Genetic variability and agronomic trait associations in hybrids of sweet corn (*Zea mays var. saccharata*) × purple Corn (*Zea mays var. indurata*)

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Abstract. Purple corn has several functional advantages, such as antioxidants and nutrients, but the total cultivation was lower than that of yellow corn. Therefore, the purposes were to characterize genetic diversity, estimate the proportion of variance due to genetic effects, and perform correlation analysis among agronomic traits, based on crossing sweet and purple corn. This study evaluated six corn populations derived from sweet and purple corn crossed, including parental lines (P1: purple corn; P2: sweet corn), F1 hybrid, F2 progeny, and two backcross generations (BC1: F1 × P1; BC2: F1 × P2). Analysis of variance revealed significant differences among populations. High genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for fresh ear weight with husk (FEW-H), ear length (EL), and kernel thickness (KT), indicating strong genetic control. Traits such as days to tasseling (DT), days to silking (DS), and Number of kernel rows per ear (NKRE) showed high broad-sense heritability. Correlation analysis indicated a strong positive relationship between DT and DS, and between FEW-H and ear diameter (ED), cob diameter (CD), and Number of kernels per row (NKR). A trade-off was observed between kernel width (KW) and NKRE. These findings support the selection of early-flowering, high-yielding genotypes for improvement.

1 Introduction

Corn (*Zea mays* L.) is one of Indonesia's principal cereal crops, serves as a staple food, a raw material for animal feed and industrial products, and an increasingly important functional food resource. According to the Indonesian Central Bureau of Statistics [1, 2], Indonesia ranks among the world's top Corn-producing countries, with approximately 12.6–13.3 million tonnes produced annually over the period 2020–2025, cultivated across about 3.5–3.7 million hectares (yield ~3.4–3.7 t/ha). Corn is estimated to meet around 50 %

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of national food consumption needs and plays a significant role in food, feed, and agribusiness sectors [3]. However, most of this production is still dominated by yellow hybrid corn for feed purposes, while the development and utilization of functional or specialty corn remain limited.

In recent years, the research interest in functional corn, particularly pigmented varieties such as purple, red, and black corn, has increased due to health-promoting, functional properties such as bioactive compounds, including anthocyanin, carotenoids, and phenolic acids [4]. Pigmented corn varieties are not only valued for nutritional content but also for application in food, nutraceutical, and cosmetic industries [5]. In Indonesia, functional corn represents promising avenues for expanding functional food production and diversifying agricultural output. Recent hybrid breeding research, such as crossing sweet corn and purple corn, aimed to combine favourable traits of high sugar content and bioactive pigment accumulation into a single cultivar, potentially adding value to fresh and processed corn products [6].

To utilize effectively such hybrid populations and breeding, one has to assess key genetic parameters, genetic diversity**,** heritability**,** and correlation among agronomic traits, as these inform selection strategies and potential genetic gain. However, few studies have relatively investigated the genetic architecture of hybrid populations specifically derived from sweet × purple corn crossed, a cross-type of growing interest in Indonesia. No previous evaluation of genetic variance, heritability, and trait correlations within such populations was essential for identifying parent lines and traits that contribute most to yield and functional parameters.

Therefore, the present study aimed to characterize the corn population generated by crossing sweet corn and purple corn, focusing on assessing genetic diversity, estimating heritability, analyzing correlations among agronomic traits, and identifying direct and indirect associations related to ear yield and quality. By integrating sweet corn's high sugar content and purple corn's rich anthocyanin profile, it contributed to the development of novel functional corn varieties with enhanced nutritional value, yield potential, and adaptability to local agro-ecological conditions.

2 Material and Methods

2.1 Genetic Materials and Experimental Site

The experiment involved six populations of corn [*Zea mays* L.] consisting of parental lines, hybrid segregating and backcross generations. The materials included: P1**:** Purple Corn [anthocyanin-rich**)** P2**:** Sweet Corn F1: Hybrid of Sweet Corn × Purple Corn F2: Selfed progeny of the F1 hybrid BC1: Backcross of F1 × P1 [Purple Corn) and BC2**:** Backcross of F1 × P2 [Sweet Corn). These populations were evaluated to analyze their yield performance and quantitative agronomic traits.

The research was conducted at the Experimental Farm of the Faculty of Agriculture and Animal Science, University of Muhammadiyah Malang (UMM), East Java, Indonesia. The site was located at an altitude of approximately 500 meters above sea level and characterized by a humid tropical climate. The experiment was carried out from February to July 2025, covering the entire growing season.

2.1 Data Collections

The following quantitative traits were recorded during the experiment: Days to tasseling (male flowering) [DT] (days), Days to silking (female flowering) [DS], Fresh ear weight with husk [FEW-H] (g), Fresh ear weight without husk [FEW-NH**]** (g), Ear length [EL**]** (cm)**.** Ear peduncle length [EPL**]** (mm), Ear diameter [ED] (mm), Cob diameter [CD] (mm), Rachis diameter [RD**]** (mm), Number of kernels per row [NKR**]. **Number of kernel rows per ear [NKRE], Kernel length [KL] (mm), Kernel width [KW] (mm), Kernel thickness [KT] (mm), 100-kernel weight [100-KW] (g). Data collection followed standard agronomic protocols and was performed on selected representative plants within each plot.

2.2 Data Analysis

2.2.1 Analysis of variance

Analysis of variance [ANOVA) was applied to establish the level of significance among the population using the Minitab. The mean values were compared using Tukey's HSD procedure.

2.2.2 Analysis of Genotypic Variance and Phenotypic Variance

The variability of each quantitative trait was estimated by simple statistical measures, including phenotypic and genotypic variances and the coefficient of variation. The phenotypic and genotypic variation and coefficient of variation were calculated following the formula suggested [7] [8]. Phenotypic and genotypic variances were computed from the respective mean squares as suggested [7].

2.2.3 Components of Variance

The formula for the components of variance and heritability used is as follows [6] at Table 1:

Table 1. Analysis of Variance Agronomical and Morphological Traits of Corn Population

Source	DF	Mean Square	F Value	Pr(> F)
Rep (r)	r-1	MS_r	$\sigma_r^2 = \sigma_e^2 + g\ \sigma_r^2$	
Genotipe (g)	g-1	MS_g	$\sigma_g^2 = \sigma_e^2 + r\ \sigma_g^2$	
Galat (e)	(g-1) (r- 1)	MS_e	σ_e^2	
Total	(g.r) -1			

$$\sigma_g^2 = \frac{MS_g - MS_e}{r} \qquad GCV = \frac{\sqrt{\sigma_g^2}}{x}\ x100\%$$

$$\sigma_p^2 = \sigma_g^2 - \sigma_e^2 \qquad PCV = \frac{\sqrt{\sigma_p^2}}{x}\ x100\%$$

Where:
MSg = mean square of genotype σ_g^2 = Genotype variance r = replication
MSe = mean square of error σ_p^2 = Phenotype variance X= grand mean for the trait considered

2.2.4 heritability

Heritability in the broad sense was calculated using the following formula:

$$H_{BS}^2 = \frac{\alpha_G^2}{\alpha_P^2}$$

Where:

$H_{BS}^2 = Broad - Sense\ heritability$

$\alpha_G^2 = Genetic\ Varian$

$\alpha_P^2 = Phenotypic\ Varian$

2.2.5 Correlation Analysis

Pearson's correlation coefficients were used to evaluate the relationships among traits, with significance tested at the 5% and 1% probability levels using Minitab version 22.

3 Results and Discussion

The Analysis of variance (ANOVA) presented in Table 2 evaluated the significance of differences among treatments for several agronomic traits. The Pr[>F] value (p-value) indicated whether the observed variations among the treatments were statistically significant, $p < 0.05$. The existence of considerable phenotypic variation in key agronomic traits—such as flowering time, yield components, and kernel arrangement, indicated strong potential for genetic selection and improvement through breeding programs. For instance, traits like days to tasseling and silking, ear/kernel characteristics, and grain yield have demonstrated substantial variability and high heritability in Corn populations, thereby enabling effective selection strategies [9].

Conversely, other traits often exhibit limited variability and low responsiveness to selection, particularly when derived from narrow germplasm pools. This underscores the critical necessity of conducting multi-environment trials (METs) and incorporating broader genetic diversity—such as tropical landrace germplasm or diverse pre-breeding lines—to unlock trait variation and ensure stability of performance across environments [10].

3.1 Genetic Diversity

Genetic diversity served as a fundamental basis in plant breeding programs, as it reflected the potential of a population to produce individuals with superior traits and determined the extent to which a trait could be selected and improved. Commonly used parameters to assess genetic diversity included the Genotypic Coefficient of Variation (GCV) and the Phenotypic Coefficient of Variation (PCV)**.** The GCV represents the variation that was genetically inherited, while the PCV encompasses the total observed variation resulting from both genetic and environmental factors. The results of genetic variability analysis for the observed traits in this study were presented in Table 3.

Table 2. Analysis of Variance for Agronomical Traits

Agronomical Trait	Df	Mean Squre	F Value	Pr[>F]	Remarks
Days to tasseling	3	25.95	64.18	0.00	Significance
Days to silking	3	25.51	486.12	0.00	Significance
Fresh ear weight with husk	5	26023	8.05	0.003	Significance
Fresh ear weight without husk	5	9446	5.87	0.009	Significance
Ear length	5	133.3	1.11	0.415	Non Significance
Ear peduncle length	5	40.58	5.24	0.013	Significance
Ear diameter	5	16.25	2.43	0.109	Non Significance
Cob diameter	5	4.46	0.78	0.592	Non Significance
Rachis diameter	5	37.90	2.12	0.146	Non Significance
Number of kernels per row	5	106.96	7.97	0.003	Significance
Number of kernel rows per ear	5	4.78	21.52	0.000	Significance
Kernel length	5	1.96	2.35	0.12	Non Significance
Kernel width	5	0.75	2.97	0.07	Non Significance
Kernel thickness	5	26.64	1.28	0.35	Non Significance
100-kernel weight	5	9.38	0.35	0.87	Non Significance

Notes : $p < 0.05$: significance level

3.2 Genotypic and Phenotypic Variance

The genotypic variance and phenotypic variance observed for agronomic traits in corn indicated the existence of substantial genetic diversity among the evaluated genotypes. Traits such as fresh ear weight with husk (FEW-H), fresh ear weight without husk (FEW-NH), Number of kernel rows (NKR), and ear length (EL) exhibited relatively high values for both genotypic and phenotypic variance, suggesting that these traits are highly variable and could be selected for genetic improvement.

In contrast, traits such as kernel width (KW), kernel thickness (KT), and 100-kernel weight (100-KW) exhibited low genotypic and phenotypic variance, indicating were more stable expression of these traits across environments or lower inherent genetic diversity. These results align with recent findings in sweet corn genetic studies, which have reported similar patterns of variance distribution [11-13].

Moderate variability was found in traits such as fresh ear weight with husk (FEW-H), fresh ear weight without husk (FEW-NH), ear length (EL), ear position length (EPL), Rachis diameter (RD), and kernel thickness (KT). These traits exhibited moderated GCV and PCV values, indicating that both genetic and environmental factors contribute to phenotypic expression. Moderate variation suggested that meaningful selection gains were achievable, albeit potentially requiring multi-generational breeding. These findings were consistent with [13], who highlighted the importance of such traits in yield optimization, and the utility of moderately variable traits in multi-environment breeding programs.

Table 3. Estimates of genetic variance, phenotypic variance, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) and broad sense heritability for agronomical traits

Agronomical Trait	Variance		Coef of Variation [%]		Heritability	
	σ_g^2	σ_p^2	GCV	PCV	h_{BS}^2	Criteria
Days to tasseling	25.82	26.22	3.03	3.06	0.98	High
Days to silking	25.49	25.54	2.98	2.99	1.00	High
Fresh ear weight with husk	24945.69	28176.58	13.66	14.52	0.89	High
Fresh ear weight without husk	8909.61	9609.90	11.03	14.69	5.53	High
Ear length	93.14	213.48	8.62	13.06	0.44	Medium
Ear peduncle length	37.99	45.74	10.84	11.89	0.83	High
Ear diameter	14.02	20.70	1.98	2.41	0.68	High
Cob diameter	2.56	8.26	1.29	2.32	0.31	Medium
Rachis diameter	31.95	49.80	9.92	12.39	0.64	High
Number of kernels per row	102.48	115.91	7.52	7.99	0.88	High
Number of kernel rows per ear	4.71	4.93	3.79	3.88	0.95	High
Kernel length	1.68	2.52	3.13	3.82	0.67	High
Kernel width	0.67	0.92	2.14	2.52	0.73	High
Kernel thickness	19.71	40.51	13.17	18.88	0.49	Medium
100-kernel weight	0.44	27.26	0.51	4.00	0.02	Low

Notes:
σ_g^2 : genetic variance; σ2p : phenotypic variance ; GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; h_{BS}^2: broad-sense heritability; Criteria: High (H) > 20%, Medium (M) = 10–20%, Low (L) < 10%

3.3 Genotypic and Phenotypic Coefficient of Variation (GCV and PCV)

The magnitude of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) offered further insights into trait variability. GCV values ranged from 0.51% (100-KW) to 13.66% (FEW-H), while PCV ranged from 2.32% (CD) to 18.88% (KT). The highest GCV and PCV were observed for FEW-H (13.66% and 14.52%), KT (13.17% and 18.88%), and FEW-NH (11.03% and 14.69%). These indicating that traits were not only under strong genetic influenced but also sensitive to environmental conditions. The relatively small differences between GCV and PCV values in traits like days to silking (DS), days to tasseling (DT), and Number of kernel rows (NKR) suggested low environmental influence, creating these traits reliable targets for selection in breeding programs. This indicates that traits were under strong genetic influence but also sensitive to environmental conditions [14].

Conversely, traits such as ear diameter (ED), cob diameter (CD), kernel row number (NKR), number of kernels per row (NKRE), kernel length (KL), and kernel width (KW) recorded and described relatively low GCV and PCV values. This suggesting limited variability and indicating that improvement through direct selection might be slow unless other sources of variability were introduced [15].

Low GCV and PCV values were recorded for traits such as ear diameter (ED)**,** cob diameter (CD)**,** kernel row number (NKR)**,** number of kernels per row (NKRE)**,** kernel length (KL)**,** kernel width (KW)**,** and 100-kernel weight (100-KW)**.** This refers that limited genetic variability for these traits within the evaluated corn populations. Low GCV and

PCV values generally directed that phenotypic expression of these traits was influenced by the environment, with minimal contribution from genetic factors [16]. As a result, the potential for improving these traits through selection might be limited unless broader genetic variability was introduced through hybridization or the use of diverse germplasm.

The narrow differences between PCV and GCV for these characters also implied relatively low environmental influenced, refer that the observed phenotypic uniformity was primarily due to inherent genetic similarity among the evaluated genotypes [15]. Nevertheless, even with low variation, these traits might still contribute significantly to grain yield if favorably correlated with more heritable yield components or exhibited stability across different environments. Moreover, kernel size traits (KL, KW, and 100-KW), despite showing low variability, were considered critical for both market preference and end-use quality in corn [17]. Therefore, maintaining stability and optimizing through indirect selection methods, such as using yield-associated molecular markers or focusing on traits with higher GCV–PCV values that were genetically correlated, might be more effective. To enhance the potential for genetic gain in these traits, future breeding programs should consider incorporating genetically diverse sources, particularly landraces or colored corn lines, which have been reported to exhibit broader variability in kernel morphology and size attributes [18].

3.4 Broad-Sense Heritability

Heritability in the broad sense ranged from very low to very high across traits (Table 3). Traits such as days to silking (1.00), days to tasseling (0.98), NKRE (0.95), and FEW-H (0.89) exhibited very high heritability, suggesting that these traits were predominantly governed by additive genetic factors and selection based on phenotype would be effective. Medium heritability was recorded for traits such as ear length (EL, 0.44), kernel thickness (KT, 0.49), and cob diameter (CD, 0.31), were indicating moderate genetic control and suggesting that selection for these traits advanced from progeny testing or advanced generation evaluation. Notably, 100-kernel weight had extremely low heritability (0.02), highlighting a strong environmental influence and minimal genetic control over this trait. Improvement through conventional selection in this trait was therefore likely to be ineffective without the aid of molecular or biotechnological tools [19]

Overall, traits with high heritability and high GCV such as FEW-H, FEW-NH, and DS were ideal candidates for selection in sweet corn breeding programs aimed at yield improvement and earliness. Moreover, traits with low heritability and low GCV (e.g., 100-KW) might require alternative breeding strategies such as marker-assisted selection.

3.5 Correlation Analysis Agronomic Traits

Pearson correlation analysis among 15 agronomic traits of Corn revealed several significant associations, indicating possible genetic and physiological linkages between traits (Figure 1).

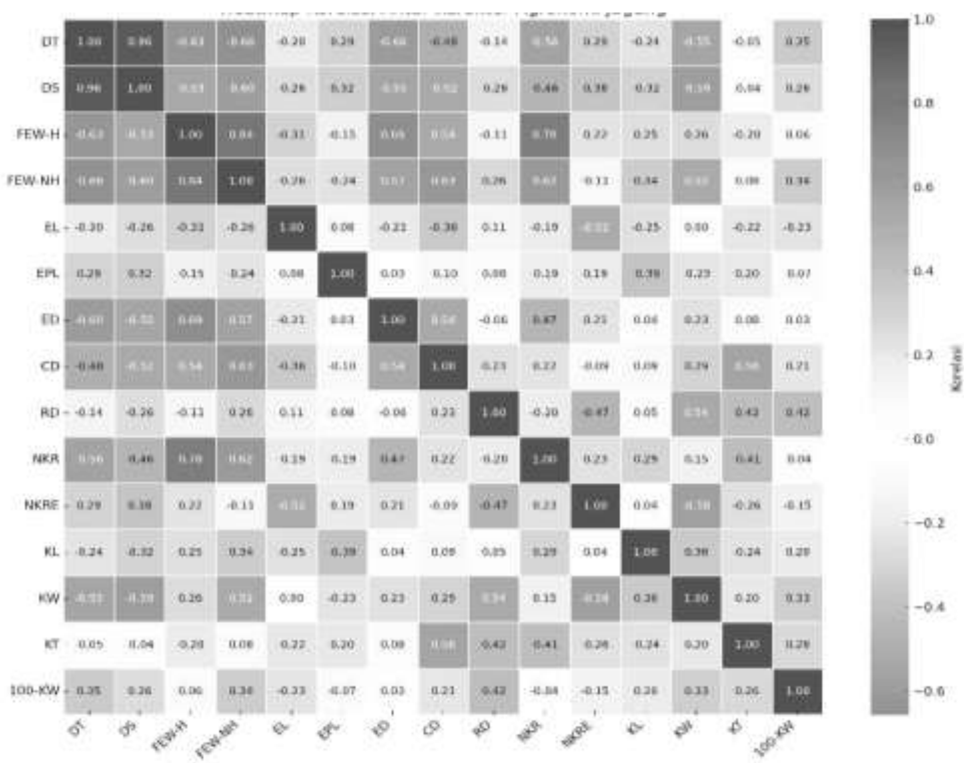

Fig. 1. Correlation Analysis Agronomic Traits

Notes:
DT: Days to tasseling (male flowering), DS: Days to silking [female flowering), FEW-H: Fresh ear weight with husk, FEW-NH: Fresh ear weight without husk, EL: Ear length. EPL: Ear peduncle length, ED: Ear diameter, CD: Cob diameter, RD: Rachis diameter, NKR: Number of kernels per row, NKRE: Number of kernel rows per ear, KL: Kernel length, KW: Kernel width, KT: Kernel thickness, 100-KW: 100-kernel weight. Blue shades indicate positive correlations, while red shades represent negative correlations. Higher absolute values (closer to 1 or –1) reflect stronger relationships between the variables.

Days to tasseling (DT) and days to silking (DS) exhibited a very strong positive correlation ($r = 0.957$; $p < 0.01$), indicated that genotypes which initiate tasseling earlier also tend to silk earlier. This association was consistent with prior findings by [11], which emphasized the genetic synchrony of flowering traits in corn as crucial for pollen viability and successful fertilization. In contrast, DT and DS were significantly negatively correlated with female ear weight under both husked (FEW-H; $r = -0.627$) and non-husked (FEW-NH; $r = -0.657$) conditions. Early-flowering genotypes tended to produce heavier ears, a finding consistent with [20,21] who noted that earlier maturity could lead more efficient resource partitioning and improved grain filling.

Strong positive correlations were observed between ear weight and yield components. FEW-H was positively associated with ear diameter (ED; **r = 0.695**), cob diameter (CD; **r = 0.535**), and number of kernel rows (NKR; **r = 0.783**), while Number of kernels per row was weak correlation (NKRE; **r = 0.222**). These results suggest that increased ear girth and row configuration contributed significantly to higher ear weight, which was consistent with the findings of [22].

Interestingly, kernel traits showed varied correlations. Kernel width (KW) had a significant positive correlation with root diameter (RD; **r = 0.535**) and FEW-NH (**r =**

0.523), while exhibiting a significant negative correlation with NKRE (**r = –0.576**). This trade-off suggested that broader kernels associated with fewer kernels per row, possibly due to space constraints within the Cob [23]. Moreover, cob diameter (CD) was positively correlated with kernel thickness (KT**;** r = 0.563**),** reflecting the structural role of cob robustness in supporting thicker kernels. A similar trend was also observed between CD and FEW-NH (**r** = 0.628), underscoring the importance of cob architecture in ear weight development. Traits such as kernel length (KL), kernel thickness (KT), and 100-kernel weight (100-KW) showed weak to moderate correlations with other traits, implying a more independent genetic control. Notably, 100-KW exhibited a positive, though non-significant, correlation with FEW-NH (r = 0.337**)** and KW (r = 0.325), highlighting its potential utility in yield selection despite lower direct correlations.

These interrelationships were critical for breeding programs, due to provide insights into trait combinations that could be targeted simultaneously for improving yield potential and agronomic efficiency. Traits with strong positive correlations to yield components served as reliable indirect selection criteria, especially in early-generation selection phases [24]. These correlation patterns suggested several key implications for breeding programs. The negative correlation between flowering time and ear number indicated that early-maturing genotypes possed yield advantages under time-limited environments. Additionally, the positive association between kernel arrangement traits (NKR, NKRE) and ear/cob dimensions (ED, CD) highlights the importance of structural ear traits in determining potential yield. However, the negative correlation between kernel number and size warrants a balanced selection strategy to optimize both yield components. Overall, understanding these correlations enables breeders to design more effective selection indices and to anticipate potential trade-offs among traits in hybrid or population improvement programs.

4 Conclusion

Substantial genetic variability in key yield traits (FEW-H, EL, NKR) supported effective selection, whereas KW and 100-KW appeared more stable. High GCV and PCV for FEW-H, KT, and FEW-NH indicated strong genetic control with some environmental effects; small GCV–PCV gaps for DS, DT, and NKR suggested limited environmental influence. Broad-sense heritability was very high for DS, DT, NKRE, and FEW-H; moderate for EL, KT, and CD; and very low for 100-KW. Correlations showed synchronized flowering (DT–DS), earlier flowering linked to heavier ears, and positive associations of ear weight with ED, CD, and NKR, alongside a KW–NKRE trade-off. These patterns could guide selection of early-flowering, heavy-ear genotypes in sweet corn.

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