



## **Genetic variability studies in mid-season cauliflower (*Brassica oleracea* var. *botrytis* L.)**

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### **ABSTRACT**

*Genetic variability was studied for sixteen quantitative traits in fifty seven genotypes of mid-season cauliflower. Analysis of variance studies revealed significant difference for majority of the characters except plant spread, curd length and curd size index. The genotypes viz. INBPCF 120, 2013/CAUMVAR-6, PCF- 93, PG-5, PCF- 7, INBPCF 117 were found more promising as they had more than one desirable traits. INBPCF 120 had highest curd yield per hectare (192.5q) whereas PCF 29 requires least days to maturity (85). Appreciable level of phenotypic and genotypic coefficient of variation (PCV and GCV) were reported for stalk length, gross plant weight, net curd weight, curd yield per hectare, marketable curd weight, harvest index and curd size index. However, lowest coefficient of variation (PCV and GCV), heritability in broad sense, genetic advance and genetic advance as a percent of mean was recorded for number of leaves per plant and days required to maturity.*

**Keywords:** Cauliflower, genetic variability, coefficient of variation, heritability and genetic advance

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### **INTRODUCTION**

Cauliflower (*Brassica oleracea* var. *botrytis* L.,  $2n = 2x = 18$ ) is an important vegetable crop cultivated throughout India [21 & 24]. Cauliflower is the most popular vegetable among the Cole crops. It is grown in all continents of the world, of which Asia is the leading one followed by Europe and cover small acreages in North America, South America, Africa, Australia and New Zealand. India is the largest producer of cauliflower in the world and other major producers are China, France, Italy, United Kingdom, United States of America, Spain, Poland, Germany and Pakistan. The leading cauliflower growing states in India constitute of West Bengal, Bihar, Haryana, Gujarat, Assam, Uttar Pradesh, Karnataka and Tamil Nadu. In India, area under cauliflower is about 410.9 thousand hectares with production of 7925.85 thousand metric tonnes and productivity is 19.2 tonnes/ha. In world, area under cauliflower is 1258.1 thousand hectares, with production of 22840.0 thousand metric tonnes and productivity of 18.2 tonnes/ha [14]. 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. It is originated from wild cabbage known as 'Cole warts', through mutation, human selection and adoption. Dr. Jemson at Saharanpur introduced it to India in 1822 during the period of East India Company [23]. The present tropical Indian cauliflower developed as a result of inter crossing between European and Cornish type, perhaps the first to introduced in India, has itself gone out of cultivation after contributing many genes to Indian varieties like resistance to black rot, self-incompatibility, curd flavour, open plant habit, exposed yellow loose curds etc [23]. Most of the open pollinated varieties are poor in curd quality with low yield and have variation in maturity, shape and other quality characters. Progress in cauliflower breeding is at a lower pace in India thereby crop yield is not improving to an appreciable extent. The primary objective behind a plant breeding programme is to create variability and select best recombinants with desirable characters. The nature and extent of genetic variability in the germplasm indicate the scope of improvement in the character through selection. Genetic variability in a population is of immense importance for biodiversity because variability, not only helps in crop improvement but also provide crop adaptability to environmental changes and therefore, makes it less prone to extinction. Therefore an

attempt was made to study the genetic variability, heritability and genetic advance studies in mid-season cauliflower.

## MATERIALS AND METHODS

The present investigation was conducted at Vegetable Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar (Uttarakhand) during 2015-2016. The experimental material comprised of fifty two genotypes and five checks (Table 1). The experiment was laid out in Augmented Block Design with four blocks at Vegetable Research Centre, G.B. Pant University of Agriculture and Technology. Observations were recorded for sixteen quantitative characters *viz.*, leaf length (cm), leaf width (cm), Petiole length (cm), plant height (cm), plant spread (cm), number of leaves per plant, stalk length (cm), days to curd maturity, gross plant weight (g), marketable curd weight (g), net curd weight (g), curd length (cm), curd breadth (cm), harvest index (%), curd size index (cm<sup>2</sup>) and curd yield per hectare (q/ha). The analysis of variance was carried out using the method given by [6] and [7]. Genotypic and phenotypic coefficients of variation were calculated according to the method suggested by [2]. Heritability estimates were obtained [9].

## RESULTS AND DISCUSSION

Analysis of variance studies revealed significant differences in all the genotypes for majority of the characters except plant spread, curd length and curd size index (Table 2). The mean estimates of genotypes (Table 3) for various characters revealed that the wide range was recorded for all the characters.

Phenotypic coefficient of variation is the sum total of genotypic and environmental coefficient of variation which mean that morphological characters of any cultivars are under the influence of environment condition and its genetic characters. Character showing high PCV is not effective for selection in breeding program. So, it is important that selection should be performed on the basis of its calculated genetic values. In the present study a narrow range of genetic differences between the PCV and GCV indicates that the traits are mostly governed by genetic factors with minimum environmental influence on the phenotypic expression of these traits. Maximum Higher magnitude of phenotypic and genotypic coefficients of variation (> 20%) was recorded for net curd weight, curd yield per hectare and marketable curd weight indicating the maximum variability among the genotypes for these parameters. Similar results were also reported by [17] and [3]. Highest value of PCV was observed for stalk length as confirmed by [20]. Higher values of PCV were also observed for harvest index and curd size index as suggested by [13].

Phenotypic coefficient of variation was observed maximum for stalk length (25.74%) followed by net curd weight (25.34%), gross plant weight (25.23%), curd yield (21.86%), marketable curd weight (21.80%), harvest index (20.52%), curd size index (20.17%), petiole length (19.64%), curd length (17.81%), leaf length (12.16%), plant height (11.90%), leaf width (11.54%), plant spread (10.72%), curd breadth (9.07%), number of leaves per plant (8.01%) and days to maturity (3.85%). Higher value of phenotypic coefficient of variation for all the traits than the corresponding value of genotypic coefficient of variation indicates that the characters remained uninfluenced by environmental effects. This was further confirmed by [11], [16] [17], [20] & [22]. PCV values were higher for net curd weight, stalk length, marketable curd yield per plant, gross plant weight and harvest index as reported by [19].

Genotypic coefficient of variation was observed maximum for stalk length (25.70%) followed by net curd weight (25.28%), gross plant weight (25.09%), marketable curd weight (21.61%), curd yield (21.53%), harvest index (20.44%), curd size index (20.09%), petiole length (19.53%), curd length (17.75%), plant height (11.75%), leaf width (11.40%), leaf length (11.18%), plant spread (10.56%), curd breadth (8.88%), number of leaves per plant (7.76%), days to maturity (3.41%). Higher values of GCV for gross plant weight, net curd weight, curd yield per hectare and marketable curd weight was observed by [3], [17] & [18]. Lowest coefficient for variation was reported for days to curd maturity as suggested by [3]. [19] obtained moderate values of GCV for harvest index.

The study of genotypic coefficient of variation helps to measure the range of genotypic variation existing at specified environmental site for a particular character and to compare the variability existing in various characters. However, it cannot measure the heritable variation; the genotypic coefficient of variation together with heritability estimates would give reliable indication of the expected improvement through selection as reported by [2]. Estimates of heritability in broad sense ranges from 99.66 to 78.78. Highest heritability estimates was recorded for stalk length (99.66%) followed by net curd weight (99.48%), curd length (99.32%), curd size index (99.20%), harvest index (99.19%), gross plant weight (98.92%), petiole length (98.83%), marketable curd weight (98.26%), plant height (97.50%), leaf width (97.47%), plant spread (97.08%), curd yield per hectare (96.98%), curd breadth (95.76%), leaf length

(95.08%), number of leaves per plant (93.78%) and days to maturity (78.78%). Similar to the above results high heritability was recorded for gross curd weight, net curd weight and stalk length by [10] and [12]. [5] suggested net curd weight, gross plant weight and harvest index as most important traits for improving the genotypes while leaf length as the second most important character. Good level of heritability was also reported for net curd weight, marketable curd weight, gross curd weight and curd yield per hectare by [3] and [17]. Harvest index also acquired high heritability as suggested by [3], [4], [8] and [22] observed high heritability for plant spread. Similarly, Low heritability was also obtained for days to curd maturity as suggested by [3].

Estimates of genetic advance range from low 2.07 to high 443.13. Highest genetic advance was observed for gross plant weight (443.13) followed by marketable curd weight (192.90), net curd weight (132.47), curd yield per hectare (57.18), curd size index (35.34), harvest index (13.17), plant spread (12.24), plant height (11.20), leaf length (9.88), days to maturity (5.74), petiole length (4.54), leaf width (4.28), curd length (2.70), number of leaves per plant (2.55), stalk length (2.51) and curd breadth (2.07). High genetic advance was observed for gross curd weight and net curd weight as reported by [3], [5], [8], [10] and [17]. Similar to the above results low genetic advance was shown by stalk length and days to maturity also observed by [15]. [3] also observed lower genetic advance for days to curd maturity.

Genetic advance as percent of mean varied from 6.24% to 52.85%. High value of genetic advance as percent of mean was recorded for stalk length (52.85%) followed by gross plant weight (51.41%). Moderate value of genetic advance as percent of mean was observed for net curd weight (49.88%), marketable curd weight (44.13%), curd yield per hectare (43.67%), harvest index (41.93%), curd size index (41.21%), petiole length (39.99%) and curd length (36.43%). Genetic advance as percent of mean was observed low for plant height (23.89%), leaf length (23.81%), leaf width (23.18%), plant spread (21.44%), curd breadth (17.89%), number of leaves per plant (15.48%) and days to maturity (6.24%).

**Table 1: List of genotypes of mid-season cauliflower under study**

Sl. No.	Genotypes	Sl. No.	Genotypes
1	PCF 246	31	INB 10-2
2	PCF 108	32	PCF 249
3	PCF 248	33	INBPCF 117
4	PC 77	34	INBPCF-3
5	PCF 251	35	CAUVAR-2
6	DC-98-4-2	36	PCF 247
7	PCF-86	37	PCF 253
8	DC 541-5	38	PCF 243
9	CAUVAR-5	39	PCF 1-1
10	PG 3-1-1	40	PCF 70
11	INB 16-2	41	INB 79
12	INBPCF 120	42	INB 20
13	C1	43	PCF 255
14	PCF 252	44	PCF 14-2
15	Comp-3	45	PC-98
16	PCF-65	46	PC 20-8
17	PCF 244	47	PC 100
18	PG-5	48	PCF-7
19	PCF 245	49	PC 98-4-3
20	INB 20-3	50	PCF 250
21	PCF-117	51	PCF 87
22	INB-9-2	52	2013/ CAUMVAR-6
23	PCF 254	53	Pusa Early Synthetic (check)
24	PCF-4-2	54	Pant Gobi-4 (check)
25	PCF-93	55	Pant Gobi-3 (check)
26	PG-6	56	Pusa Sharad (check)
27	PCPGR- 2004	57	Pusa Pausjha (check)
28	DC-94		
29	PCF 256		
30	PCF 29		

High heritability along with high genetic advance results from heritability due to additive gene effect thereby making the selection effective and rewarding whereas high heritability coupled with low genetic advance results in non-additive gene effects, thereby rendering the selection ineffective. The above results are also found to be in accordance with the findings of [3] and [15] who also observed high genetic advance as percent of mean for gross curd weight and net curd weight. [12] reported maximum genetic advance as percent of mean for stalk length whereas moderate for net curd weight and gross curd weight. Plant spread and days to curd maturity exhibited higher heritability coupled with low genetic advance indicating non-additive gene effects. Plant spread and curd breadth exhibited low genetic advance as suggested by [22].

**Table 2: Analysis of variance (ANOVA) for various characters of cauliflower genotypes**

S. N.	Characters	Mean sum of square			
		Blocks (3)	Checks (4)	Total (19)	Error (12)
1	Leaf length (cm)	2.64	122.46*	44.39	28.81
2	Leaf width (cm)	4.34	25.76*	9.56	5.47
3	Petiole length (cm)	0.22	28.66**	7.48	2.23
4	Plant height (cm)	85.21	152.84*	65.48	31.42
5	Plant spread (cm)	29.99	147.12	77.77	66.59
6	Number of leaves per plant	3.93	16.18*	6.64	4.14
7	Stalk length (cm)	0.74	3.13*	1.23	0.72
8	Days to maturity	66.87	686.07**	228.41	116.24
9	Gross plant weight (g)	11500.00	1031667.00**	258313.26*	62231.93
10	Marketable curd weight (g)	333.33	135975.25**	37723.63	14320.67
11	Net curd weight (g)	924.2	58463.07**	15430.68	4713.79
12	Curd length (cm)	0.19	0.46	0.66	0.84
13	Curd breadth (cm)	0.19	12.92*	5.02	3.18
14	Harvest index	18.18	140.58**	41.82	14.81
15	Curd size index (cm <sup>2</sup> )	69.18	892.71	364.63	262.46
16	Curd yield (q/ha.)	111.40	12240.05**	3391.31	1261.72

\* Significant at 5% level of probability

\*\* Significant at 1% level of probability

Degree of freedom are shown in parenthesis

**Table 3: Mean, range, coefficient of variation and genetic parameters for different quantitative characters of Cauliflower**

CHARACTERS	RANGE	GM	Coefficient of variation (%)			Heritability (h <sup>2</sup> %)	Genetic advance	Genetic advance as (%) of mean
			PCV (%)	GCV (%)	ECV (%)			
Leaf length(cm)	27.54-64.94	41.91	12.157	11.184	2.696	95.08	9.875	23.812
Leaf width(cm)	13.00-28.50	18.58	11.543	11.396	1.835	97.47	4.276	23.177
Petiole length(cm)	05.47-19.47	11.56	19.641	19.526	2.123	98.83	4.539	39.988
Plant height(cm)	32.31-70.31	47.52	11.896	11.746	1.879	97.50	11.201	23.893
Plant spread(cm)	40.57-71.95	57.60	10.719	10.561	1.832	97.08	12.237	21.436
Number of leaves per plant	12.16-16.00	16.61	8.012	7.759	1.999	93.78	2.554	15.478
Stalk length(cm)	03.12-10.60	4.76	25.741	25.697	1.503	99.66	2.507	52.846
Days to maturity	84.70-123.75	92.71	3.846	3.414	1.772	78.78	5.737	6.242
Gross plant weight(gm)	271.95-2101.75	901.94	25.230	25.094	2.617	98.92	443.133	51.414
Marketable curd	213.90-905.50	454.31	21.804	21.613	2.879	98.26	192.900	44.134

<b>weight(gm)</b>								
<b>Net curd weight(gm)</b>	144.90-514.50	275.04	24.339	24.276	1.751	99.48	132.466	49.879
<b>Curd length(cm)</b>	05.54-14.04	7.38	17.807	17.746	1.471	99.32	2.703	36.431
<b>Curd breadth(cm)</b>	08.96-14.42	11.67	9.071	8.876	1.868	95.76	2.065	17.893
<b>Harvest index</b>	17.98-56.78	31.18	20.522	20.438	1.850	99.19	13.168	41.931
<b>Curd size index(cm<sup>2</sup>)</b>	54.44-141.38	86.30	20.169	20.088	1.805	99.20	35.341	41.214
<b>Curd yield (q/ha.)</b>	63.95-271.5	136.18	21.857	21.525	3.797	96.98	57.178	43.667

## CONCLUSION

From the above result, it is concluded that there is a wide range of variability present among the germplasm for almost all characters indicating that a wide scope for genetic improvement of crop. The narrow difference was retained between GCV and PCV indicating a little effect of environment in the expression of characters. So, selection of these traits on the basis of their phenotypic values becomes effective. High heritability coupled with greater genetic advance was observed for gross plant weight, marketable curd weight followed by net curd weight which indicates that these characters are govern with additive gene effect with minimum environment effect so we can go prefer direct selection for crop improvement.

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