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Estimation of existing genetic variability, heritability and genetic advance in tropical cauliflower (*Brassica oleracea* var *botrytis* L.)

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Abstract
Nineteen genotypes of cauliflower were evaluated to study the magnitude of genetic variability, heritability and genetic advance. The genotypes were evaluated for eleven quantitative characters *viz.,* days to 50 per cent curd initiation, days to 50 per cent curd maturity, number of leaves per plant, curd equatorial diameter (cm), curd polar diameter (cm), plant canopy diameter, net curd weight (g), marketable curd weight (g), harvest index, curd compactness and biological weight of plant (g). The present study showed that PCV was higher than GCV for all the traits indicated the presence of environmental effect for traits expression. High magnitude of broad sense heritability was observed for most of the traits except number of leaves, curd equatorial diameter, curd polar diameter and curd compactness. The high genetic advance as per cent of mean showed by plant canopy width, net and marketable curd weight, biological curd weight, curd compactness and harvest index. High heritability coupled with high genetic advance was observed for plant canopy width, net and marketable curd weight, biological curd weight, curd compactness and harvest index which are governed by additive gene and could be effectively improved through selection.

Keywords: genetic, tropical, cauliflower, *Brassica oleracea*

Introduction
Cauliflower (*Brassica oleracea* var *botrytis* L.) is an important member of the cole crops, commonly known as 'Phoolgobhi', grown and consumed widely in all pockets of India (Meena *et al,* 2012) [7]. This is cultivated worldwide in different climatic conditions, ranging from temperate to tropics during most of the cropping seasons and is available round the year in the market. Curd the economic part of cauliflower is an intermediate stage between vegetative and reproductive stage (Singh *et al.*, 2013) [8]. In India, area under cauliflower cultivation was 4.34 mha and the production was 85.732 MT (NHB 2013-14). India is major grower in the world after china but as far as productivity is concern we fall on the sixth position (19.8 MT/ha) in the world. Further study of genetic variability for cauliflower requires improving the existing germplasm in desirable direction. Therefore an attempt has been made to study the genetic variability, heritability and genetic advance studies in tropical cauliflower.

Materials and Methods
A group of twenty one parents including two testers were taken and made thirty eight cross in line × testers mating design in the present studies. 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). Phenotypic and Genotypic coefficients of variation were calculated by the method suggested by Burton (1952) [1]. Heritability in broad sense is the ratio of genotypic variance to the total variance and is

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calculated by the formula given by Lush (1940). The estimates of genetic advance as percent of mean were obtained by the formula given by Lush (1949) [5, 6] and Johnson et al. (1955) [4].

Results and Discussion

Analysis of variance clearly depicted that the significant genetic variations was observed for all the characters under study (Table 1). The genotypes included in the study were genetically diverse and considerable amount of variability were present among the genotypes. Hence, there is ample scope for isolating promising entries for high yield and other desirable traits.. Information on genetic variability of yield and its component traits is of paramount importance in crop improvement programme. The extent of genotypic variability indicates the amenability of given character for its improvement as reported by Burton, (1952) [1]. The estimate of genotypic co-efficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance as per cent of mean for yield and its contributing characters are presented (Table 2). Pooled analysis of two year data revealed that moderate genotypic co-efficient of variation in net curd weight (19.42) followed by harvest index (16.06), marketable curd weight (16.06), biological weight (14.02) and curd compactness (13.54). While, the low GCV was observed for days to 50 % curd initiation (6.95), days to 50 % curd maturity (6.62), number of leaf (5.01), curd equatorial diameter (3.31), curd polar diameter (4.04) and plant canopy width (8.59). PCV was higher than GCV for all the traits indicated that the characters to some extend were influenced by environment. Singh et al. (2010) also found that the PCV was higher than the GCV for net curd weight and moderate for gross weight. Mehra and Singh (2013) [8] was observed high PCV value for marketable curd weight, net curd weight and harvest index moderate for number of leaf and low for days to 50 % curd initiation. The high magnitude of GCV further suggested that great extent of variability exist. High heritability alone is not enough to make efficient selection in segregating generation unless the information is accompanied for substantial amount of genetic

advance (Singh et al. 2006) [11]. Burton (1952) [1] and Panse (1957) viewed that if a character is governed by non-additive gene action, it may have high heritability but low genetic advance, whereas, if it is governed by additive gene action, heritability and genetic advance both would be high. Heritability was high for plant canopy width (89.96%) followed by days to 50% curd maturity (77.33%), net curd weight (77.13%), marketable curd weight (76.75%), days to 50 % curd initiation (74.16%) biological weight (72.98%), while moderate heritability was observed for rest of all the characters. Knowledge on heritability coupled with expected genetic advance of characters is necessary for assessing the scope of improvement of a character through selection. Expected genetic advance indicated the expected genetic progress for particular traits under a suitable selection system. From the pooled analysis (Table 2), data revealed that high expected genetic advance was found for net curd weight (35.13), marketable curd weight (28.98), biological weight (24.61), and harvest index (27.21) moderated genetic advance was observed for the character curd compactness (18.56) plant canopy width (16.68), days to 50% curd initiation (12.34) and days to 50% curd maturity (12.00), while the low genetic advance was observed for number of leaf, curd polar diameter and curd equatorial diameter. These results are in accordance with the findings of Dhatt and Garg 2008; [3] Singh et al., 2010 [12]. Understanding of the genetic variability among the present genotypes of cauliflower is prerequisite for planning any breeding programme (Singh et al., 2010) [12]. Further, the partitioning of the total variability into heritable and non-heritable components enables to know whether the superiority of selection is inherited by the progenies or not. Therefore, estimates of heritability and genetic advance expected after selection indicates the possibility and extent to which improvement is possible through selection. From the above experiment it may concluded that the characters net curd weight, harvest index, marketable curd weight and biological weight were found to be highly heritable and high genetic advance as a per cent of mean. It indicates selection of parental line for these traits could be effective.

Table 1: Pooled Mean sum of squares for eleven quantitative characters in L × T analysis in early cauliflower.

Sources	DF	D50%CI	D50%CM	NL	CED	CPD	PCW	NCW	CC	HI	MCW	BW
Rep	1	18.72	16.04	2.58	0.22	0.17	4.81	666.36	6.06	13.49	1129.40	460.92
Tr	58	77.18**	86.98**	2.60**	0.70*	0.42*	42.61**	5612.93**	26.82**	92.87**	6523.38**	21624.81**
Er	58	11.45	11.12	1.24	0.36	0.16	2.49	724.74	10.36	17.96	858.08	3431.51
SE m (±)		2.39	2.36	0.79	0.42	0.29	1.12	19.04	2.28	0.03	20.72	41.43
CD		6.77	6.68	2.23	1.20	0.81	3.16	53.89	6.44	0.08	58.64	117.26
CV		4.11	3.59	6.74	4.82	4.57	3.03	10.57	15.20	11.12	8.84	8.61

D50%CI- Days to 50% curd initiation, D50%CM- Days to 50% curd maturity, NL- Number of leaf, CED- Curd equatorial diameter, CPD- Curd polar diameter, PCW- plant canopy width, NCW- Net curd weight, CC- curd compactness, HI- harvest index, MCW- marketable curd weight, BW- biological weight.

Table 2: Pooled estimates of variability parameters for earliness and yield contributing traits in cauliflower

S. No	character	GCV	PCV	Heritability	Genetic Advance	GA (% of Mean)
1	D50%CI	6.95	8.08	74.16	10.17	12.34
2	D50%CM	6.62	7.53	77.33	11.16	12.00
3	NOL	5.01	8.40	35.55	1.01	6.15
4	CED (cm)	3.31	5.85	31.95	0.48	3.85
5	CPD (cm)	4.04	6.10	43.85	0.49	5.51
6	PCW (cm)	8.59	9.10	88.96	8.70	16.68
7	NCW(g)	19.42	22.11	77.13	89.44	35.13
8	CC (g/cm3)	13.54	20.36	44.25	3.93	18.56
9	HI (%)	16.06	19.54	67.60	0.10	27.21
10	MCW (g)	16.06	18.33	76.75	96.05	28.98
11	BW (g)	14.02	16.45	72.98	167.42	24.61

D50%CI- Days to 50% curd initiation, D50%CM- Days to 50% curd maturity, NL- Number of leaf, CED- Curd equatorial diameter, CPD- Curd polar diameter, PCW- plant canopy width, NCW- Net curd weight, CC- curd compactness, HI- harvest index, MCW- marketable curd weight, BW- biological weight.

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