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Genetic Variability, Correlation, and Path Coefficient Analysis in Cauliflower (*Brassica oleracea var. botrytis* L.) Genotypes

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Abstract

A field experiment was carried out during the 2022–2023 growing season to assess 12 cauliflower genotypes (*Brassica oleracea var. botrytis* L.) sourced from the All India Coordinated Research Project (AICRP) on Vegetables. Eleven agronomic traits were evaluated to estimate genetic variability, heritability, correlation, and path coefficients in relation to yield. Analysis of variance indicated highly significant differences ($P<0.01$) among the genotypes for all traits studied. For every trait, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), highlighting environmental influence. High genetic variability was observed for traits such as yield per plot, net curd weight, curd compactness, and curd size. Heritability estimates exceeded 60% for all traits, with all showing high heritability and high genetic advance as a percentage of the mean, except for crude diameter. Correlation analysis showed strong genotypic and phenotypic associations between yield and traits like plant height, plant spread, stalk length, curd diameter, gross and net curd weights, curd compactness, and ascorbic acid content. Path coefficient analysis revealed that net curd weight, curd diameter, and curd compactness had the most substantial direct positive effects on yield.

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Introduction

Cauliflower (*Brassica oleracea var. botrytis* L.) is a major crop of the *Brassica*ceae family, valued for its edible white curd.[1] Native to the Mediterranean region, it has gained global popularity due to its rich nutritional profile, comprising essential vitamins, minerals, and antioxidants. Its ability to thrive under diverse climatic conditions has facilitated widespread cultivation across temperate and tropical regions.[2] In India, cauliflower plays a significant economic

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role, being one of the most extensively cultivated vegetables. The country's varied agro-climatic zones enable year-round production, fulfilling both domestic consumption and export demands.[3] However, to meet the increasing demand and overcome various biotic and abiotic stresses, it is imperative to improve both the yield and quality of cauliflower. This requires an in-depth understanding of the genetic variability present in the crop.[4]

Genetic variability refers to the variation in genetic composition among individuals within a species and serves as a cornerstone of plant breeding. Assessing this variability is crucial as it determines the scope for selecting and improving elite genotypes.[5] A broader genetic base enhances the potential to develop varieties that are high-yielding, nutritionally superior, and resilient to stresses.[6] To effectively utilize this variability, it is essential to understand the interrelationships among various agronomic traits. Correlation analysis facilitates the identification of the strength and direction of associations between traits.[7] However, correlation alone does not imply causation.[8] To overcome this limitation, path coefficient analysis is employed, which partitions correlation coefficients into direct and indirect effects, thereby clarifying the actual impact of individual traits on yield.[9] This approach helps differentiate traits that influence yield directly from those that act indirectly through other characters.[10] Such analytical tools are invaluable to plant breeders, offering a targeted framework for selecting traits that significantly enhance yield and quality, thus streamlining cultivar development.

In this context, the present study was designed to evaluate 12 cauliflower genotypes obtained from the All India Coordinated Research Project (AICRP) on Vegetables. These genotypes represent a wide genetic spectrum, providing an ideal resource to assess genetic variability and analyze inter-trait associations. By employing correlation and path coefficient analyses, the study seeks to identify key traits contributing to yield and quality, offering insights that can guide the development of improved cauliflower varieties tailored to agronomic requirements and market expectations.

Materials and Methods

During the 2022–2023 growing season, a field experiment was conducted at the Experimental Research Farm of Horticulture, School of Agricultural Sciences, Nagaland University, Medziphema Campus, Nagaland. The primary objective was to evaluate 12 cauliflower (*Brassica oleracea var. botrytis* L.) genotypes obtained from the All India Coordinated Research Project (AICRP) on Vegetables. The experiment was arranged in a Randomized Block Design (RBD) with three replications to ensure statistical validity and reduce environmental variability.[11] Recommended agronomic practices were meticulously followed throughout the crop cycle to maintain ideal conditions for plant growth and yield performance.

A total of eleven quantitative traits were recorded for phenotypic evaluation: 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), yield per plot (kg), curd compactness, and ascorbic acid content (mg/100g). These measurements were taken in accordance with the standard guidelines set by the Protection of Plant Varieties and Farmers' Rights Authority (PPVFRA).

The collected data were analyzed using OPSTAT, an open-source statistical software, to ensure precise and dependable results.[12] Analysis of variance (ANOVA) and genetic variability parameters were computed using the formulae proposed earlier.[13] Genotypic, phenotypic, and environmental coefficients of variation were estimated following the methods outlined by Lnu *et.al.*[14] Heritability and genetic advance were determined based on the approach described by Sarker *et al*.[15] Correlation coefficients were calculated using standard procedures,[16] while path coefficient analysis was conducted as per the methodology suggested by Chatterjee *et al*.[17]

Results

Analysis of Variance

The analysis of variance (ANOVA) revealed highly significant differences ($P < 0.01$) among the 12 cauliflower genotypes for the agronomic traits evaluated (Table 1). This indicates the presence of substantial genetic variation within the population, highlighting the potential for identifying and selecting superior genotypes for use in breeding programs.

Table 1: Analysis of variance for eleven agronomic traits among twelve cauliflower genotypes

Character	Mean Squares			CD at 5 %	CV (%)
	Replication df (2)	Treatments df (11)	Error df (22)		
Yield per plot (kg)	1.262	10.204**	0.401	1.073	12.666
Plant height (cm)	4.044	59.564**	1.605	2.145	3.466
Plant spread (cm)	1.909	166.862**	1.417	2.016	2.757
Stalk length (cm)	0.841	8.271**	0.335	0.98	6.266
Number of leaves per plant	0.249	16.073**	1.431	2.026	7.936
Curd diameter (cm)	0.409	3.828**	0.655	1.37	7.216
Curd size (cm2)	502.59	755.164**	66.039	13.761	11.174
Gross curd weight (g)	238.256	16062.433**	802.095	47.957	4.934
Net curd weight (g)	5,644.11	40924.093**	1,776.12	71.363	13.443
Curd compactness	21.56	315.039**	31.811	9.55	12.965
Ascorbic acid (mg/100g)	0.104	9.304**	0.392	1.061	3.724

** = Significant at 1 % and * = Significant at 5 % level of significance

Estimates of Genetic Variability Among Twelve Cauliflower Genotypes

Assessing genetic variability is crucial for determining the extent of differences among genotypes, which facilitates effective selection and crop improvement. The genetic variability parameters for twelve agronomic traits in cauliflower genotypes are summarized in Table 2.

Table 2: Estimation of genetic parameters for eleven agronomic traits among twelve cauliflower genotypes

Response Variable	SED	Heritability	GCV	PCV	Gen-Advance	Gen-Adv % Means
Yield per plot (kg)	1.073	89.06	36.139	38.294	3.514	70.255
Plant height (cm)	2.145	92.331	12.026	12.516	8.7	23.805
Plant spread (cm)	2.016	97.495	17.198	17.417	15.105	34.981
Stalk length (cm)	0.98	88.77	17.616	18.698	3.157	34.192
Number of leaves per plant	2.026	77.327	14.656	16.667	4.002	26.55
Curd diameter (cm)	1.37	61.76	9.171	11.669	1.665	14.846
Curd size (cm2)	13.761	77.671	20.841	23.647	27.516	37.836
Gross curd weight (g)	47.957	86.379	12.425	13.369	136.551	23.789
Net curd weight (g)	71.363	88.02	36.439	38.84	220.776	70.425
Curd compactness	9.55	74.797	22.336	25.826	17.311	39.793
Ascorbic acid (mg/100g)	1.061	88.33	10.245	10.9	3.337	19.835

The results revealed that the phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV) for all traits, indicating the influence of environmental factors on the expression of these traits. Among the traits studied, PCV ranged from 10.90% for ascorbic acid content to 38.84% for net curd weight, while GCV ranged from 9.17% for curd diameter to 36.44% for net curd weight. Traits such as yield per plot, net curd weight, curd compactness, and curd size exhibited high genetic variability, suggesting they hold strong potential for improvement through selection. Traits like plant height, plant spread, stalk length, number of leaves per plant, curd diameter, and gross curd weight showed moderate variability, indicating that selection may still be effective, though environmental influences may play a role. Ascorbic acid content was the only trait that exhibited low genetic variability. All the evaluated traits recorded high heritability estimates (>60%), suggesting strong genetic control and a favorable response to selection. Furthermore, all traits except curd diameter displayed high genetic advance as a percentage of the mean, indicating the predominance of additive gene action. This reinforces their suitability for genetic improvement through direct selection. All investigated traits exhibited both high heritability and high genetic advance as a percentage of the mean except crude diameter. Which intricate these traits controlled by additive gene action and selection among genotypes might be reward.

Correlation

The genotypic and phenotypic correlation coefficients of twelve agronomic traits with yield per plot are presented in Table 3. The results indicate that most traits show a positive and significant correlation with yield at both the genotypic and phenotypic levels, highlighting their importance in improving productivity. Traits such as plant height, plant spread, stalk length, curd diameter, gross curd weight, net curd weight, curd compactness, and ascorbic acid content demonstrated strong and significant associations with yield per plot. These findings suggest that selection based on these traits could effectively enhance cauliflower yield. Furthermore, the genotypic correlation coefficients were generally higher than the phenotypic ones, indicating a strong underlying genetic association among these traits with relatively lower environmental influence. This emphasizes the potential for successful selection and genetic improvement based on these key agronomic characteristics.

Table 3: Estimation of genotypic and phenotypic correlation for eleven agronomic traits among twelve cauliflower genotypes

Pheno-typic corre-lations	YPP	PH	PS	SL	NOL	CD	CS	GCW	NCW	CC	ACC	Geno-typic corre-lation
	YPP	1	0.786**	0.988**	0.485**	0.21	0.745**	0.007	0.569**	1	0.750**	0.790**
	PH	0.704**	1	0.792**	0.691**	-0.191	0.444**	0.046	0.685**	0.788**	0.881**	0.372*
	PS	0.915**	0.742**	1	0.373*	0.136	0.800**	0.076	0.593**	0.992**	0.746**	0.708**
	SL	0.392*	0.628**	0.343*	1	-0.01	-0.118	-0.235	0.247	0.482**	0.393*	0.114
	NOL	0.159	-0.123	0.1	-0.02	1	0.529**	0.363*	0.203	0.214	-0.137	0.305
	CD	0.571**	0.373*	0.610**	-0.08	0.324	1	0.281	0.755**	0.750**	0.604**	0.575**
	CS	-0.006	0.03	0.053	-0.181	0.349*	0.159	1	0.032	0.023	0.377*	0.218
	GCW	0.533**	0.592**	0.532**	0.245	0.19	0.586**	0.079	1	0.567**	0.668**	0.359*
	NCW	0.999**	0.701**	0.912**	0.386*	0.16	0.571**	0.006	0.528**	1	0.756**	0.796**
	CC	0.691**	0.686**	0.659**	0.317	-0.115	0.335*	0.222	0.579**	0.691**	1	0.667**
	ACC	0.662**	0.340*	0.662**	0.098	0.296	0.467**	0.163	0.301	0.664**	0.507**	1

** = Significant at 1 % and * = Significant at 5 % level of significance

Path Analysis

Path coefficient analysis was conducted at the genotypic level, and the results are summarized in Table 4. This analysis helps to dissect the direct and indirect effects of various agronomic traits on yield per plot, offering valuable insights into the most influential traits for selection. The findings revealed that traits such as stalk length, number of leaves per plant, curd diameter, net curd weight, and curd compactness had a direct positive effect on yield. Among these, net curd weight emerged as the most influential trait, indicating its strong contribution to yield enhancement. The low residual effect observed suggests that the traits included in the analysis account for nearly all the variation in yield per plot, leaving very little unexplained. This emphasizes the effectiveness of these traits in selection strategies and their potential to significantly improve cauliflower productivity.

Table 4: Estimation of genotypic path coefficient analysis for eleven agronomic traits among twelve cauliflower genotypes

	PH	PS	SL	NOL	CD	CS	GCW	NCW	CC	ACC	YPP (rg)
PH	-0.009	-0.021	0.017	-0.002	0.028	-0.002	-0.03	0.756	0.05	-0.003	0.786**
PS	-0.007	-0.026	0.009	0.001	0.05	-0.004	-0.026	0.952	0.043	-0.005	0.988**
SL	-0.006	-0.01	0.024	0.000	-0.007	0.011	-0.011	0.462	0.022	-0.001	0.485**
NOL	0.002	-0.004	0.000	0.010	0.033	-0.017	-0.009	0.205	-0.008	-0.002	0.210
CD	-0.004	-0.021	-0.003	0.005	0.063	-0.013	-0.033	0.72	0.035	-0.004	0.745**
CS	0.000	-0.002	-0.006	0.004	0.018	-0.047	-0.001	0.022	0.022	-0.001	0.007
GCW	-0.006	-0.015	0.006	0.002	0.048	-0.002	-0.044	0.544	0.038	-0.002	0.569**
NCW	-0.007	-0.026	0.012	0.002	0.047	-0.001	-0.025	0.96	0.043	-0.005	0.999
CC	-0.008	-0.019	0.01	-0.001	0.038	-0.018	-0.029	0.725	0.057	-0.005	0.750**
ACC	-0.003	-0.018	0.003	0.003	0.036	-0.01	-0.016	0.764	0.038	-0.007	0.790**

Discussion

This study offers a comprehensive evaluation of genetic variability, heritability, correlation, and path coefficient analysis for key agronomic traits in cauliflower, providing valuable insights for crop improvement programs.[16] Understanding the magnitude of genetic variation and the interrelationships among traits is crucial for identifying superior genotypes with desirable characteristics. The findings lay a solid foundation for future cauliflower breeding efforts aimed at enhancing yield potential and stability.[17] Additionally, this research contributes to a broader understanding of the genetic parameters that influence trait expression, supporting applications in marker-assisted selection and advanced breeding strategies.[18]

The results are consistent with earlier studies that reported significant genetic variation among *Brassica genotypes*. The highly significant differences ($P < 0.01$) observed in ANOVA among the 12 cauliflower genotypes confirm substantial genetic variability, which is critical for effective selection.[12] Similar trends have been documented in cabbage, reinforcing the potential for genetic improvement.[12]

In this study, the phenotypic coefficient of variation (PCV) consistently exceeded the genotypic coefficient of variation (GCV) across all traits, indicating a notable influence of environmental factors on trait expression.[3] This pattern is consistent with findings in cabbage and other *Brassica* crops, where environmental variability impacts quantitative traits such as yield and nutritional quality.[19] High genetic variability was recorded for traits like yield per plot, net curd weight, curd compactness, and curd size, while moderate variability was observed in plant height, plant spread, stalk length, curd diameter, and gross curd weight. In contrast, ascorbic acid content exhibited low genetic variability.[20,21]

All evaluated traits showed high heritability estimates (>60%), suggesting strong genetic control.[4] Traits with both high heritability and high genetic advance as a percentage of the mean indicate additive gene action.[5] However, curd diameter, despite its high heritability, showed lower genetic advance, implying the involvement of dominance or epistatic effects, which favors heterosis breeding.[13] Similar observations were reported in cabbage for traits such as head weight and compactness.[5.6]

Positive and significant genotypic correlations with yield were found for traits including plant height,[7] plant spread,[21] curd diameter,[8] curd compactness,[7] and ascorbic acid content.[22] Genotypic correlations were generally stronger than phenotypic ones, indicating robust genetic associations.[4,9,21] Path coefficient analysis revealed that net curd weight had the most substantial direct effect on yield,[21] followed by curd diameter and curd compactness, with plant spread and stalk length also contributing positively.[18] The minimal residual effect observed confirmed the effectiveness of these traits in improving yield.[3]

Conclusion

The present study revealed significant genetic variation among 12 cauliflower genotypes, highlighting their potential for yield improvement. Characters such as net curd weight, curd compactness, and curd size exhibited high genetic variability, heritability, and genetic advance, indicating their suitability for selection-based breeding programs. The consistently higher PCV than GCV across all traits suggests environmental influence, but the strong genotypic correlations and direct effects on yield confirm the predominance of genetic control. Net curd weight showed the highest direct positive effect on yield, making it the most critical trait for selection. The low residual effect in path analysis indicates that the studied traits explain nearly all the yield variation, ensuring selection efficiency. These findings underscore the importance of net curd weight, curd compactness, and plant spread as primary selection criteria for genetic enhancement in cauliflower breeding programs. Future research should integrate molecular breeding and genotype-by-environment studies to further refine selection strategies and enhance cauliflower productivity.

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Not Applicable

Author Contributions

All authors contributed significantly in the preparation of the manuscript. All authors have read and approved the final version of the manuscript.

- **Satya Prakash Kanaujia:** Conceptualization, experimental design, and data interpretation.
- **Rishabh Kumar Singh:** Conducted the field experiments and collected the necessary data.
- **Ashwini Ananda:** Statistical analysis and data visualization.
- **Moakala Changkiri:** Literature review and contributed to manuscript writing.
- **Ravi Shankar:** Laboratory analysis and validation of results.
- **Hanuman Prasad Chaturvedi:** Reviewed and edited the manuscript.
- **Rajat Rajput:** Formatting and references, ensuring adherence to journal guidelines.
- **Ajeet Kumar:** Data collection and analysis, providing valuable inputs to the study.

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