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Variability studies in cauliflower (*Brassica oleracea* L. var. *botrytis* L.) for horticultural traits under mid hill conditions of North-Western Himalayas, India

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Abstract
The present investigation was undertaken to assess the variability, heritability and genetic advance in late maturing group of cauliflower. The experiment was undertaken in Randomized Block Design (RBD) with three replications at the Experimental Farm of the Department of Vegetable Science and Floriculture, CSK HPKV Palampur. Twenty five genotypes of cauliflower were evaluated including Madhuri as check during Rabi season of 2014-15. Analysis of variance revealed significant variability for most of the traits. High estimates of PCV and GCV were observed for curd solidity indicated that there is substantial variability ensuring ample scope for improvement of this trait through selection. High heritability coupled with high genetic advance was observed for ascorbic acid content and curd solidity. The result suggested the importance of additive gene action for the inheritance of these characters thus improvement can be brought about by phenotypic selection for these characters.

Keywords: cauliflower, heritability, genetic advance, variability

Introduction
Cauliflower is an important vegetable crop of family *Brassicaceae* and is grown in many countries across the globe. The name cauliflower has originated from the Latin words *'caulis'* and *'floris'* which means cabbage and flower, respectively. It has been rightly described as "Aristocrat of cole crops" and is grown throughout the world for tender white curds (Nimkar and Korla, 2014) [1]. It is commonly used as a vegetable, in curry, soup and for pickling. The edible portion of this vegetable is approximately 45 per cent of the plant (Rai and Yadav, 2005) [2].

Globally, cauliflower is grown in an area of 1382.5 thousand ha with the production of 24175 thousand metric tonnes and its productivity is 17.49 metric tonnes/ ha (Anonymous, 2015) [3]. China amounts to a multi-billion-dollar trade boost for the Asian powerhouse being the leading producer of cauliflower in the world and contributing 34 per cent in area (478.3 thousand ha) and 42.9 per cent in production (9365.7 thousand metric tonnes) with the productivity of 19.58 metric tonnes/ ha. India is the second major cauliflower producing country after China in the world and contributes 32 per cent in area and 36 per cent in the world production share. In India, productivity of cauliflower is 19.76 metric tonnes/ ha but its potential productivity is 35-40 metric tonnes/ha and maximum productivity of 50 metric tonnes/ ha has been achieved in New Zealand followed by Kuwait (38 metric tonnes/ ha), Bahrain (36 metric tonnes/ ha) and Cyprus (36 metric tonnes /ha) (Anonymous, 2015) [3]. Apart from India and China, the other major producers of cauliflower are France, Italy, United Kingdom, United States of America, Spain, Poland, Germany, and Pakistan (Sharma *et al.,* 2005) [4].

Genetic variability is the basis of all plant improvement programmes. Exploitation of genetic potential for yield delivers varieties for enhancing the productivity of a crop (Ameta *et al.,* 2016) [5]. In cauliflower high genetic variation exists for yield and yield contributing traits. Yield is a complex character governed by several other yield attributing characters, therefore an observation with respect to the extent of genetic variability for the major agro-morphological traits reflects the status of variation available in hand for its effective utilization to breed improved varieties. An estimation of variability parameters viz., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance of the important yield contributing traits suggest the strategy to be adopted for its utilization in genetic improvement. Keeping in view the present experiment was laid to assess the variability parameters in cauliflower.

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Material and Methods

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. Seeds were sown in nursery beds of size 3m × 1m × 0.15m on September 30, 2014 and seedlings were transplanted in the field on November 1, 2014 at an inter and intra-row spacing of 45cm × 45cm. Besides the application of Farm Yard Manure @ 20 tonnes/ha, chemical fertilizers were applied as per the recommended package of practices (150 kg N, 100 kg P_2O_5, 50 kg K_2O /ha). Half dose of N and full dose of P_2O_5 and K_2O were applied at the time of field preparation and remaining half dose was dressed in two equal amounts, first at twenty five days after transplanting and second at the time of curd initiation. The intercultural operations, irrigations and pest-control were carried out in accordance with the recommended schedule. 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. The data for different characters was analyzed as per Gomez and Gomez (1983) [6]. The genotypic, phenotypic and environmental coefficients of variation were estimated by following method of Burton and De Vane (1953) [7]. Heritability in broad sense (h^2_{bs}) expected genetic advance (GA) resulting from the selection of 5% superior individuals was calculated as per Burton and De Vane (1953) [7] and Johnson et al., (1955) [8].

Table 1: Limits used for parameters of variability

Parameters	High	Moderate	Low
PCV and GCV:	>20 %	10 – 20 %	<10 %
Heritability in broad sense	>60 %	30 – 60 %	<30 %
Genetic advance:	>30 %	10 – 30 %	<10 %

PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation

Results and Discussion
Parameters of variability

The estimates of mean, range and parameters of variability viz., phenotypic and genotypic coefficients of variability (PCV and GCV) along with heritability (h^2bs) in broad sense and expected genetic advance as per cent of mean for different characters are presented (Table 2).

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV)

The knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is helpful in predicting the amount of variation present in the given genetic stock which in turn helps in formulating an efficient breeding programme. The estimates of PCV were higher than corresponding GCV for all characters studied which indicated that the apparent variation is not only due to genotypes but also due to the influence of environment. Therefore, caution has to be exercised in making selection for these characters on the basis of phenotype alone as environmental variation is unpredictable in nature. Singh et al., (2006) [9] and Kumar et al., (2011) [10] also reported higher estimates of PCV than the corresponding GCV.

PCV and GCV were high for curd solidity which indicated that there is substantial variability ensuring ample scope for improvement of these traits through selection and moderate for ascorbic acid content, stalk length, marketable yield per plant, curd size index, dry matter content and harvest index and gross weight per plant which could be due to differences in genetic material and growing conditions. The results are in consonance for ascorbic acid (Kumar et al., 2011) [10], marketable yield and gross weight (Chittora and Singh, 2015) [11], curd size index (Sharma et al., 2006) [12] and stalk length (Kumar et al., 2011) [10].

Heritability and genetic advance

The coefficient of variation alone cannot be used to partition the heritable components of variation (Burton, 1952) [13]. This suggested that genetic coefficient of variation together with heritability estimates would give the best picture of the amount of advance to be expected from selection. Heritability is a measure of the genetic relationship between parents and progeny and had widely used in determining the degree to which a character may be transmitted from parents to offspring. The information on heritability estimates is helpful in studying the inheritance of quantitative characters as well as for planning breeding programmes with desired degree of expected general progress. Heritability in broad sense is of tremendous significance to the breeders as its magnitude indicates the reliability with which a genotype can be recognized by its phenotypic expression (Lush 1940) [14].

High heritability estimates were observed for ascorbic acid, days to initiation of curd from transplanting, curd size index, harvest index, curd depth, days to marketable curd maturity from date of transplanting, stalk length, per cent marketable curds, curd diameter, plant height and total soluble solids, marketable yield per plant, gross weight per plant and curd solidity. These high estimates revealed the lesser influence of environment and greater role of genetic component of variation. Earlier researchers have also found similar results for ascorbic acid (Singh et al., 2013) [15], days to initiation of curd from transplanting and days to marketable curd maturity from date of transplanting (Singh et al., 2006 and Kumar et al., 2011) [9, 10], gross weight per plant and marketable yield per plant (Dubey et al., 2003) [16], stalk length (Kumar et al., 2011) [10], plant height (Singh et al., 2013) [15] and harvest index by Dubey et al., (2003) [16]. Moderate level of heritability was recorded for curd compactness, dry matter content and number of leaves per plant. Similar findings were reported for number of leaves per plant (Kumar et al., 2011 and Chittora and Singh, 2015) [10, 11].

Selection for a particular trait is generally made on the basis of its phenotypic expression which is the outcome of genotype and environment. Therefore, the phenotypic superiority of plants over the original population is not solely due to favourable environmental factors. In such a situation, genetic advance gives good idea for actual gain to be made in the population under evaluation. Johnson et al., (1955) [8] stressed that for estimating the real effects of selection, heritability alone is not sufficient and genetic advance along with heritability is more useful. Genetic advance may or may not be in proportion to genetic variability and heritability estimates because both high heritability and genetic variability are important to obtain higher genetic gain (Kumari, 2010) [17]. The high heritability does not necessarily

mean high genetic gain and alone it is not sufficient to make improvement through selection. Thus, the genetic advance has an edge over heritability as a guiding factor to breeders in selection programme.

In the present study, high genetic advance expressed as per cent of mean was observed for ascorbic acid content and curd solidity. The findings are confirmatory for ascorbic acid (Kumar and Korla, 2011) [18]. The estimates were moderate for curd size index, stalk length, harvest index, marketable yield per plant, curd depth, gross weight per plant, curd diameter, total soluble solids, dry matter content and days to initiation of curd from transplanting. The findings are in line for curd size index (Singh *et al.,* 2006) [9], harvest index, marketable yield per plant (Singh *et al.,* 2006 and Singh *et al.,* 2013) [9, 15] and curd diameter (Dubey *et al.,* 2003) [16]. High heritability coupled with high genetic advance was observed for ascorbic acid content and curd solidity. The result suggested the importance of additive gene action for the inheritance of these characters thus improvement can be brought about by phenotypic selection for these characters. Similar results have been observed for ascorbic acid content (Kumar *et al.,* 2011 and Singh *et al.,* 2013) [10, 15]. High heritability along with moderate genetic advance was observed for days to initiation of curd from transplanting, curd size index, harvest index, curd depth, curd diameter, stalk length, total soluble solids, marketable yield per plant and gross weight per plant which may be attributed to non-additive gene effects. The results are in line with the observation for gross weight per plant (Sharma *et al.,* 2006) [12], harvest index (Kumar, 1998) [19] and stalk length (Singh *et al.,* 2006) [9]. High heritability with low genetic advance was marked for days to marketable curd maturity from date of transplanting, per cent marketable curds and plant height indicating that this trait is more likely under the control of non-additive gene action and selection for this trait would be less effective. Similar findings have also been reported for days to marketable curd maturity from date of transplanting and plant height (Kumar and Thakur, 2004; Dhatt and Garg, 2008 and Singh *et al.,* 2010) [20, 21, 22]. Moderate heritability coupled with low genetic advance indicating the role of dominance and epistasis and hence improvement in traits can be brought about by recombination. This was observed for curd compactness and number of leaves per plant. The results are in confirmatory for number of leaves and curd compactness with Singh *et al.,* (2006) [9].

Table 2: Estimates of parameters of variability for different characters in cauliflower hybrids

Traits	Mean ±SE	Range	PCV (%)	GCV (%)	Heritability h^2bs (%)	GA (%)
Days to initiation of curd from transplanting	102.47±0.46	93.00-112.00	5.68	5.56	98.82	11.56
Days to marketable curd maturity from date of transplanting	119.15±0.66	107.33-128.00	4.86	4.74	95.06	9.52
Gross weight per plant (g)	1182.99±3.22	940.20-1413.15	10.76	10.43	73.12	17.60
Marketable yield per plant (g)	759.56±2.81	529.31-1021.78	14.68	14.31	79.26	25.39
Curd depth (cm)	7.68±0.22	6.51-9.15	9.18	8.97	95.47	18.05
Curd diameter (cm)	11.28±0.32	10.00-13.27	7.70	7.24	88.31	14.02
Curd size index (cm^2)	86.88±0.73	65.65-112.80	14.59	14.47	98.32	29.55
Curd compactness (^{0})	111.69±0.88	105.83-115.22	8.89	7.95	54.98	8.48
Curd solidity (g/cm)	99.04±2.19	66.78-125.30	26.39	20.80	62.14	33.78
% Marketable curds	84.94±0.66	78.33-100.00	4.89	4.69	92.01	9.27
Stalk length (cm)	3.36±0.22	2.67-4.78	14.76	14.25	93.20	28.34
Number of leaves per plant	12.12±0.55	10.67-13.33	9.08	5.17	32.43	6.07
Plant height (cm)	43.84±0.59	36.40-47.69	5.78	5.25	82.61	9.82
Dry matter content (%)	9.08±0.58	7.00-10.67	14.37	9.25	41.39	12.25
Ascorbic acid content (mg/100g)	50.10±0.54	35.00-67.13	16.64	16.55	98.91	33.91
Total soluble solids (^{0} Brix)	6.46±0.27	5.43-7.40	8.34	7.56	82.29	14.13
Harvest index (%)	63.76±0.65	47.25-80.93	13.96	13.77	97.23	27.96

PCV: Phenotypic Coefficient of Variation; GCV: Genotypic Coefficient of Variation; h^2bs (%): Heritability in broad sense; GA: Genetic Advance (%) of mean

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