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Genetic variability, correlation and path coefficient analysis in cauliflower (*Brassica oleracea* var. *botrytis*) genotypes

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Abstract

Genetic variability, correlation and path coefficient analysis was studied in cauliflower (*Brassica oleracea* var. *botrytis*) genotypes. The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating a high degree of variability in the material. High PCV and GCV were recorded for yield per plot, yield per hectare, net curd weight, gross curd weight, curd size, curd compactness and number of leaves per plant indicating variation among these traits. High heritability and genetic advance as percent of mean were recorded for curd diameter, plant height, plant spread, number of leaves per hectare, curd size, curd compactness, net curd weight, gross curd weight, yield per plot and yield per hectare. Therefore, selection for these traits may accumulate more additive genes and leads to further development in their performance in cauliflower breeding programme. The yield per hectare showed significant positive correlation with plant height, plant spread, curd diameter, curd size, gross curd weight, net curd weight, curd compactness and yield per plot. Hence, selection for these traits helps in the yield improvement. Path analysis showed that yield per plot, net curd weight, number of leaves per plant, curd diameter, plant spread and curd compactness exerted positive direct effect on yield per hectare and also showed positive significant correlation with yield per hectare indicating true relationship between the traits.

Keywords: Cauliflower, genotypes, genetic variability, heritability, correlation, path coefficient

Introduction

Cauliflower (*Brassica oleracea* L var *botrytis*) has wide adaptability and cultivated throughout India (Varalakshmi, 2009) [12]. It is believed that it has been originated in the island of Cyprus (Verma *et al.*, 2011) [13]. Cauliflower is mainly grown for its curds which are rich in vitamin C (ascorbic acid) and protein. Cauliflower is low in fat, but high in dietary fibre, foliate and water, possessing a high nutritional density. Cauliflower contains 56 mg/100 g vitamin B. Among the minerals, it constitutes of 0.76 percent P, 3.58 percent K, 117 mg Fe and 36 mg Cu. Besides vitamins and minerals cauliflower also contains, 4.9 percent total carbohydrate, 0.2 percent fat. In addition, cauliflower is fairly a high source of glucosinolates (40-80 mg/100 g) predominantly sin grin and glucobrassicin which have predominantly anti-carcinogenic property. It contains several phytochemicals, common in the cabbage family that may be beneficial to human health. Sulforaphane, a compound released when cauliflower is chopped or chewed, may protect against cancer. Other glucosinolates, Carotenoids, Indole-3-carbinol, a chemical that enhances DNA repair and acts as an estrogen antagonist, slowing the growth of cancer cells. A high intake of cauliflower has been associated with reduced risk of aggressive prostate cancer.

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 provides crop adaptability to environmental changes. Hence study of genetic variability along with heritability and genetic advance is required for formulating breeding method. Therefore, the present study was undertaken to assess the nature and magnitude of genetic variability present in different genotypes of cauliflower. An attempt has also been made to study the correlation and path coefficient which are helpful in selecting the desirable traits.

Materials and Methods

The present investigation was carried out in the experimental farm of Department of Horticulture, School of agricultural Sciences and Rural Development, Nagaland University,

Medziphema campus. The experiment was done during the month of October 2021 to February 2022 in Randomized Block Design with three replications. Twelve genotypes were studied to see the performance on growth, yield and quality characters like- Plant height, stalk length, number of leaves per plant, plant spread, curd diameter, curd size, gross curd weight, net curd weight, yield per plot, yield per hectare, curd compactness and ascorbic acid content. The analysis of variance was carried out according to Panse and Sukhatme (1957) [11] by using the mean performance of the genotypes. The phenotypic, genotypic and environmental coefficient of variation was calculated according to Burton and De Vane (1953) [3]. Heritability was calculated according to Allard (1960) [2]. Genetic advance possible through selection was calculated according to Johnson *et al.* (1955) [8]. Phenotypic and genotypic correlation coefficients were worked out as suggested by Al-Jibouri *et al.* (1958) [1]. The partitioning of genotypic correlation coefficient of traits into direct and indirect effects was carried out using the procedure suggested by Dewey and Lu (1959) [6].

Results and Discussion

The Analysis of variance showed significant difference among the genotypes for all the traits studied which specifies a high degree of variability in the material. It was revealed that the estimates of phenotypic coefficient of variation (PCV) were higher than those of genotypic coefficient of variation (GCV) for all the characters studied (Table-1). High PCV and GCV were recorded for yield per plot, yield per hectare, net curd weight, gross curd weight, curd size, curd compactness and number of leaves per plant indicating variation among these traits.

A fair measure of efficiency of selection for any quantitative traits can be derived from the character under consideration because heritability in a broad sense is the ratio of genotypic variance to the total phenotypic variance. But reliability depends not only on heritability, but it also should be accompanied by genetic advances as well (Johnson *et al.* 1955) [8]. High heritability coupled with high genetic advance shows that progress can be made through selection. Heritability is actually considered to be low if it is less than 30 percent, moderate between (30-60 percent) and high if it is more than 60 percent (Johnson *et al.* 1955) [8]. The range of

genetic advance as percent of mean is classified as low if it is less than 10 percent, moderate between (10-20 percent) and high if more than 20 percent (Johnson *et al.* 1955) [8]. In the present study, high estimates of heritability and genetic advance as percent of men were recorded for curd diameter, plant height, plant spread, number of leaves per hectare, curd size, curd compactness, net curd weight, gross curd weight, yield per plot and yield per hectare (Table- 1). Thus selection for these traits may accumulate more additive genes and leads to further development in their performance in cauliflower breeding programme. Similar findings were observed by Gurubaksh *et al.* (2010) [7], Kumar *et al.* (2010) [10], Chittora *et al.* (2015) [5] and Chatterjee *et al.* (2018) [4].

Correlation coefficient is a statistical measure which is used to find out the mutual relationship between various plants characters on which selection can be based for genetic improvement in yield. Correlation coefficient enables to identify characters or combinations of characters, which might be useful indicator of high yield. Correlation studies provide better understanding of yield components which helps in plant breeder during selection (Johnson *et al.* 1955) [8]. Therefore in the present study, correlation between twelve characters was studied in all possible combinations at phenotypic and genotypic level (Table-2 & 3). In general, magnitude of genotype correlation tended to be higher than the phenotypic correlation. This suggested a strong genetic association between the traits and the phenotypic expression was suppressed due to environmental influence. The yield per hectare showed significant positive correlation with plant height, plant spread, curd diameter, curd size, gross curd weight, net curd weight, curd compactness and yield per plot. Hence, selection for these traits helps in the yield improvement. Similar findings were reported by Kumar *et al.* (2010) [10] Path analysis (Table- 4) showed that yield per plot, net curd weight, number of leaves per plant, curd diameter, plant spread and curd compactness exerted positive direct effect on yield per hectare and also showed positive significant correlation with yield per hectare indicating true relationship between the traits. This suggests that direct selection for net curd weight, curd diameter, plant spread and curd compactness would be effective in increasing seed yield. Similar results were reported by Kumar *et al.* (2005) [9] and Kumar *et al.* (2010) [10].

Table 1: Genetic parameters for growth, yield and quality traits in cauliflower

Genetic parameters	Mean \pm SEM	Range	Genotypic Coefficient of variation (%)	Phenotypic Coefficient of variation (%)	Heritability (%)	Genetic Advance (GA)	Genetic advance in % of mean
Plant height (cm)	32.078 \pm 0.53	25.50-41.33	14.79	15.066	96.374	9.594	29.91
Stalk length (cm)	9.35 \pm 0.31	7.53-11.13	10.677	12.157	77.127	1.806	19.316
Number of leaves per plant	15.708 \pm 0.82	11.00-21.73	20.011	21.963	83.012	5.9	37.558
Plant spread (cm)	43.001 \pm 1.55	36.83-55.37	14.48	15.765	84.371	11.782	27.4
Curd diameter (cm)	9.914 \pm 0.18	7.63-12.70	13.152	13.517	94.673	2.613	26.362
Curd size (cm ²)	81.255 \pm 0.76	59.37-119.02	22.578	22.636	99.493	37.697	46.393
Gross curd weight (g)	753.569 \pm 6.56	267.33-40.03	37.341	37.371	99.837	579.191	76.86
Net curd weight (g)	451.114 \pm 8.83	153.67-38.33	44.768	44.896	99.429	414.835	91.958
Yield per plot (kg)	6.85 \pm 0.13	2.46-13.41	45.357	45.474	99.485	6.383	93.182
Yield per hectare (q)	118.96 \pm 2.18	42.68-232.87	45.350	45.46	99.511	110.86	93.191
Curd compactness	83.556 \pm 1.26	50.91-107.61	22.478	22.63	98.661	38.431	45.994
Ascorbic acid (mg/100g)	16.513 \pm 0.03	14.17-19.10	8.147	8.154	99.82	2.769	16.768

Table 2: Estimates of genotypic correlation coefficient among twelve characters in cauliflower genotypes

	1	2	3	4	5	6	7	8	9	10	11
1											
2	-0.162 ^{NS}										
3	0.365*	-0.289 ^{NS}									
4	0.915**	0.106 ^{NS}	0.170 ^{NS}								
5	0.681**	-0.315 ^{NS}	-0.201 ^{NS}	0.684**							
6	0.713**	-0.373*	0.031 ^{NS}	0.658**	0.919**						
7	0.524**	0.097 ^{NS}	-0.392*	0.530**	0.609**	0.462**					
8	0.769**	0.134 ^{NS}	-0.186 ^{NS}	0.790**	0.748**	0.678**	0.874**				
9	0.441**	0.142 ^{NS}	-0.529**	0.448**	0.682**	0.478**	0.908**	0.861**			
10	-0.077 ^{NS}	0.104 ^{NS}	-0.240 ^{NS}	0.027 ^{NS}	-0.154 ^{NS}	-0.202 ^{NS}	0.192 ^{NS}	0.135 ^{NS}	0.283 ^{NS}		
11	0.702**	0.262 ^{NS}	-0.227 ^{NS}	0.757**	0.610**	0.539**	0.914**	0.928**	0.823**	0.213 ^{NS}	
12	0.702**	0.262 ^{NS}	-0.227 ^{NS}	0.757**	0.610**	0.539**	0.914**	0.928**	0.823**	0.213 ^{NS}	1.000**

*Significant at 1% level of significance, **Significant at 5% level of significance 1. Plant height (cm) 2. Stalk length (cm) 3. Number of leaves per plant 4. Plant spread (cm) 5. Curd diameter (cm) 6. Curd size (cm²) 7. Gross curd weight (g) 8. Net curd weight (g) 9. Curd compactness 10. Ascorbic acid (mg/100 g) 11. Yield per plot (kg) 12. Yield per hectare (q).

Table 3: Estimates of phenotypic correlation coefficient among twelve characters in cauliflower genotypes

	1	2	3	4	5	6	7	8	9	10	11
1											
2	-0.140 ^{NS}										
3	0.315 ^{NS}	-0.237 ^{NS}									
4	0.829**	0.028 ^{NS}	0.090 ^{NS}								
5	0.667**	-0.301 ^{NS}	-0.159 ^{NS}	0.606**							
6	0.694**	-0.327 ^{NS}	0.029 ^{NS}	0.607**	0.890**						
7	0.516**	0.086 ^{NS}	-0.364*	0.487**	0.593**	0.461**					
8	0.759**	0.117 ^{NS}	-0.171 ^{NS}	0.721**	0.726**	0.674**	0.873**				
9	0.437**	0.142 ^{NS}	-0.488**	0.411*	0.667**	0.470**	0.902**	0.855**			
10	-0.077 ^{NS}	0.094 ^{NS}	-0.228 ^{NS}	0.026 ^{NS}	-0.152 ^{NS}	-0.201 ^{NS}	0.192 ^{NS}	0.135 ^{NS}	0.281 ^{NS}		
11	0.691**	0.229 ^{NS}	-0.208 ^{NS}	0.686**	0.590**	0.535**	0.911**	0.927**	0.816**	0.213 ^{NS}	
12	0.691**	0.229 ^{NS}	-0.208 ^{NS}	0.686**	0.590**	0.535**	0.911**	0.927**	0.816**	0.213 ^{NS}	1.000**

*Significant at 1% level of significance, **Significant at 5% level of significance 1. Plant height (cm) 2. Stalk length (cm) 3. Number of leaves per plant 4. Plant spread (cm) 5. Curd diameter (cm) 6. Curd size (cm²) 7. Gross curd weight (g) 8. Net curd weight (g) 9. Curd compactness 10. Ascorbic acid (mg/100g) 11. Yield per plot (kg) 12. Yield per hectare (q).

Table 4: Direct (diagonal) and indirect effects of different characters at genotypic level in cauliflower

Characters	Plant height (cm)	Stalk length (cm)	Number of leaves per plant	Plant spread (cm)	Curd diameter (cm)	Curd size (cm ²)	Gross curd weight (g)	Net curd weight (g)	Curd compactness	Ascorbic acid (mg/100g)	genotypic correlation for Yield per plot (kg)
Plant height (cm)	-0.00104	0.00006	0.00015	0.00021	0.00022	-0.00025	-0.00034	0.00034	0.00005	0.00001	0.70248
Stalk length (cm)	0.00017	-0.00037	-0.00012	0.00002	-0.00010	0.00013	-0.00006	0.00006	0.00002	-0.00002	0.26192
Number of leaves per plant	-0.00038	0.00011	0.00041	0.00004	-0.00007	-0.00001	0.00025	-0.00008	-0.00006	0.00004	-0.22749
Plant spread (cm)	-0.00095	-0.00004	0.00007	0.00023	0.00022	-0.00023	-0.00034	0.00035	0.00005	0.00000	0.75747
Curd diameter (cm)	-0.00071	0.00012	-0.00008	0.00016	0.00033	-0.00032	-0.00039	0.00033	0.00008	0.00003	0.61025
Curd size (cm ²)	-0.00074	0.00014	0.00001	0.00015	0.00030	-0.00035	-0.00030	0.00030	0.00005	0.00003	0.53922
Gross curd weight (g)	-0.00054	-0.00004	-0.00016	0.00012	0.00020	-0.00016	-0.00065	0.00039	0.00010	-0.00003	0.91478
Net curd weight (g)	-0.00080	-0.00005	-0.00008	0.00018	0.00024	-0.00024	-0.00057	0.00044	0.00010	-0.00002	0.92847
Curd compactness	-0.00046	-0.00005	-0.00022	0.00010	0.00022	-0.00017	-0.00059	0.00038	0.00011	-0.00005	0.82368
Ascorbic acid (mg/100g)	0.00008	-0.00004	-0.00010	0.00001	-0.00005	0.00007	-0.00012	0.00006	0.00003	-0.00017	0.21365
Yield per plot (kg)	-0.00073	-0.00010	-0.00009	0.00017	0.00020	-0.00019	-0.00059	0.00041	0.00009	-0.00004	1.00086

Residual value = 0.00012

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