

GENETIC VARIABILITY AND CHARACTER ASSOCIATION FOR QUANTITATIVE TRAITS IN CAULIFLOWER (*Brassica Oleracea* Var. *Bsotrytis*) GENOTYPES

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Abstract

The present study was conducted to evaluate sixteen cauliflower (*Brassica oleracea* var. *botrytis* L.) genotypes under the agro-climatic conditions of Gazipur, Bangladesh during 07 November 2024 to 24 February 2025, to find out their variability, character association and path coefficient of curd yield and its related traits at the Research Field of Olericulture Division of Horticulture Research Center, Bangladesh Agriculture Research Institute. The experiment was laid out in a randomized complete block design with three replications. Significant variation ($p \leq 0.001$) was observed among genotypes for all traits, indicating ample genetic diversity suitable for selection and improvement of cauliflower. Early maturing genotypes such as CL-1, CL-2, and CL-4 showed the shortest duration for curd initiation and harvest but produced smaller curds and lower yields. In contrast, CL-5, CL-7, CL-9, CL-12 and CL-13 recorded superior vegetative growth, larger curd size and the highest curd yield per hectare (58.56-67.07 t/ha). High heritability coupled with high genetic advance as percent of mean for traits such as whole plant weight, marketable curd weight, days to first curd initiation, days to fifty percent curd initiation and net curd weight indicated that additive gene effects play a major role and simple selection methods would be successful. However, the less deviations between phenotypic coefficient of variation and genotypic coefficient of variation suggested low influence of growing environment for all traits and these traits are mostly controlled by gene. Correlation and path coefficient analyses revealed that days to first curd initiation, whole plant weight, marketable curd weight, curd breadth, and leaf length had strong positive associations and direct effects on curd yield, identifying them as major selection indices, suggesting these traits as key selection criteria for curd yield improvement in cauliflower genotypes.

Keywords: Genetic variability, heritability, path coefficient, correlation, cauliflower, *Brassica oleracea* var. *botrytis*.

Introduction

Cauliflower (*Brassica oleracea* var. *botrytis* L., $2n = 2x = 18$), an important nutritious vegetable crop of the Brassicaceae family, is popularly known as

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‘Fulcopi’ in Bangladesh. It is a vital member of cole crops, which is cultivated worldwide including Bangladesh. It protects heart health, lowers cholesterol, establishes immune system, prevents bone loss, reduces cancer risk, protects skin from UV rays and aids in digestion; nutrition quality of its 100 g head is-2.6 g protein, 30 mg carotene, 33 mg Ca, 4 Kcal energy, 57 mg P, 1.2 mg iron and 56 mg vitamin (Udaysinh *et al.*, 2024). Cauliflower is generally used as cooked vegetable either singly or mixed with potato, carrot, and peas. In Bangladesh, annually cauliflower occupies an area of 23,534 ha with a production of 429,670 MT and productivity of 18.25 t/ha (Anon., 2025). In Bangladesh, cauliflower plays a significant role in improving nutritional security and farmers livelihoods. Generally, this crop is grown only in winter season due to its temperate origin; however, with the development of tropical heat-tolerant varieties, its cultivation window has significantly expanded (Rahman *et al.*, 2020; Hussien *et al.*, 2021). Bangladesh’s diverse agro-climatic conditions, ranging from humid sub-tropical summers to cool, dry winters, provide opportunities for year-round cultivation of cauliflower. This has encouraged the introduction of both tropical and temperate genotypes with varying adaptability and productivity. Tropical types are generally early maturing and heat-tolerant, while temperate types tend to exhibit better curd quality and higher yields under cooler conditions (Singh *et al.*, 2023). However, the adaptability, curd yield, and quality, as well as seed production capacity, are critical traits that require assessment for breeding purposes. Temperate genotypes often require specific vernalization conditions for seed production, while tropical genotypes may offer more flexibility in seed set under warmer environments (Thakur and Sharma, 2023).

In cauliflower high genetic variation exists for yield and yield contributing traits and exploitation of genetic potential for enhancing the productivity of this crop helps develop varieties using breeding method. An estimation of variability parameters viz. genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent of mean of the yield contributing traits suggests the strategy to be adopted for its utilization in genetic improvement (Ullah *et al.*, 2012). The magnitude of variability and its quantitative estimation for each character would indicate the potential of each plant and scope for improving the desirable and economic characters through selection. Knowledge regarding association i.e., correlation and path coefficient analysis between yield and its component traits are important in determining the component characters that could be used as selection parameters for effective improvement of the crop. The study was, therefore, carried out to investigate the genetic variability, correlation and path analysis in sixteen cauliflower genotypes with a view to

identifying promising genotypes for future breeding program under the agroclimatic conditions of Gazipur, Bangladesh.

Materials and Methods

The experiment was conducted at the research field of Olericulture Division, Horticulture Research Center (HRC), Bangladesh Agricultural Research Institute (BARI), Gazipur, Bangladesh during the period from 07 November 2024 to 24 February 2025 to evaluate sixteen cauliflower genotypes using a randomized block design with three replications. The study area is situated in 23.9917° N longitude and 90.4137° E latitude at an altitude of 9 meter above the sea level. Seedlings were sown in seed bed on 07 November 2024 and then the seedlings were transferred to the 2nd seed bed 14 days after emergence (double transplanting). Thirty-day-old healthy seedlings (4-leaf stage) were transplanted in the main field on 07 December 2024. The unit plot size and plant spacing were maintained at 10.0 × 1.0 m and 50 cm × 50 cm, respectively. A total of 40 seedlings were planted in each unit plot. Fertilization was done at @ 70-50-75-18-4.2-2 kg ha⁻¹ NPKSZnB along with 10 tons cow dung per hectare. Half of the cow dung and half of the phosphorus, along with the entire sulfur and boron, were applied during final land preparation. The remaining cow dung and phosphorus were applied during pit preparation one week before planting. Nitrogen and potassium were applied in three equal installments at 20, 35, and 50 days after transplanting. Irrigation was provided as needed. Other cultural practices and plant protection measures were followed during the cultivation of the crop. Data were recorded on days to first curd initiation, days to 50% curd initiation, days to first harvest, whole plant weight, plant height, number of leaves per plant, individual marketable curd weight, net curd weight, curd length, curd breadth, leaf length, leaf breadth and curd yield per plant. Per plot yield was then converted to yield per hectare. All the recorded data were analyzed statistically using R software. Mean separation was done by least significant difference (LSD) test at 5% level of probability. From the recorded data, range (maximum and minimum), grand mean, Standard Error of Mean ((SEm), Environmental Coefficient of Variation (ECV), Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Heritability (broad sense), Genetic advance and Genetic advance as percentage of mean were analyzed using R software. Pearson Correlation Coefficient and Path Coefficient Analysis were also done by R software.

Results and Discussion

Analysis of variance for various growth and yield related traits

Analysis of variance (ANOVA) revealed highly significant differences ($p \leq 0.001$) among the 16 cauliflower genotypes for all vegetative growth and yield-related characters investigated (Table 1). Significant treatment mean squares for days to first curd initiation (MS = 1678.84), days to 50% curd initiation (MS = 1783.77), days to harvest (MS = 1631.96), whole plant weight (MS = 1,705,002), marketable curd weight (MS = 536,656), net curd weight (MS = 370,370) and yield per hectare (MS = 214.662) indicate that the observed variation for both earliness and yield components was mainly attributable to genotypic differences rather than experimental error (Kotha Keerthana *et al.*, 2025). The presence of significant variation for earliness traits (days to curd initiation and days to harvest) suggests that the evaluated germplasm contains early and late types, providing scope to select genotypes adapted to specific planting windows and to target multiple markets. Similar reports of significant genotypic variation for earliness in cauliflower have been documented in variability studies (Lav Kumar *et al.*, 2019). Vegetative traits including whole plant weight, plant height, number of leaves, leaf length and breadth also showed highly significant treatment effects. Large treatment mean squares for whole plant weight and curd weight components indicate these are promising selection targets for improving marketable yield. Other authors have likewise found that curd weight and whole plant biomass are among the most variable and heritable traits contributing to yield, and therefore useful targets in selection and hybridization programs (Subhrajyoti Chatterjee *et al.*, 2018). The relatively small error mean squares for many characters (Table 1) indicate good experimental precision and reliability of the observed differences. Because treatment variance substantially exceeded error variance for key yield components, the estimates of genotypic differences are likely robust, supporting confident selection decisions (Kotha Keerthana *et al.*, 2025). Overall, the highly significant genotypic differences recorded for both earliness and yield-related traits point to a considerable scope for genetic improvement of cauliflower through selection and hybridization. The results support continued evaluation of the identified superior genotypes in multi-location trials and incorporation of high-performing lines into crossing programs to combine earliness and yield-related favorable traits—an approach recommended in prior cauliflower breeding and genetic variability studies (Hussein *et al.*, 2021).

Table 1. Analysis of variance (ANOVA) for various vegetative growth and yield related traits in 16 cauliflower genotypes

Characters	Mean Sum Square		
	Replication Df (2)	Treatment Df (15)	Error Df (30)
Days to first curd initiation	1.94	1678.84**	0.96
Days to fifty percent curd initiation	2.15	1783.77**	0.83
Days to harvest	21.82	1631.96**	7.34
Whole plant weight	14160	1705002**	319173
Plant height	9.69	283.60**	5.61
Number of leaves per plant	1.04	54.01**	1.53
Marketable curd weight	31584	536656**	7368
Curd length	0.74	98.22**	0.62
Curd breadth	0.32	57.63**	1.02
Leaf length	2.59	194.37**	6.66
Leaf breadth	2.17	50.47**	1.63
Net curd weight	6795	370370**	3943
Yield ton per hectare	12.63	214.66**	2.94

* & **, indicate significant at 5% and 1% probability levels, respectively.

Mean performance of cauliflower genotypes

Mean performance of sixteen cauliflower genotypes was evaluated based on their growth duration, morphological characteristics, and yield related traits under Gazipur condition (Table 2). Significant variation ($P < 0.01$) was observed among 16 genotypes for all studied traits, indicating ample genetic variability suitable for selection and improvement (Rahman *et al.*, 2020; Hussien *et al.*, 2021). The lowest days to first curd initiation (DFCI), days to fifty percent curd initiation (DFPCI) and days to harvest (DH) were recorded in genotype CL-2 (23, 26, 41.10 days, respectively) followed by genotypes CL-4 (26, 29 and 42.67 days, respectively), CL-1 (37, 42 and 55 days, respectively), CL-6 (42, 44.67 and 58.33 days, respectively) and CL-3 (42.33, 46 and 72.67 days, respectively). The maximum days to first curd initiation (DFCI) was found in CL-9 (90.33 days) closely followed by CL-12 (90 days) and then followed by CL-13 (88.33 days) and CL-14

(87.67 days). The highest days to fifty percent curd initiation (DFPCI) and days to harvest (DH) were observed in CL-10 (97 and 106 days, respectively) followed by CL-9 (96.33 and 104 days, respectively), CL-12 (94 and 103 days, respectively) and CL-13 (92 and 102.67 days, respectively). From these results it is revealed that the earliest genotypes in terms of DFCI, DFPCI and DH were CL-2, CL-1, CL-4 and CL-6. In contrast, it showed that the latest genotypes were CL-9, CL-10, CL-13, and CL-14 with regard to DFCI, DFPCI and DH. Such variation in maturity duration (41–107 days) offers flexibility for staggered harvesting. Earliness is a desirable trait for early market advantage and extended harvesting periods, as supported by Thakur and Sharma (2023) and Nehra (2023). Marked differences were also noted in plant morphological traits such as whole plant weight (WPW), plant height (PH) and number of leaves per plant (NLPP). The maximum whole plant weights (heaviest plants) (WHP) were recorded in CL-7 (3161 g) followed by CL-13 (2628.67 g), CL-5 (2627.67 g), CL-3 (2575 g), CL-9 (2483.33 g) and CL-12 (2373.33 g), indicating strong vegetative vigor, while CL-2 (716.67 g) and CL-4 (783.33 g) exhibited the lowest plant biomass. The tallest plant was noted in CL-16 (76.67 cm) followed by CL-7 (72.33 cm), CL-15 (69.33 cm), CL-5 (62.27 cm) CL-13 (63.00 cm) and the shortest plant was observed in CL-2 (42.10 cm) and CL-4 (44.90 cm). The highest number of leaves/plant (NLPP) (26.00) was observed in CL-13 (26) followed by CL-7 (24.33), CL-9 (22.67), CL-5 (22.39) and CL-12 (21.33), whereas the lowest NLPP was recorded in CL-2 (11.30) followed by CL-4 (12.07). The genotypes having higher leaves/plant suggest their potential for higher photosynthetic capacity and biomass accumulation (Singh *et al.*, 2023; Hussien *et al.*, 2021), and the genotypes with lower number of leaves/plants gave lower whole plant weight i.e. lower biomass due to their low photosynthetic capacity because of lower number of leaves in the present investigation. Significant variation was also observed in marketable curd weight (MCW). The Genotype CL-9 produced the maximum marketable curd weight (MCW) (1676.67 g), which was statistically similar with CL-13 (1597.67 g) and CL-12 (1540.00 g) and then followed by CL-5 (1463.69 g) and CL-7 (1415.77 g), while genotypes CL-2 (351.33 g) recorded the smallest MCW (351.33 g) on par with CL-4 (379.67 g). These findings indicate that early maturing genotypes tend to have smaller curds, reflecting a trade-off between earliness and curd size, as reported in previous studies (Rahman *et al.*, 2020; Nehra, 2023). Curd and leaf morphology also showed substantial variation among genotypes. The longest curd (21.43 cm) was observed in CL-5 which was on par with CL-12 (19.67 cm) and the maximum breadth (25.33 cm) was noticed in CL-5 closely followed by CL-9 (24.67 cm), CL-12 (24.67 cm), CL-13 (24.33 cm) and CL-7 (23.67 cm)., indicating superior curd development. Conversely, CL-2 and CL-4 exhibited the smallest curd dimensions (L x B: 5.50 cm x 10.93 cm and L x B: 5.70 cm x 11.90 cm. Leaf traits such as leaf length (LL)

and breadth (LB) were found highest in CL-7 (63 cm, 31.33 cm) followed by CL-13 (54.67 cm, 25.33 cm) and CL-9 (53 cm, 26.33 cm), suggesting a positive relationship between leaf area and curd yield. Yield per hectare (YTPH) varied significantly among genotypes, ranging from 14.05 t/ha (CL-2) to 67.07 t/ha (CL-9). The highest yield was recorded in CL-9 (67.07 t/ha), closely followed by CL-13 (63.91 t/ha), CL-12 (61.60 t/ha) and CL-5 (58.56 t/ha). These high-yielding genotypes exhibited favorable combinations of plant biomass due to higher whole plant weight, Number of leaves/plant, higher leaf length and leaf breadth, marketable curd weight, and curd dimensions. In contrast, CL-2 produced the lowest yield (14.05 t/ha) being on par with CL-4 (15.19 t/ha) despite its early maturity, highlighting the trade-off between earliness and yield potential (Hussien *et al.*, 2021; Singh *et al.*, 2023).

Table 2. Mean performance of 16 cauliflower genotypes for 14 quantitative traits

Genotype	DFCI	DFPCI	DH	WPW (g)	PH (cm)	NLPP	MCW (g)
CL-1	37.00	42.00	55.00	1022.00	52.00	14.66	633.22
CL-2	23.00	26.00	41.10	716.67	42.10	11.30	351.33
CL-3	42.33	46.00	72.67	2575.00	60.78	18.00	1205.55
CL-4	26.00	29.00	42.67	783.33	44.90	12.07	379.67
CL-5	56.00	59.00	72.67	2627.67	62.27	22.39	1463.89
CL-6	42.00	44.67	58.33	1433.33	58.33	18.00	855.55
CL-7	60.00	63.33	73.67	3161.00	72.33	24.33	1415.77
CL-8	81.00	85.00	104.33	1222.33	50.44	18.00	928.44
CL-9	90.33	96.33	104.00	2483.33	53.33	22.67	1676.67
CL-10	86.00	97.00	106.00	1791.33	50.00	20.00	1162.33
CL-11	74.67	76.00	90.33	1430.00	61.33	21.00	930.00
CL-12	90.00	94.00	103.00	2373.33	62.00	21.33	1540.00
CL-13	88.33	92.00	102.67	2628.67	63.00	26.00	1597.67
CL-14	87.67	89.67	107.00	1175.00	50.63	16.07	795.00
CL-15	60.33	62.33	93.00	1502.33	69.33	16.00	772.33
CL-16	73.33	77.00	95.00	1702.67	76.67	15.33	740.00
CV (%)	1.54	1.35	3.28	5.35	4.08	6.68	8.35
LSD (0.05)	1.63	1.52	4.52	159.69	3.95	2.07	143.14

DFCI=Days to first curd initiation, DFPCI=Days to fifty percent curd initiation, DH=Days to harvest, WPW=Whole plant fresh weight, PH=Plant height, NLPP=Number of leaves per plant, MCW=Marketable curd weight, CV=Co-efficient of Variation, LSD=Least Significant Difference.

Table 2. Continued

Genotype	CL (cm)	CB (cm)	LL (cm)	LB (cm)	NCW (g)	YTPH
CL-1	7.23	17.50	42.11	19.28	402.78	25.33
CL-2	5.50	10.93	31.00	14.47	210.00	14.05
CL-3	8.58	24.57	51.03	24.82	882.22	48.22
CL-4	5.70	11.90	34.00	15.13	250.67	15.19
CL-5	21.43	25.33	52.10	23.61	1123.33	58.56
CL-6	8.00	20.00	46.33	21.00	613.33	34.22
CL-7	18.33	23.67	63.00	31.33	823.33	56.63
CL-8	15.00	21.00	43.67	20.33	633.33	37.14
CL-9	17.00	24.67	53.00	26.33	1100.00	67.07
CL-10	13.00	21.33	42.00	20.00	896.67	46.49
CL-11	7.67	19.33	46.67	23.33	733.33	37.20
CL-12	19.67	24.67	50.67	22.33	1353.33	61.60
CL-13	18.00	24.33	54.67	25.33	1330.00	63.91
CL-14	9.57	18.10	41.63	21.48	625.00	31.80
CL-15	19.33	20.67	53.00	21.00	436.67	30.89
CL-16	19.00	18.00	51.00	20.33	556.67	29.60
CV (%)	5.94	4.97	5.46	5.85	8.39	8.35
LSD (0.05)	1.32	1.69	4.30	2.13	191.11	5.73

CL=Curd length, CB=Curd breadth, LL=Leaf length, LB=Leaf breadth, YTPH=Yield tons per hectare

Estimation of genetic variability

A wide range of variability was observed among the sixteen cauliflower genotypes for all the studied traits (Table 3). The values for days to first curd initiation ranged from 23 to 91 days, fifty percent curd initiation 26 to 98 days, and days to harvest 40 to 108 days with mean values of 63.63 ± 0.57 , 67.46 ± 0.53 and 82.59 ± 1.56 days, respectively that revealed notable variations exist in maturity behaviour of cauliflower genotypes. Similarly, the wide ranges in whole plant weight and marketable curd weight were observed 700–3433 g and 342–1800 g with mean values of 1789 ± 55.29 and 1027.96 ± 49.56 g, respectively, reflecting considerable variations in these traits which contributed much in the variability of yield potential of cauliflower genotypes. The ranges for plant height (PH), number of leaves/plant (NLPP), leaf length (LL) and leaf breadth (LB) were observed 41.50–78.00 cm, 10.90–27.00, 30–68 cm and 14.20–32 cm,

respectively and their mean values were recorded 58.09 ± 1.37 cm, 18.57 ± 0.72 , 47.24 ± 1.49 cm and 21.88 ± 0.74 cm, respectively, indicating considerable variability in vegetative growth. Curd length (CL) varied from 5.3 to 22.0 cm, curd breadth (CB) from 10.3 to 27.0 cm, net curd weight (NCW) from 195 to 1480 g and yield per hectare (YTPH) from 13.68 to 72.00 t/ha, with their mean values 13.31 ± 0.46 cm, 20.38 ± 0.58 cm, 748.17 ± 36.26 g and 41.12 ± 1.98 t/ha, respectively that indicates a lot of variability were present in yield and yield related traits. The low environmental coefficient of variation (1.35–8.39%) were noticed in the traits suggested minimal environmental influence in 14 quantitative traits. The phenotypic coefficient of variations in 14 characters was always higher than the genotypic coefficient of variations of those characters, but lower differences were found. This close correspondence between genotypic and phenotypic coefficients of variations indicated that most of the variability was genetic in nature and selection based on phenotype can be effective for improvement of these traits (Begum *et al.*, 2016). Heritability estimates in broad sense for all traits were found very high (0.92–1.00), indicating the low influence of environment on the studied characters and implying strong genetic control and high selection efficiency of these traits. High estimates of heritability for most of the variables suggested that variations were passed down to progeny, implying that a high-yielding variety may be developed by selecting desirable genotypes. High heritability provided more options for selecting plant material with the desired features. High genetic advance (genetic gain) and genetic advance as percentage of mean were recorded for WPW (1536.38 and 85.87%), MCW (847.75 and 82.47%), NCW (708.60 and 94.71%) and curd initiation traits viz. DFCI (48.68 and 76.50%) and DFCI (50.18 and 74.39%), suggesting predominance of additive gene action and high effectiveness of selection for these traits. Johnson *et al.* (1955) reported that heritability estimates with high genetic advance are more helpful in predicting the gain under selection. Traits with high heritability integrated with high genetic advance can be improved effectively through direct selection (Mohana Krishna *et al.*, 2009). High heritability (0.96–0.98) coupled with high genetic advance for CL (0.98 and 87.42%), and YTPH (0.96 and 82.47%) suggested the predominance of additive gene action and high effectiveness of selection for these two traits conversely, traits such as leaf breadth (LB) and curd breadth (CB) exhibited moderate genetic advance as % mean, indicating partial non-additive gene effects (Mohana Krishna *et al.*, 2009).

Table 3. Estimates of variability characters for 14 quantitative traits in 16 cauliflower genotypes

Traits	Range		Mean± SEm	ECV	GCV	PCV	h ₂ b	GA	GAM
	Mini.	Max.							
DFCI	23.00	91.00	1331±0.57	1.54	37.17	37.20	1.00	48.68	76.50
DFPCI	26.00	98.00	67.46±0.53	1.35	36.14	36.16	1.00	50.18	74.39
DH	40.00	108.00	82.59±1.56	3.28	28.17	28.36	0.99	47.61	57.65
WPW	700.00	3433.00	1789.25±55.29	5.35	42.02	42.36	0.98	1536.38	85.67
PH	41.00	78.00	58.09±1.37	4.08	16.57	17.07	0.94	19.25	33.15
NLPP	10.90	27.00	18.57±0.72	6.68	22.52	23.49	0.92	8.26	44.48
MCW	342.00	1800.00	1027.96±49.56	8.35	40.86	41.71	0.96	847.75	82.47
CL	5.30	22.00	13.31±0.46	5.94	42.84	43.25	0.98	11.64	87.42
CB	10.50	27.00	20.38±0.58	4.97	21.32	21.89	0.95	8.72	42.78
LL	30.00	68.00	47.24±1.49	5.46	16.74	17.61	0.90	15.49	32.79
LB	14.20	32.00	21.88±0.74	5.85	18.44	19.34	0.91	7.92	36.20
NCW	195.00	1480.00	748.17±36.26	8.39	46.71	47.46	0.97	708.60	94.71
YTPH	13.68	72.00	41.12±1.98	8.35	40.86	41.71	0.96	33.91	82.47

Min.= Minimum, Max. = Maximum, SEm = Standard Error of mean, ECV = Environmental Coefficient of Variation, GCV = Genotypic Coefficient of Variation (GCV), PCV = Phenotypic Coefficient of Variation, h₂b = Heritability in broad sense, GA = Genetic advance, GAM = Genetic Advance as percentage of mean

DFCI=Days to first curd initiation, DFPCI=Days to fifty percent curd initiation, DH=Days to harvest, WPW=Whole plant weight, PH=Plant height, NLPP=Number of leaves per plant, MCW=Marketable curd weight, CL=Curd length, CB=Curd breadth, LL=Leaf length, LB=Leaf breadth, NCW= Net curd weight; YTPH=Yield ton per hectare.

Correlation between various traits of cauliflower genotypes

Pearson's correlation coefficient matrix was estimated (Fig. 1) to determine the value of association among the various growth, yield and yield attributes of cauliflower genotypes. Most traits exhibited strong and significant positive correlations, suggesting that improvement in one trait would likely enhance others, thereby contributing to higher yield potential (Sandhu *et al.*, 2024; Nehra, 2023). The analysis revealed yield per hectare (YTPH) was positively and significantly correlated with all the traits studied. YTPH reflected a significant and strong positive correlation with whole plant weight, WPW (0.90***), number of leaves per plant, NLPP (0.89***), marketable curd weight, MCW (1.00***), curd breadth, CB (0.91***), and net curd weight, NCW (0.94***), suggesting that these traits are the most influential determinants of yield per hectare. A very strong positive correlation was observed between net curd weight (NCW) and marketable curd weight (MCW), indicating that heavier curds directly contribute to overall

marketable curd yield. Similarly, MCW showed a highly significant association with curd breadth (0.91**), curd length, CL (0.66***), number of leaves per plant, NLPP (0.89***), leaf breadth, LB (0.78***), and WPW (0.90***). These results imply that plants with greater vegetative biomass and larger curd size tend to produce higher yields. Morphological traits such as plant height, PH (0.38*) and days to harvest, DH (0.56**) showed moderate correlations with yield attributes. PH exhibited a positive but weaker association with MCW (0.38**) and YTPH (0.38**), suggesting that taller plants do not always correspond to higher yield. In contrast, earliness traits, days to first curd initiation (DFCI) and days to 50% curd initiation (DFPCI) showed comparatively weak correlations with most yield parameters, implying that early-maturing genotypes tend to have lower yield due to shorter growth duration and smaller curd development (Singh *et al.*, 2023). Overall, the strong positive correlations among WPW, LB, MCW, CL, CB, NCW, NLPP, and YTPH suggest that these traits are the major contributors to yield improvement in cauliflower genotypes. Therefore, these parameters may be considered as key selection criteria for identifying high-yielding cauliflower genotypes under Gazipur condition.

Path Coefficient Analysis

Path coefficient analysis was performed to partition the correlation coefficients into direct and indirect effects of various traits on curd yield per hectare (YTPH), thereby identifying the most influential yield-contributing parameters (Fig. 2). The analysis revealed that marketable curd weight (MCW) exerted the highest positive direct effect (1.00) on YTPH, indicating that this trait is the principal determinant of curd yield. This finding aligns with the correlation analysis, where MCW also showed the strongest positive association with YTPH, suggesting that genotypes producing heavier curds directly enhance productivity and Singh *et al.*, (2025) found the similar result. Among morphological traits, curd breadth (CB) (0.001) exhibited substantial positive direct effects on YTPH, implying that curd breadth contributes significantly to total yield. The whole plant weight (WPW) (0.001) and leaf length (0.001) showed positive direct effects on yield. The number of leaves per plant (NLPP) (0.0001) showed positive smaller direct effect, indicating their indirect influence on yield through helping in accumulation of photo-synthates contributing in curd development. In contrast, days to 50% curd initiation (DFPCI) (-0.002) and days to harvest (DH) (-0.001), plant height

(PH) (-0.001) and leaf breath (LB) (0.0001) displayed negative direct effects, confirming that early-maturing genotypes generally produce lower yields due to shorter vegetative and curd growth periods. Leaf attributes such as leaf length (LL) and leaf breadth (LB) had moderate indirect effects on curd yield and primarily mediated through their influence on MCW and CB suggesting that larger leaf area enhances photosynthetic capacity and assimilate supply for curd growth.

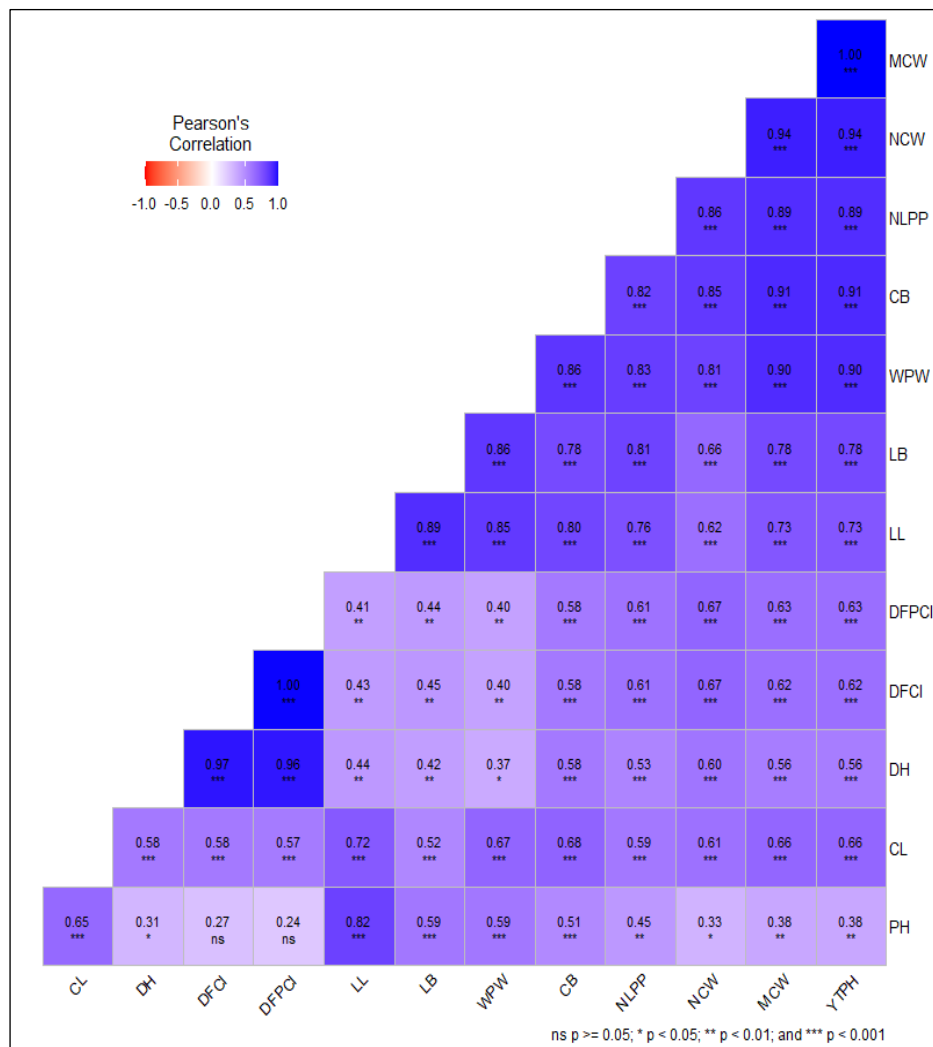


Fig. 1. Pearson correlation for various quantitative traits under study.

[*, **, *** indicate significance at 0.05, 0.01 and 0.001 probability levels, respectively. [DFCI: Days to first curd initiation, DFPCI: Days to 50% curd initiation, DH: days to harvest, WPW: Whole plant weight, PH: Plant height, NLPP: Number of leaves per plant, MCW: Marketable curd weight, CL: Curd Length, CB: Curd breadth, LL: Leaf length, LB: Leaf breadth, NCW: Net Curd weight; YTPH= Yield ton per hectare].

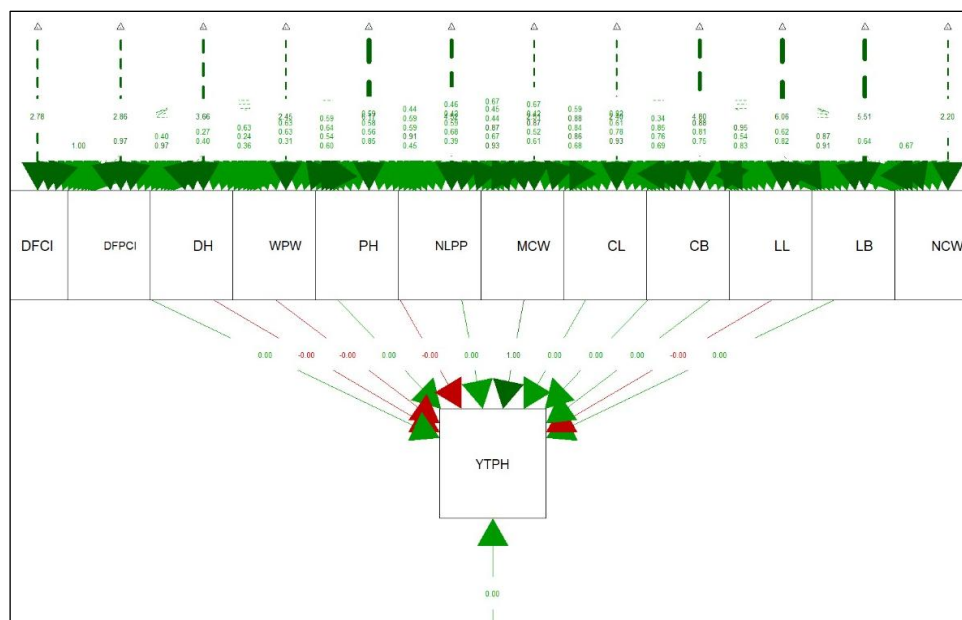


Fig. 2. Path coefficient analysis of 14 characters in 16 cauliflower genotypes.

[DFCI: Days to first curd initiation, DFPCI: Days to 50% curd initiation, DH: days to harvest, WPW: Whole plant weight, PH: Plant height, NLPP: Number of leaves per plant, MCW: Marketable curd weight, CL: Curd Length, CB: Curd breadth, LL: Leaf length, LB: Leaf breadth, NCW: Net Curd weight, YTPH=Yield ton per hectare.]

Conclusion

The experimental results revealed that early-maturing genotypes, namely CL-1, CL-2, and CL-4 showed potential for early market supply due to their short vegetative growth and curd growth period but were generally associated with smaller curds and lower curd yields. In contrast, CL-9, CL-5, CL-7, CL-12, and CL-13 exhibited superior vegetative vigour, larger curd size and higher yield per hectare, making them promising candidates for producing higher yields. The strong positive correlations among marketable curd weight, curd length, curd breadth, net curd weight and number of leaves per plant, whole plant weight and yield per plant suggest that these traits are the major contributors to yield improvement in cauliflower genotypes. Therefore, these parameters may be considered as key selection criteria for identifying high-yielding genotypes under Gazipur condition. The low environmental coefficient of variation (1.35–8.39%) were noticed in the traits studied in present investigation, and the phenotypic coefficient of variations were higher than the genotypic coefficient of variations for all the characters, but due to lower differences, the environment had less influence on the studied

characters and implying strong genetic control and high selection efficiency; also indicated that most of the variability was genetic in nature and selection on the basis of phenotype can be effective for improvement for all traits. High heritability (>0.90) combined with high genetic advance as percent of mean ($>70\%$) for days to first curd initiation, days to 50% curd initiation, marketable curd weight, curd length, and net curd weight along with yield per hectare indicated that these traits are commanded by additive gene action. The path analysis emphasized that whole plant weight, leaf length, curd breadth and marketable curd weight are the most critical direct contributors to yield, while plant vigour traits influenced by whole plant weight and number of leaves per plant play supportive indirect roles for yield. Overall, the results revealed ample genetic variability among genotypes, which may be effectively exploited for yield and curd improvement in future cauliflower breeding programs.

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