Biological Forum – An International Journal 13(1): 762-767(2021)

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Correlation and Genetic Divergence Studies of Cauliflower (*Brassica oleracea* var. *botrytis*) under Lower Hilly Region of Himachal Pradesh

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(Received 12 March 2021, Accepted 20 May, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Availability of diverse parental lines is of paramount importance for crop improvement, thus an attempt was made to estimate the association of characters and genetic divergence between twenty five cauliflower genotypes. Significant variations were observed for almost all the traits. Net curd weight had the highest positive significant correlation with the curd yield indicating that the net curd weight is the optimum parameter for selection of high yielding genotypes. However, days to marketable maturity imposed negative non significant correlation on curd yield. Among the twenty five genotypes curd yield (kg/plot and q/ha) was greater in local genotypes namely Jachh CF-2, Jachh CF-7 and Jachh CF-17, hence these local varieties can be utilized in further breeding programmes. It was found that cluster I and cluster V were most divergent due to presence of maximum inter cluster distance between them. Therefore, they can be used for further breeding programmes such as hybridization.

Keywords: Cauliflower, Correlation, Genetic divergence, Path analysis, Yield

INTRODUCTION

Cauliflower is nutritionally rich important cruciferous vegetable crop that is naturally high in fiber and B-vitamins. It provides antioxidants and phytonutrients that can protect against cancer. It also contains fiber to enhance weight loss and digestion, choline that is essential for learning and memory, and many other body functions.100 g edible serving of cauliflower contains 1.9% protein, 5% carbohydrate, 95% water, 48.2 mg vitamin C, 199 mg potassium. It can immensely improve human health and have been symbolized as ‘Super food’ owing to its oxidative defense systems (Gopalan *et al*., 2011). Presently it is cultivated on an area of 469,000 ha with production of 9103,000 MT in India (Anonymous, 2018) while in Himachal Pradesh the area under cauliflower is 5310 ha with production of 124,330 MT (Anonymous, 2017).

The association of different horticultural traits is of tremendous value for any strategic breeding programme besides yield betterment. The extent of observed relationship between two characters is indicated by phenotypic correlation which includes both hereditary and environmental influences, while the real association between the two characters is indicated by genotypic correlation coefficient which may be useful for selection (Johnson *et al*., 1955). To develop high yielding varieties genetic diversity is of utmost importance. The extent and nature of genetic variability in the available germplasm implies the extent to which various characters can be improved through selection. Greater variability offers great chances of selecting superior genotypes (Simmonds, 1962).

Genetic diversity is an important factor in any crop improvement programme for obtaining high yielding variety. Multivariate analysis such as D^2 cluster and factor analysis have been proved to be useful in selecting accessions for hybridization. Mahalanobis (1949) D^2 analysis has been successfully used in measuring the diversity in several crops. An understanding of nature and magnitude of variability among the existing lime germplasm is a prerequisite for its improvement. Divergence analysis is a useful tool in quantifying the degree of divergence between biological population of geographical level and to access in assessing relative contribution of different components to the total divergence both at intra and inter cluster levels Precise information on the nature and degree of genetic divergence helps the plant breeder in choosing the diverse parents for purposeful hybridization

MATERIAL AND METHOD

The investigation was carried out during Rabi 2019 at the experimental farm of Regional Horticultural Research & Training Station, Jachh (Nurpur), District-Kangra, Himachal Pradesh. The experimental Farm of the Research Station Jachh, Nurpur is situated 428 m above mean sea level lying between 32° $18^{'}$ N latitude and longitude of 75° $55^{'}$ E under sub- mountain low hill sub tropical areas, zone 1 of Himachal Pradesh, India. The temperature goes as high as 43.50°C in summers and as low as -0.1°C during winter months. The mean annual rainfall of 1500 mm and soil of the experimental farm is sandy loam to clayey loam with pH of nearly 6.8.

Correlation among different traits is of vital importance to know their association, as yield is an important outcome of many correlated characters. Thus it becomes necessary to study the association for effective selection

Experimental material: The experimental material comprised of 25 genotypes of cauliflower (*Brassica oleracea* L. var. *botrytis* L.) out of which two are commercially grown cultivars Pusa Snowball K-1 and Pusa Snowball K-25 (Check) from IARI, Regional Station, Katrain, Kullu (H.P.). These genotypes were transplanted on in a Randomized Block Design with three replications at spacing of 60×45 cm in the plots of 1.8m× 1.8m. Crop was raised by following the package and practice recommended by the university.

The list of genotypes along with source is as under.

Sr. No.	GENOTYPE	SOURCE
1.	Jachh CF-1	RHR&TS, Jachh
2.	Jachh CF-2	RHR&TS, Jachh
3.	Jachh CF-3	RHR&TS, Jachh
4.	Jachh CF-4	RHR&TS, Jachh
5.	Jachh CF-5	RHR&TS, Jachh
6.	Jachh CF-6	RHR&TS, Jachh
7.	Jachh CF-7	RHR&TS, Jachh
8.	Jachh CF-8	RHR&TS, Jachh
9.	Jachh CF-9	RHR&TS, Jachh
10.	Jachh CF-10	RHR&TS, Jachh
11.	Jachh CF-11	RHR&TS, Jachh
12.	Jachh CF-12	RHR&TS, Jachh
13.	Jachh CF-13	RHR&TS, Jachh
14.	Jachh CF-14	RHR&TS, Jachh
15.	Jachh CF-15	RHR&TS, Jachh
16.	Jachh CF-16	RHR&TS, Jachh
17.	Jachh CF-17	RHR&TS, Jachh
18.	Jachh CF-18	RHR&TS, Jachh
19.	Pusa Sharad	IARI,New Delhi
20.	Pusa Deepali	IARI,New Delhi
21.	Pusa Ashwini	IARI,New Delhi
22.	Pusa Himjyoti	IARI, Regional Station, Katrain, Kullu valley, Kullu (H.P.)
23.	Pusa Snowball-1	IARI, Regional Station, Katrain, Kullu valley, Kullu (H.P.)
24.	Pusa Snowball K-1 (C)	IARI, Regional Station, Katrain, Kulluvalley, Kullu (H.P.)
25.	Pusa Snowball K-25 (C)	IARI, Regional Station, Katrain, Kullu valley, Kullu (H.P.)

Observations were recorded on ten randomly selected plants from each plot and their means were calculated out for statistical analysis. Observations were recorded for days to marketable maturity, number of leaves per plant, plant height (cm), leaf length (cm), leaf breadth (cm), gross plant weight (kg), stalk length (cm), net curd weight (g), curd compactness (compact/medium/loose), curd depth (cm), curd breadth (cm), curd yield (kg/plot), curd yield (q/ha), harvest index (per cent). Mean of the various observations were subjected to the following statistical analysis recommended by Gomez and Gomez (1984) for Randomized Block Design (RBD).

Statistical analysis: The statistical analysis for all the characters studied was done by following the method recommended by Gomez and Gomez (1984) for Randomized Block Design (RBD). The correlation coefficients (genotypic and phenotypic) were calculated by the method of analysis of variance and covariance matrix as per Al Jibouri *et al*. (1958). The path coefficient analysis of phenotypic and genotypic correlation was used to determine the direct and indirect contribution towards net curd weight. The direct and indirect paths were obtained by the formula given by Dewy and Lu (1959). The genetic divergence in cauliflower genotypes (twenty five) was estimated by

Mahalanobis D^2 values which were estimated by the method suggested by Mahalanobis (1936). Grouping of populations into number of clusters was carried out according to the method described by Rao, (1952). Two genotypes of the similar cluster, which showed a lesser D^2 value as compared to those belonging to non similar clusters were grouped together. Therefore, if genotypes X_1 and X_2 were close together and X_3 genotype was distant from both as depicted by their generalized distance, than X_1 and X_2 were classified, in the same cluster. The average D^2 values of all possible genotypes combinations in one cluster with those in the other were computed and its square root was used to represent the 'statistical distance' between two clusters.

RESULT AND DISCUSSION

The measure of degree of association between the two traits simultaneously is coined as correlation coefficient. The association of different horticultural traits is of tremendous value for any strategic breeding programme besides yield betterment. The extent of observed relationship between two characters is indicated by phenotypic correlation which includes both hereditary and environmental influences, while the real association between the two characters is indicated by genotypic correlation coefficient which may be useful for selection (Johnson *et al*., 1955).

A. Genotypic correlation

Generally the study undertaken depicted higher genotypic correlation coefficients as compared to phenotypic correlation coefficients in all the traits. This was also in accordance to earlier findings of Chittora *et al.,* (2017) and Meena *et al.,* (2013). The slight variation between the values of both correlation coefficients reflected robust inheritance among several characters observed (Table 1). Net curd weight (1.012) followed by curd breadth (0.965), harvest index (0.922), gross plant weight (0.879), number of leaves per plant (0.715), curd depth (0.672), leaf breadth (0.362), leaf length (0.336) and plant height (0.260) demonstrated positive and significant correlation with curd yield. Whereas stalk length (-0.144) and days to marketable maturity (-0.219) showed negative and non significant correlation with curd yield.

Table 1: Genotypic coefficients of correlation for different characters in cauliflower.

Characters	DMCM	NLPP	PH	LL	LB	GPW	SL	NCW	CD	CB	HI	CY
DMCM	1.00	-0.733^{**}	0.643^{**}	0.420^{**}	-0.263^{*}	-0.454^{**}	-0.883^{**}	-0.225^{*}	0.430^{**}	-0.181^{NS}	0.012^{NS}	-0.219^{NS}
NLPP		1.00	-0.321^{**}	0.023^{NS}	0.437^{**}	0.833^{**}	0.442^{**}	0.726^{**}	0.079^{NS}	0.696^{**}	0.484^{**}	0.715^{**}
PH			1.00	0.402^{**}	-0.297^{**}	-0.011^{NS}	-0.755^{**}	0.262^{*}	0.516^{**}	0.353^{**}	0.422^{**}	0.260^{*}
LL				1.00	0.111^{NS}	0.266^{*}	-0.484^{**}	0.335^{**}	0.751^{**}	0.406^{**}	0.328^{**}	0.336^{**}
LB					1.00	0.248^{*}	0.100^{NS}	0.373^{**}	0.293^{**}	0.363^{**}	0.406^{**}	0.362^{**}
GPW						1.00	0.169^{NS}	0.870^{**}	0.411^{**}	0.838^{**}	0.586^{**}	0.879^{**}
SL							1.00	-0.145^{NS}	-0.635^{**}	-0.172^{NS}	-0.380^{**}	-0.144^{NS}
NCW								1.00	0.672^{**}	0.969^{**}	0.911^{**}	1.012^{**}
CD									1.00	0.603^{**}	0.772^{**}	0.672^{**}
CB										1.00	0.892^{**}	0.965^{**}
HI											1.00	0.922^{**}
CY												1.00

*Significant at 5% level of significance

**Significant at 10% level of significance

Where, DMCM= Days to marketable maturity, NLPP= Number of leaves per plant, PH= Plant height, LL= Leaf length, LB= Leaf breadth, GPW= Gross plant weight, SL= Stalk length, NCW= Net curd weight, CD= Curd depth, CB= Curd breadth, HI= Harvest Index, CY=Curd yield per hectare

Days to marketable maturity imposed negative non significant correlation on curd yield (-0.219) which was nearby to Chittora *et al.,* (2017). Plant height showed non significant association with curd yield similar to Santosha *et al.,* (2011).

Net curd weight had the maximum positive significant correlation with curd yield which was approximate to findings of Meena *et al.,* (2013). It also had positive significant correlation with plant height (0.262), leaf length (0.335) and leaf breadth (0.373) which was not far off from studies of Kumar *et al.,* (2011); Santhosha *et al.,* (2015). Number of leaves per plant had higher significant correlation (0.715) which was in line with Jha *et al.,* (2014).

B. Phenotypic Correlation

The values here were almost close by the value of genotypic correlation and therefore they followed a regular matching trend (Table 2). The manner in which phenotypic correlation decreased for the given characters was similar to decrease in genotypic correlation and vice versa. Nevertheless all the values of phenotypic correlation were smaller than genotypic correlation.

Table 2: Phenotypic coefficients of correlation for different characters in cauliflower.

Characters	DMCM	NLPP	PH	LL	LB	GPW	SL	NCW	CD	CB	HI	CY
DMCM	1.00	-0.690^{**}	0.589^{**}	0.327^{**}	-0.195^{NS}	-0.387^{**}	-0.848^{**}	-0.195^{NS}	0.384^{**}	-0.170^{NS}	0.014^{NS}	-0.205^{NS}
NLPP		1.00	-0.282^{*}	0.022^{NS}	0.365^{**}	0.718^{**}	0.408^{**}	0.662^{**}	0.107^{NS}	0.651^{**}	0.397^{**}	0.682^{**}
PH			1.00	0.294^{**}	-0.201^{NS}	-0.004^{NS}	-0.657^{**}	0.211^{NS}	0.407^{**}	0.277^{*}	0.312^{**}	0.215^{NS}
LL				1.00	0.120^{NS}	0.267^{*}	-0.416^{**}	0.294^{**}	0.596^{**}	0.326^{**}	0.221^{NS}	0.293^{**}
LB					1.00	0.154^{NS}	0.064^{NS}	0.309^{**}	0.240^{*}	0.278^{*}	0.340^{**}	0.327^{**}
GPW						1.00	0.141^{NS}	0.805^{**}	0.351^{**}	0.741^{**}	0.371^{**}	0.789^{**}
SL							1.00	-0.139^{NS}	-0.582^{**}	-0.174^{NS}	-0.317^{**}	-0.140^{NS}
NCW								1.00	0.609^{**}	0.874^{**}	0.841^{**}	0.977^{**}
CD									1.00	0.559^{**}	0.636^{**}	0.609^{**}
CB										1.00	0.701^{**}	0.881^{**}
HI											1.00	0.822^{**}
CY												1.00

*Significant at 5% level of significance

**Significant at 10% level of significance

Where, DMCM= Days to marketable maturity, NLPP= Number of leaves per plant, PH= Plant height, LL= Leaf length, LB= Leaf breadth, GPW= Gross plant weight, SL= Stalk length, NCW= Net curd weight, CD= Curd depth, CB= Curd breadth, HI= Harvest Index, CY=Curd yield per hectare

C. Path coefficient analysis

Clarified approach is followed by path coefficient analysis during association of several horticultural traits. Correlation values only guide us through only positive and negative significant, non-significant knowledge and devoid of any direct or indirect dependence. Path coefficient analysis renders the bifurcation of phenotypic and genotypic correlation coefficients together in terms of direct and indirect effects. The rate of several yield components in miscellaneous crops stratify the superior genotypes resolved by path coefficient analysis. Dewey and Lu (1959) were the first to suggest the use of path coefficient analysis in breeding programmes.

Harvest index had highest positive direct effect (1.030) on curd yield proceeded by gross plant weight (0.932), curd depth (0.493), curd breadth (0.356), number of leaves per plant (0.347), days to marketable maturity (0.077) and plant height (0.067). Simultaneously highest negative direct effect was shown by leaf breadth (-0.079), leaf length (-0.0269) and net curd weight (-1.533). Days to marketable maturity through plant height (0.050), leaf length (0.032), curd depth (0.033) and harvest index (0.001) showed positive indirect effect on curd yield. Number of leaves per plant imposed positive indirect effect on gross plant weight (0.289), net curd weight (0.252), curd breadth (0.242), harvest index (0.168), stalk length, (0.153), leaf breadth (0.152), curd depth (0.028) and leaf length (0.008) while plant height imposed positive indirect effect on days to marketable maturity (0.043), curd depth (0.035), harvest index (0.028), leaf length (0.027), curd breadth (0.024) and net curd weight (0.018). Kumar *et al.*, (2011) and Santhosha *et al.*, (2015) had also reported similar observations.

Curd yield via curd depth had positive indirect effect on harvest index (0.381), leaf length (0.370), net curd weight (0.332), curd breadth (0.297), plant height (0.255), days to marketable maturity (0.212) and gross plant weight (0.203). Contrarily curd breadth imposed positive and indirect effect on net curd weight (0.345), harvest index (0.317), gross plant weight (0.298), curd depth (0.214) and leaf length (0.144).

Chittora *et al.*, (2017) showed positive direct effect via curd depth, days to marketable maturity and plant height. Similar results were reported Kumar *et al.*, (2011); Chittora *et al.*, (2017); Jha *et al.*, (2014) also reported negative direct effect of leaf length on curd yield.

D. Genetic divergence

All the twenty five genotypes were grouped into five clusters (Table 3). Eight genotypes were classified under cluster V (Jachh CF-3, Jachh CF-4 and Jachh CF-5, Jachh CF-5, Jachh CF-6, Jachh CF-11, Jachh CF-12, Jachh CF-15 and Jachh CF-16). Seven genotypes were categorized under cluster II (Jachh CF-1, Jachh CF-8, Jachh CF-9, Jachh CF-13, Jachh CF-14, Pusa Ashwini and Pusa Himjyoti). Four genotypes were grouped under cluster IV (Jachh CF-10, Pusa Snowball -1, Pusa Snowball K-1 and Pusa Snowball K-25). Cluster I had three genotypes (Jachh CF-2, Jachh CF-7 and Jachh CF-17). Cluster III also had three genotypes (Jachh CF-18, Pusa Sharad and Pusa Deepali).

Cluster I expressed highest mean for maximum traits which included gross plant weight (g) (1655.53), net curd weight (g) (960.21), number of leaves per plant (18.86), plant height (cm) (52.86), leaf length (cm) (39.95), curd depth (cm) (10.91), curd breadth (cm) (14.63), harvest index (%) (58.09) and curd yield (q/ha) (355.63). Cluster V showed maximum mean for only one trait namely days to marketable maturity (128.55). Similarly cluster IV had maximum mean for only leaf breadth (cm) (17.93) and cluster III had maximum mean for only stalk length (cm) (9.37). These results are in conformity with Santhosha *et al*., (2011).

Table 3: Clustering pattern of twenty five genotypes of cauliflower on the basis of genetic divergence.

Clusters	Number of genotypes	Genotypes
I	3	Jachh CF-2, Jachh CF-7 and Jachh CF-17
II	7	Jachh CF-1, Jachh CF-8, Jachh CF-9, Jachh CF-13, Jachh CF-14, Pusa Ashwini and Pusa Himjyoti
III	3	Jachh CF-18, Pusa Sharad and Pusa Deepali
IV	4	Jachh CF-10, Pusa Snowball-1, Pusa Snowball K-1 and Pusa Snowball K-25
V	8	Jachh CF-3, Jachh CF-4, Jachh CF-5, Jachh CF-6, Jachh CF-11, Jachh CF-12, Jachh CF-15 and Jachh CF-16

The utmost requirement in a breeding programme is undoubtedly the availability of genetic divergence in the present population. Besides degree of genetic divergence it also focus on selection of superior genotypes thereby availing promising varieties for the future. Highly significant differences were revealed by analysis of variance and it further accomplished grouping into various clusters on the mean performance of several traits in the present study. Intra and inter cluster distances both were calculated concluding that same cluster genotypes had not necessarily superior yield (Table 4). The highest intra cluster distance was shown by cluster I (76.12) which highlighted high heterogeneity whereas minimum distance was shown by cluster V (11.75). The highest inter cluster distance was found between cluster I and cluster V (637.28) depicting wide genetic divergence thereby higher possibilities of better segregants in F_2 and subsequent generations. More authenticate information was guaranteed by calculating the cluster mean. Previous studies done by Santhosha *et al*., (2011); Verma and Kalia (2016) also stipulated similar results in cauliflower.

The highest per cent contribution towards divergence was shown by curd yield (11.76 %), net curd weight (11.76 %), curd breadth (11.52 %), harvest index (10.95 %), gross plant weight (10.41 %), curd depth (9.65 %), number of leaves per plant (9.21 %), leaf length (7.38 %), leaf breadth (7.02 %), plant height (6.03 %) and the lowest contribution was by days to marketable maturity (2.48 %) and stalk length (1.82 %). The characters contributing maximum to the divergence are given greater emphasis for deciding on the clusters for the purpose of further selection and choice of parents for hybridization.

Table 4: Cluster means for the characters among twenty five genotypes of cauliflower.

Characters	I	II	III	IV	V
Days to marketable maturity	107.94	114.93	91.96	112.90	128.55
Number of leaves per plant	18.86	15.14	15.87	16.98	12.77
Plant height(cm)	52.86	49.16	45.00	50.33	50.83
Leaf length(cm)	39.95	37.89	36.70	39.19	38.04
Leaf breadth(cm)	16.68	16.95	15.47	17.93	16.38
Gross plant weight(g)	1655.53	1345.41	1465.22	1501.21	1193.02
Stalk length(cm)	5.18	5.98	9.37	5.34	4.79
Net curd weight(g)	960.21	603.51	593.35	844.56	549.76
Curd depth(cm)	10.91	9.13	8.41	10.68	9.46
Curd breadth(cm)	14.63	11.39	11.08	13.93	10.69
Harvest index(%)	58.09	44.74	40.56	56.36	46.14
Curd yield(q/ha)	355.63	223.52	219.76	312.80	203.61

Table 5: Average Inter and Intra cluster distance between the cluster mean (D^2).

Cluster	I	II	III	IV	V
I	**76.12**				
II	491.05	**21.91**			
III	435.83	122.68	**51.37**		
IV	197.65	300.84	271.69	**46.78**	
V	637.28	163.42	278.73	440.67	**11.75**

CONCLUSION

Net curd weight had the highest positive significant correlation with the curd yield indicating that the net curd weight is the optimum parameter for selection of high yielding genotypes. This study revealed highest positive direct effect of harvest index on curd yield. Twenty five genotypes were classified into five clusters on the basis of D^2 analysis. It was found that cluster I and cluster V were most divergent due to presence of maximum inter cluster distance between them. Therefore, they can be used for further breeding programmes such as hybridization. The highest intra cluster distance in cluster I depicted presence of high heterogeneity.

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How to cite this article: Kumar, D., Chaudhary, D., Bhardwaj, R., Dogra, R., Chauhan, A., Kumar, S., Shiwani, K. and Chandel, V.G.S. (2021). Correlation and Genetic Divergence Studies of Cauliflower (*Brassica oleracea* var. *botrytis*) under Lower Hilly Region of Himachal Pradesh. *Biological Forum – An International Journal*, *13*(1): 762-767.