87.10
% Marketable curds	91.56	93.48	96.7	96.70	91.56	93.91
Stalk length	3.63	3.05	3.41	3.63	3.05	3.36
Number of leaves	12.83	11.43	12.17	12.83	11.43	12.14
Plant height	43.32	45.76	42.99	45.76	42.99	44.02
Dry matter content	8	9.02	9.65	9.65	8	8.89
Ascorbic acid	50.58	54.1	47.53	54.10	47.53	50.74
TSS	6.45	6.32	6.55	6.55	6.32	6.44
Harvest index	53.39	49.29	57.91	57.91	49.29	53.53

Conclusion

On the basis of D^2 analysis, it can be concluded that genotypes from Cluster 1 for earliness and yield characters and from cluster II for morphological and quality characters, present the best choice for hybridization for obtaining useful segregants for further exploitation in cauliflower improvement programme.

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