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Genetic diversity and agronomic morphological characteristics of 22 hybrid purple sweet corn genotypes

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Abstract. *Todingrante AT, Ritonga AW, Marwiyah S. 2025. Genetic diversity and agronomic morphological characteristics of 22 hybrid purple sweet corn genotypes. Biodiversitas 26: 4124-4136.* Purple sweet corn (*Zea mays* var. *saccharata*) is a nutritionally valuable crop known for its high anthocyanin content, which functions as a potent antioxidant. This study aimed to assess the genetic diversity and agronomic performance of 22 hybrid genotypes of purple sweet corn developed by Institut Pertanian Bogor. Field trials were conducted at the Pasir Kuda Experimental Station using a Randomized Complete Block Design (RCBD) with three replications. Eighteen quantitative and fifteen qualitative traits were evaluated to estimate genetic variability, heritability, and phenotypic expression. Analysis of variance indicated significant genotypic differences for the majority of traits. Broad-sense heritability estimates ranged from 8.24% (leaf width) to 96.99% (silking date), with high heritability observed for ear diameter (57.08%), ear weight with husk (66.40%), and Productivity (67.68%). The genotypic and phenotypic coefficients of variation revealed substantial genetic diversity across genotypes. Correlation analysis demonstrated that ear weight with husk ($r = 0.68$) and ear weight without husk exhibited strong and significant positive correlations with overall yield, highlighting their importance as effective selection criteria in breeding programs. Additional yield-contributing traits such as ear length, ear diameter, and number of kernel rows also showed positive associations with productivity, reinforcing their utility in selecting superior genotypes. Cluster analysis grouped the genotypes based on morphological and agronomic similarities. Genotype G19 showed exceptional performance, with a high yield (18.55 tons ha^{-1}) and deep kernel pigmentation, making it a promising candidate for future breeding. These results provide valuable insights for developing high-yielding, anthocyanin rich purple sweet corn cultivars with enhanced agronomic performance and nutritional quality.

Keywords: GCV, genetic diversity, heritability, PCV, purple sweet corn

Abbreviations: CV: Coefficient of Variance, GCV: Genotypic Coefficient of Variation, h^2 bs: Broad sense heritability, PCV: Phenotypic Coefficient of Variation

INTRODUCTION

Sweet corn (*Zea mays* L. var. *saccharata*) is a horticultural crop widely cultivated and consumed in Indonesia. It is a rich source of lutein, zeaxanthin, and carotenoids, which are known to support eye health by protecting against oxidative damage and reducing the risk of age-related macular degeneration (Koraneeyakijkulchai et al. 2023). In addition to these compounds, sweet corn contains a complex nutritional profile, including vitamins, minerals, and antioxidants, which contribute to overall health and serve as a balanced nutritional source (Mushtaq et al. 2025). The development of improved sweet corn varieties is essential to meet consumer preferences and nutritional needs. One of the major goals in corn breeding programs is to increase productivity, which can be achieved through the development of superior cultivars (Sa'adah et al. 2022). Current breeding efforts largely focus on enhancing yield and resistance to pests. However, pest pressure remains one of the leading causes of productivity decline in sweet corn (Dimaspatti et al. 2023). Despite progress in increasing sweetness primarily associated with the recessive *sh2sh2* allele other quality traits have not been significantly improved (Harakotr et al. 2022). To achieve comprehensive quality enhancement, breeding strategies should incorporate nutritional biofortification. Biofortification is a promising approach to enrich staple crops with essential micronutrients through conventional breeding, agronomic practices, or genetic engineering (Monika et al. 2023).

Purple corn, known for its high anthocyanin content, presents an opportunity for the development of sweet corn varieties with improved nutritional value. Anthocyanins exhibit strong antioxidant properties and have been shown to inhibit cancer cell proliferation by modulating apoptosis and angiogenesis (Salehi et al. 2020; Kowalczyk et al. 2024). These compounds also interact with key molecular pathways involved in inflammation and tumor progression. Structural genes directly encode enzymes required in the anthocyanin biosynthesis pathway, such as Phenylalanine ammonia-lyase, Chalcone synthase, Chalcone isomerase, flavanone-3-hydroxylase, flavonoid-3'-hydroxylase, dihydro flavonol-4-reductase, leukoanthocyanidin dioxygenase, and anthocyanidin-3-O-glucosyltransferase (Li et al. 2020; Liu et al. 2021; Kaur et al. 2022). In Indonesia, purple corn is primarily available in the form of flint kernels, and the development of sweet purple corn remains limited. Only one seed producer currently cultivates sweet purple corn, and production levels are insufficient to meet growing consumer demand. Given its high anthocyanin content and potential health benefits, purple sweet corn represents a promising target for breeding programs. To improve purple sweet corn, it is essential to assess the genetic variability within available germplasm.

Genetic variation is the foundation for trait improvement in breeding programs (Niji et al. 2018; Ritonga et al. 2018, 2025; Putri et al. 2025). Harakotr et al. (2016) reported that the inheritance of anthocyanin content in purple waxy corn is primarily governed by additive gene action. This finding suggests that conventional breeding methods, particularly early-generation selection based on phenotypic traits, are effective for enhancing antioxidant levels and improving the nutritional quality of maize. Similarly (Khampas et al. 2015) emphasized the importance of selecting purple corn genotypes with consistently high anthocyanin levels, as stable expression across environments is essential for effective breeding strategies targeting functional food production.

Cluster analysis enables the classification of genotypes based on phenotypic similarity and serves as a valuable tool for genotype selection (Heryanto et al. 2022; Tan et al. 2022; Pangestu et al. 2023). Correlation analysis provides insight into the relationships among traits, offering further guidance for selection strategies (Schober et al. 2018; Popet et al. 2022). Purple sweet corn represents a highly promising target for future research due to its unique combination of sweetness and high anthocyanin content, which offers both nutritional and functional food value. Its potential to address consumer demands for health-promoting crops makes it a strategic focus in the development of biofortified and specialty corn varieties. Purple corn has emerged as a prominent subject in recent research due to its remarkably high concentrations of anthocyanins and phenolic compounds, which contribute to its strong potential as a functional and health promoting crop (Cai et al. 2023). The parental lines used in this study were derived from purple corn genotypes with high anthocyanin content. The male parent was a selected line carrying dominant alleles responsible for purple pigmentation in the kernels. The resulting hybrids exhibited stable purple kernel phenotypes, indicating successful inheritance of the anthocyanin related traits.

The purple sweet corn hybrid collection developed at Institut Pertanian Bogor has not yet undergone a comprehensive evaluation of its genetic diversity. Therefore, this study aims to evaluate the morphological variation, yield potential, and quality characteristics of purple sweet corn genotypes.

MATERIALS AND METHODS

Study area and genetic material

This study was conducted at the Pasir Kuda Experimental Field, Institut Pertanian Bogor, located in Ciomas, Bogor, Indonesia (6°36'36.4″ S, 106°47'04.1″ E), at an elevation of approximately 240 m above sea level. The study area is characterized by a humid tropical climate, with monthly rainfall ranging from 204.56 to 832.97 mm, average daily temperatures between 26.87°C and 27.71°C, and relative humidity levels ranging from 73.7% to 83.7%. The genetic materials evaluated in this study consisted of 22 purple sweet corn genotypes, including 21 hybrid lines developed by the Plant Breeding Laboratory, Institut Pertanian Bogor and one commercial variety (Mira F1). These genotypes resulted from two types of cross combinations: genotypes G1 to G11 were developed from crosses between sweet corn (female parent) and purple corn (male parent), while genotypes G12 to G21 were derived from crosses between purple corn lines. These hybrid combinations were specifically designed to combine the sweetness and kernel tenderness of sweet corn with the anthocyanin-rich pigmentation, antioxidant capacity, and nutritional benefits of purple corn. The objective of this study was to develop novel hybrid lines with enhanced agronomic performance, higher yield potential, attractive kernel coloration, and improved nutritional quality. Detailed information on the parental combinations of all genotypes is provided in Table 1.

Procedures

Land preparation was carried out using a tractor, followed by the manual formation of planting rows with a hoe. Planting holes were spaced at 80 cm × 20 cm, and one seed was sown per hole. To prevent early pest attacks, Furadan 3R, a granular insecticide containing carbofuran as the active ingredient, was applied directly into each planting hole before covering it with soil.

Table 1. Genetic material of 22 purple sweet corn genotypes

Code	Genotype	Source
G1	Sm6.3.7 × Jmu11.2	Hybrid
G2	Sm6.3.7 × Jmu26.7.8.9	Hybrid
G3	Sm9.3.7 × Jmu26.7.8.9	Hybrid
G4	Sm1.9.27 × Jmu10.1	Hybrid
G5	Sm1.9.27 × Jmu26.3.2.1.2	Hybrid
G6	T8.3.2 × Jmu26.3.2.1	Hybrid
G7	Sm9.3.7 × Jmu24.3.7.9	Hybrid
G8	Sm9.3.7 × Jmu26.7.9.8	Hybrid
G9	Sm1.9.27 × Jmu10.2	Hybrid
G10	Sm9.3.7 × Jmu11.1.2.3	Hybrid
G11	Sm9.3.7 × Jmu10.1.2	Hybrid
G12	Jmu11.1.2.3 × Jmu10.1.2.	Hybrid
G13	Jmu10.1.2 × Jmu24.3.4.7	Hybrid
G14	Jmu24.2.3.11 × Jmu10.1.2	Hybrid
G15	Jmu11.1.2.3 × Jmut10.10	Hybrid
G16	Jmu11.1.2.3 × Jmu10.1	Hybrid
G17	Jmu11.1 × Jmut 7.3	Hybrid
G18	Jmu24.3.4.7.2 × Jmut 7.3	Hybrid
G19	Jmu10.1.2 × Jmut10.10	Hybrid
G20	Jmu10.1.2 × Jmu11.1.2.3	Hybrid
G21	Jmu11.1 × Jmu10.1.2	Hybrid
G22	Mira F1	Comercial variety

Fertilization was performed in two stages. The first application occurred at 7-10 Days After Planting (DAP), using 200 kg ha^{-1} each of urea, SP-36, and KCl. The second application was carried out at 30 DAP, using 200 kg ha^{-1} of urea. Crop management practices included weeding, hilling, soil loosening, thinning, and pest and disease control. The first and second weeding operations were conducted at 7 and 28 DAP, respectively, using hoes. Hilling and soil loosening were also performed at 28 DAP to improve soil aeration and promote root development. Pest and disease control measures were implemented as needed, based on visual observations of plant health, using Demorf 60 WP (a fungicide) and Sagri-beat 7/30 WP (an insecticide). Harvesting was performed manually at the physiological maturity stage, which was identified by the browning and drying of corn silks. Ears were harvested by hand using a twisting motion to detach them from the plant.

Quantitative and qualitative traits were observed from 10 representative plants per genotype in each replication, following the guidelines of (UPOV 2009). The study evaluated 18 quantitative traits and 15 qualitative traits. The quantitative traits assessed included: plant height, ear height, stem diameter, leaf length, leaf width, anthesis date, silking date, anthesis-silking interval, ear weight with husk, ear weight without husk, ear diameter, ear length, ear length with kernels, number of kernel rows, and number of kernels per row. The qualitative traits recorded included: leaf tip shape, leaf orientation, angle between leaf blade and stem, waving of leaf blade, anthocyanin pigmentation on leaves, anthocyanin pigmentation on leaf sheath, anthocyanin pigmentation on internodes, anthocyanin pigmentation on ear husk, anthocyanin staining on anthers, anthocyanin staining at the base of the husk, grain density, angle between main and lateral branches, number of main branches, anthocyanin pigmentation on silks, and anthocyanin pigmentation on kernels.

Data analysis

The experiment was arranged in a Randomized Complete Block Design (RCBD) with one treatment factor consisting of 22 genotypes, including 21 IPB purple sweet corn hybrids and one commercial variety (Mira F1). Each genotype was replicated three times, resulting in a total of 33 experimental units. Quantitative data were subjected to Analysis of Variance (ANOVA) using PKBT STAT 3.2 (http://pbstat.com/pkbt-stat/), and significant differences among genotypes were further evaluated using Tukey's Honest Significant Difference (HSD) test at the 5% significance level. The genetic parameters including genotypic variance (σ^2g), phenotypic variance (σ^2p), environmental variance (σ^2e), Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), and broad-sense heritability (h^2bs) were estimated using the following formulas (Magar et al. 2021):

Environmental variance: $\sigma^2_e = \text{MSE}$

Genotypic variance: $\sigma^2 g = \frac{\text{MSG}-\text{MSE}}{r}$

Phenotypic variance: $\sigma^2 p = \sigma^2 g + \sigma^2_e$

Genotypic Coefficient of Variation (GCV):

$$\text{GCV} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100\%$$

Phenotypic Coefficient of Variation (PCV):

$$\text{PCV} = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100\%$$

Broad-sense heritability (h^2bs): $h^2bs = \frac{\sigma^2 g}{\sigma^2 p} \times 100\%$

Where:
MSG: Mean square of genotype
MSE: Mean square of error
r : Number of replications
$\bar{x}$: Grand mean of the population

Qualitative traits were analyzed descriptively and classified based on observed phenotypic expressions. To evaluate the genetic diversity and similarity among genotypes based on qualitative traits, a cluster analysis was performed using Euclidean distance and complete linkage method. The clustering analysis was conducted using Microsoft Excel and Minitab version 21. Pearson correlation was conducted using RStudio (R version 4.1.2)

RESULTS AND DISCUSSION

Quantitative characterization and analysis of purple sweet corn genotypes

The Analysis of Variance (ANOVA) for quantitative traits of IPB purple sweet corn hybrids is presented in Table 2. The results showed that genotype had a highly significant effect ($p<0.01$) on most agronomic traits, except for leaf width and total soluble solids, which did not differ significantly among genotypes. These findings suggest the presence of substantial phenotypic variability among the evaluated genotypes. The observed differences are likely influenced by both genetic factors (parental inheritance) and environmental conditions, which together contribute to the expression of distinct phenotypic traits (Samudin et al. 2022). These results are consistent with the findings of Alam et al. (2022), who observed that phenotypic variation in agronomic traits is commonly shaped by the combined influence of genetic inheritance and environmental factors.

Agronomic traits and yield components of hybrid purple sweet corn

Agronomic traits are critical indicators of crop growth and play a key role in determining the quality of yield components. The average values of these traits across genotypes are presented in Table 3. Significant variation was observed in plant height among the genotypes, with G9 being the tallest (221.9 cm) and G21 the shortest (142.99 cm). The variation in plant height observed among genotypes is presumed to be influenced by differences in the genetic background of the parental lines used, as well as by environmental factors that affect phenotypic expression (Yang et al. 2021). Similarly, ear height ranged from 52.12 cm in G21 to 94.58 cm in G9. Excessive plant and ear heights may increase the risk of lodging, potentially reducing overall productivity (Jafari et al. 2024). Stem diameter also varied among genotypes, with G22 exhibiting the largest diameter (27.04 mm), while G16 had the smallest (20.5 mm). A thicker stem enhances structural support and provides greater resistance to lodging caused by wind, rainfall, and cob weight (Zhou et al. 2023).

Genetic enhancement through conventional breeding is achieved via recurrent selection processes that allow for the accumulation and recombination of favorable traits. This strategy facilitates the development of new inbred lines and germplasm with superior agronomic performance compared to the original parental lines (Yang et al. 2024). Regarding foliage traits, G9 had the highest number of leaves (12.39) and the longest leaf length (89.51 cm), whereas G12 had the fewest leaves (7.89) and G16 had the shortest leaf length (72.67 cm). While leaf number and leaf length significantly influenced plant development, leaf area did not show a significant effect. Leaves are essential for photosynthesis, the process that generates energy required for growth and seed development. Increased photosynthetic activity during the seed-filling phase contributes to enhanced protein accumulation in seeds (Fu et al. 2023).

The average flowering durations are summarized in Table 4. The earliest male flowering (anthesis) was observed in genotype G19 (42.30 days), while the latest occurred in genotype G17 (47.11 days). For female flowering (silking), genotype G14 exhibited the earliest onset (44.48 days), whereas G20 recorded the latest (48.95 days). Generally, male flowers emerge 1-3 days earlier than female flowers. Anthesis Silking Interval (ASI) is a critical phenological trait in corn that influences reproductive success. A reduced ASI enhances the synchrony between pollen release and silk emergence, thereby improving fertilization efficiency and ultimately contributing to higher grain yield (Anjum et al. 2024).

The ASI is calculated by subtracting the 50% Silking Date (SD) from the 50% Anthesis Date (AD) (Zhang 2002). In this study, the shortest ASI was recorded in G17 (1.61 days), while the longest was found in G22 (3.11 days). A shorter or near-zero ASI is considered optimal, as it ensures synchronization between pollen release and silk receptivity, thereby enhancing pollination efficiency and seed development (Zhuang et al. 2024). A prolonged ASI often reflects poor synchrony between pollen shed and silk receptivity, resulting in reduced kernel set and grain yield (Lima et al. 2023).

Yield characteristics and their components are essential determinants of productivity potential in maize. The average values of yield traits across genotypes are presented in Table 5. Ear weight with husk ranged from 183.61 to 371.07 g, with the highest value observed in genotype G19 and the lowest in genotype G16. For ear weight without husk, values ranged from 95.61 g (G16) to 272.89 g (G19). The average ear weight with husk was 375.53 g, while the average ear weight without husk was 287.03 g, in accordance with findings by Jan et al. (2023). Ear length varied between 15.19 cm (G16) and 21.79 cm (G6), while ear length with kernels ranged from 11.69 cm (G16) to 18.96 cm (G19). These traits are associated with the seed-filling rate, which is influenced by both genetic variation and environmental factors (Aisah et al. 2021). Comparatively, purple corn varieties in Mexico exhibited cob lengths ranging from 8.43 to 18.95 cm (Romero-Cortes et al. 2022).

Table 2. Analysis of variance for agronomic traits in 22 genotypes of purple sweet corn

Traits	**Mean square**		**CV(%)**
	Reply	**Genotype**	
Plant height	689.15^{ns}	1304.67**	9.82
Ear height	730.84**	749.89**	10.88
Ear diameter	1.71^{ns}	9.78**	5.54
Anthesis date	0.26^{ns}	21.97**	1.18
Silking date	0.00^{ns}	23.44**	1.02
Anthesis siliking interval	0.20^{ns}	0.49**	19.23
Number of leaf	3.42^{ns}	3.61**	11.02
Leaf length	841.90**	81.28**	6.04
Leaf width	8.06*	2.92^{ns}	15.83
Ear weight with husk	3462.14^{ns}	11006.56**	12.18
Ear weight unhusked	3026.31^{ns}	8260.62**	21.37
Ear length	2.11^{ns}	6.90**	6.15
Ear length with kernel	1.59^{ns}	8.9**	9.86
Ear diameter	15.26^{ns}	36.73**	4.79
Number row on ear	3.24^{ns}	68.75**	9.61
Number kernel of row	5.18*	4.30**	8.33
Total Soluble Solids	1.34^{ns}	2.35^{ns}	8.94
Productivity	8.04^{ns}	28.25**	12.09

Note: CV: Coefficient of Variance, *: Significant effect at $\alpha = 5\%$, **: Significant effect at $\alpha = 1\%$, ns: No significant effect at $\alpha = 5\%$

Table 3. Average and morphological agronomic traits of hybrid purple sweet corn genotypes

Genotype	**PH (cm)**	**EH (cm)**	**DS (mm)**	**NL**	**LL (cm)**	**LW (cm)**
G1	194.98^{abc}	84.78^{abc}	24.57^{abc}	10.33^{ab}	87.50^{abc}	9
G2	193.22^{abc}	76.11^{abcd}	24.18^{abc}	8.95^{ab}	86.89^{abc}	9.43
G3	190.74^{abc}	72.62^{abcd}	24.87^{ab}	10.66^{ab}	79.64^{abc}	9.29
G4	199.92^{abc}	79.83^{abcd}	24.81^{ab}	10.33^{ab}	85.10^{abc}	9.24
G5	205.65^{abc}	92.40^{a}	26.36^{ab}	11.21^{ab}	84.56^{abc}	9.41
G6	201.69^{abc}	85.32^{abc}	25.72^{ab}	10.67^{ab}	87.89^{ab}	13.69
G7	196.17^{abc}	87.31^{ab}	25.31^{ab}	9.94^{ab}	79.11^{abc}	8.6
G8	206.87^{abc}	72.83^{abcd}	25.12^{ab}	10.47^{ab}	87.89^{ab}	9.05
G9	221.50^{a}	94.58^{a}	26.44^{ab}	12.39^{a}	89.51^{a}	9.77
G10	191.61^{abc}	81.72^{abcd}	25.04^{ab}	10.11^{ab}	82.77^{abc}	9.32
G11	150.55^{bc}	70.50^{abcd}	24.32^{abc}	9.28^{ab}	84.16^{abc}	9.88
G12	177.78^{abc}	62.22^{bcd}	24.85^{ab}	7.89^{b}	78.50^{abc}	9.67
G13	200.32^{abc}	80.10^{abcd}	25.58^{ab}	10.40^{ab}	82.45^{abc}	9.56
G14	202.59^{abc}	80.75^{abcd}	25.63^{ab}	9.66^{ab}	77.92^{abc}	9.58
G15	185.43^{abc}	67.51^{abcd}	22.31^{bc}	9.87^{ab}	77.30^{abc}	9.13
G16	169.78^{abc}	56.44^{cd}	20.57^{c}	9.00^{ab}	72.67^{c}	7.83
G17	211.39^{ab}	76.72^{abcd}	25.20^{ab}	10.50^{ab}	83.56^{abc}	9.07
G18	196.81^{abc}	83.25^{abc}	24.71^{ab}	9.21^{ab}	83.00^{abc}	9.51
G19	204.51^{abc}	79.55^{abcd}	24.74^{ab}	10.31^{ab}	80.85^{abc}	9.05
G20	178.28^{abc}	60.94^{bcd}	24.19^{abc}	10.33^{ab}	74.56^{abc}	10.39
G21	142.99^{c}	52.15^{d}	22.79^{bc}	9.95^{ab}	73.04^{bc}	9.21
G22	213.28^{ab}	84.22^{abc}	27.04^{a}	10.94^{ab}	85.17^{abc}	9.94

Note: PH: Plant Height (cm), EH: Ear Height (cm), DS: Diameter of Stem (cm), NL: Number of Leaf, LL: Leaf Length (cm), LW: Leaf Width (cm). Numbers followed by the same letter in the same column are not significantly different based on the HSD test at a 5% level

Table 5. Yield characteristics and yield components of hybrid purple sweet corn

Genotype	EWH (g)	EWUH (g)	EL (cm)	ELK (cm)	ED (mm)	NR	NSR	TSS (°brix)	PRD (ton ha^{-1})
G1	352.44^{ab}	155.44^{ab}	19.61^{abc}	17.03^{ab}	46.23^{ab}	33.94^{a}	14.22^{a}	14.5	17.62^{a}
G2	316.33^{ab}	193.39^{ab}	19.83^{abc}	17.36^{ab}	46.11^{ab}	32.33^{a}	14.00^{a}	14.6	15.82^{ab}
G3	332.19^{ab}	234.70^{a}	19.03^{abcd}	16.14^{ab}	48.83^{ab}	33.08^{a}	14.51^{a}	15.3	16.61^{ab}
G4	329.32^{ab}	255.35^{a}	20.90^{ab}	18.46^{a}	47.74^{ab}	37.01^{a}	14.00^{a}	16.1	16.46^{ab}
G5	345.18^{ab}	211.45^{ab}	20.83^{ab}	17.15^{ab}	45.24^{ab}	32.18^{a}	14.29^{a}	13.6	17.26^{ab}
G6	360.36^{a}	264.31^{a}	21.79^{a}	18.49^{a}	47.49^{ab}	34.49^{a}	14.86^{a}	14.9	18.02^{a}
G7	303.00^{abc}	204.11^{ab}	18.33^{abcd}	15.36^{ab}	46.98^{ab}	32.72^{a}	14.67^{a}	14.0	15.15^{abc}
G8	309.66^{ab}	245.42^{a}	20.51^{abc}	18.00^{a}	46.64^{ab}	36.79^{a}	14.60^{a}	15.3	15.49^{ab}
G9	335.94^{ab}	228.33^{ab}	21.11^{ab}	17.64^{a}	46.01^{ab}	34.06^{a}	14.44^{a}	15.3	16.80^{ab}
G10	352.83^{a}	225.67^{ab}	18.75^{abcd}	16.67^{ab}	46.31^{ab}	33.78^{a}	14.89^{a}	13.8	17.64^{a}
G11	290.72^{abc}	193.11^{ab}	18.69^{abcd}	15.55^{ab}	45.04^{ab}	32.61^{a}	13.67^{a}	13.4	14.54^{abc}
G12	271.00^{abc}	153.33^{ab}	19.11^{abcd}	16.67^{ab}	42.45^{bc}	27.67^{ab}	13.55^{a}	15.6	13.55^{abc}
G13	266.56^{abc}	171.61^{ab}	19.08^{abcd}	17.45^{ab}	41.90^{bc}	27.83^{ab}	14.11^{a}	13.7	13.33^{abc}
G14	352.04^{ab}	241.33^{a}	18.11^{abcd}	17.39^{ab}	47.52^{ab}	29.94^{a}	14.30^{a}	13.4	17.60^{a}
G15	308.40^{ab}	186.08^{ab}	18.46^{abcd}	16.45^{ab}	45.95^{ab}	28.79^{ab}	13.75^{a}	13.3	15.42^{ab}
G16	183.61^{c}	95.61^{b}	15.19^{d}	11.69^{b}	35.48^{c}	19.06^{b}	8.89^{b}	14.8	9.18^{c}
G17	312.28^{ab}	201.20^{ab}	19.31^{abc}	17.70^{a}	43.94^{b}	34.17^{a}	14.34^{a}	14.5	13.76^{abc}
G18	227.96^{bc}	176.78^{ab}	16.75^{cd}	15.99^{ab}	43.55^{b}	30.57^{a}	14.73^{a}	15.0	11.40^{bc}
G19	371.07^{a}	272.89^{a}	20.05^{abc}	18.96^{a}	46.64^{ab}	33.10^{a}	15.32^{a}	15.0	18.55^{a}
G20	295.11^{abc}	150.72^{ab}	18.44^{abcd}	17.44^{ab}	41.81^{bc}	28.17^{ab}	14.00^{a}	13.5	14.76^{abc}
G21	274.72^{abc}	161.56^{ab}	17.70^{bcd}	15.06^{ab}	42.95^{b}	28.44^{ab}	14.11^{a}	14.2	13.74^{abc}
G22	359.83^{a}	271.00^{a}	18.67^{abcd}	17.91^{a}	52.05^{a}	32.50^{a}	15.00^{a}	13.5	17.99^{a}

Note: EL: Ear Length (cm), ELK: Ear Length with Kernel (cm), ED: Ear Diameter (cm), EWH: Ear Weight with Husk (g), EWUH: Ear Weight Unhusked (g), NR: Number Row on ear, NSR: Number kernel of Row, TSS: Total Soluble Solids, PRD: Productivity. Numbers followed by the same letter in the same column are not significantly different based on the HSD test at a 5% level

Table 4. Genotypic variation in days to anthesis and silking in hybrid purple sweet corn

Genotype	AD (day)	SD (day)	ASI (day)
G1	46.44^{ab}	48.44^{abc}	2.00^{ab}
G2	44.11^{d}	46.78^{def}	2.67^{ab}
G3	44.67^{cd}	47.19^{bcdef}	2.52^{ab}
G4	44.19^{d}	46.95^{cdef}	2.76^{ab}
G5	44.99^{bcd}	47.41^{abcdef}	2.42^{ab}
G6	44.58^{d}	47.13^{cdef}	2.56^{ab}
G7	44.78^{cd}	47.22^{bcdef}	2.45^{ab}
G8	43.87^{de}	46.12^{f}	2.25^{ab}
G9	44.17^{d}	46.06^{f}	1.89^{ab}
G10	46.17^{abc}	48.33^{abcd}	2.17^{ab}
G11	45.00^{bcd}	47.50^{abcdef}	2.50^{ab}
G12	44.72^{cd}	47.17^{bcdef}	2.44^{ab}
G13	44.67^{cd}	47.37^{bcdef}	2.70^{ab}
G14	42.41^{ef}	44.48^{g}	2.06^{ab}
G15	43.80^{def}	46.69^{ef}	2.89^{ab}
G16	45.17^{bcd}	47.06^{cdef}	1.89^{ab}
G17	47.11^{a}	48.72^{ab}	1.61^{a}
G18	44.36^{d}	46.62^{ef}	2.26^{ab}
G19	42.30^{f}	44.05^{g}	1.75^{ab}
G20	46.78^{a}	48.95^{a}	2.17^{ab}
G21	44.22^{d}	47.28^{bcdef}	3.06^{b}
G22	44.61^{d}	47.72^{abcde}	3.11^{b}

Note: AD: Anthesis Date 50%, SD: Silking Date 50%, ASI: Anthesis Siliking Interval. Numbers followed by the same letter in the same column are not significantly different based on the HSD test at a 5% level

The largest ear diameter was recorded in genotype G22 (52.05 mm), whereas G16 had the smallest (35.48 mm). The number of kernels per row varied from 19.06 (G16) to 37.01 (G4). The number of kernel rows ranged from 8.89 (G16) to 15.32 (G19). These yield components significantly contributed to the productivity potential of each genotype. Grain yield ranged from 9.18 to 18.55 tons ha^{-1}. Genotype G19 exhibited the highest yield (18.55 tons ha^{-1}), whereas G16 showed the lowest (9.18 tons ha^{-1}), demonstrating the considerable influence of genetic background on productivity. The yield values obtained in this study were higher than those reported by Rabanal-Atalaya and Medina-Hoyos (2022), indicating improved agronomic potential under the evaluated conditions. The inheritance of yield components and related agronomic traits is governed by both additive and non-additive genetic effects, suggesting that a combination of gene actions contributes to the expression and improvement of these complex quantitative traits (Khamphasan et al. 2020).

Genetic parameters and heritability estimates of quantitative traits in hybrid purple sweet corn

Genotypic and phenotypic coefficients of variation (GCV and PCV) are important metrics for quantifying genetic variability and evaluating the relative influence of genetic and environmental factors on agronomic traits (Ritonga et al. 2025). The estimates of genetic variance and broad-sense heritability in purple sweet corn genotypes are presented in Table 6. In this study, GCV values ranged from 4.74% to 21.41%, with traits such as plant height, ear diameter, number of leaves, leaf length, leaf width, ear length, ear length with kernel, and number of kernel rows classified as having low genetic variability. Ear height, ear weight with husk, and number of rows per ear fell under the medium category, while ear weight without husk was categorized as having high genetic variability. According to (Magar et al. 2021), GCV and PCV values are typically classified as low (<10%), medium (10-20%), and high

(>20%). Overall, PCV values exceeded the corresponding GCV values across traits, suggesting that environmental factors significantly contributed to trait variation. This finding is consistent with the report by Abe and Adelegan (2019), who observed a strong environmental influence on several maize traits. Environmental conditions such as elevated temperature can enhance plant growth and increase biomass accumulation during the reproductive stage, leading to taller plants and larger ears (Mansilla et al. 2021).

The broad-sense heritability values ranged from 8.24% to 96.99% (Table 6). According to Stanfield (1991), heritability estimates are classified as high (≥0.50), moderate (0.20-0.49), and low (<0.20). Traits with high heritability included ear height, ear diameter, anthesis date, silking date, ear weight with husk, ear length, and number of kernel rows per ear. Traits with moderate heritability included plant height, anthesis-silking interval, number of leaves, leaf length, ear weight without husk, ear length with kernels, and number of kernels per row. In contrast, leaf width showed low heritability (8.24%). Heritability in agronomic traits reflects the proportion of phenotypic variation attributable to genetic factors. High heritability values indicate that selection for such traits is likely to be effective, as genetic influence outweighs environmental variability (Marwan et al. 2022).

Characteristic and morphological of hybrid purple sweet corn on leaf antocyanin and internodes antocyanin

The results of qualitative characterization and anthocyanin expression in leaf and internode traits are presented in Table 7 and Figure 1. The genotypes exhibited a broad variation in leaf morphology. Leaf tip shape was classified into two categories: pointed (18 genotypes) and pointed to rounded (4 genotypes). Leaf orientation was grouped into slightly recurved (11 genotypes), recurved (9 genotypes), and strongly recurved (2 genotypes). The angle between the leaf blade and stem was primarily categorized as medium (19 genotypes) and small (3 genotypes). All genotypes exhibited intermediate levels of blade margin waviness, except for one genotype, which was categorized as medium. Anthocyanin intensity in the leaf was visually assessed and classified into four levels: very weak (8 genotypes), weak (7 genotypes), medium (1 genotype), and strong (6 genotypes). A similar classification was applied to anthocyanin accumulation in the leaf sheath: very weak (9 genotypes), weak (7 genotypes), and medium (6 genotypes). These visual traits suggest differential expression of anthocyanin among the genotypes. The internode, anthocyanin pigmentation was qualitatively categorized into five groups: very weak (4 genotypes), weak (5 genotypes), moderate (4 genotypes), strong (2 genotypes), and very strong (5 genotypes), as illustrated in Figure 2. Variations in anthocyanin expression observed in sheath, glumes, internodes, and leaf organs are likely influenced by both nuclear genetic factors and parental inheritance effects (Pamandungan and Ogie 2018). Such diversity provides valuable information for the selection and development of purple corn cultivars with enhanced pigment content and desirable morphological traits.

Morphological and anthocyanin expression characteristics in the flowering organs and seeds of hybrid purple sweet corn

The results of qualitative characterization of anthocyanin expression in glumes and seeds revealed considerable phenotypic diversity in pigmentation intensity (Table 8). In the glumes, anthocyanin pigmentation was categorized into three levels: weak (2 genotypes), moderate (13 genotypes), and strong (7 genotypes), indicating variation in anthocyanin accumulation among genotypes. Similarly, anthocyanin staining in the anthers showed weak (2 genotypes), moderate (12 genotypes), and strong (8 genotypes) levels. At the base of the glumes, pigmentation intensity also varied among genotypes, with weak (2 genotypes), moderate (12 genotypes), and strong (8 genotypes) classifications.

Table 6. Estimation of genetic parameters: Genotypic and phenotypic coefficient of variation in hybrid purple sweet corn

Character	**Mean**	**σ2g**	**σ2e**	**σ2p**	**HBS**	**GCV**	**PCV**
Plant height	197.1	310.04	374.54	684.58	45.29	8.93	13.27
Ear height	81.29	223.9	78.2	302.1	74.11	18.41	21.38
Ear diameter	25.24	2.61	1.96	4.57	57.08	6.4	8.47
Anthesis date	45.45	7.23	0.29	7.52	96.14	5.91	6.03
Silking date	47.83	7.73	0.24	7.97	96.99	5.81	5.9
Anthesis siliking interval	2.39	0.09	0.21	0.3	30.77	12.78	23.04
Number of leaf	10.38	0.77	1.31	2.08	36.92	8.44	13.88
Leaf length	83.06	18.71	25.15	43.86	42.66	5.21	7.97
Leaf width	9.59	0.21	2.3	2.51	8.24	4.74	16.51
Ear weight with husk	327.21	3139.32	1588.59	4727.91	66.4	17.12	21.01
Ear weight unhusked	212.37	2066.85	2060.08	4126.93	50.08	21.41	30.25
Ear length	19.33	1.83	1.41	3.24	56.48	7	9.31
Ear length with kernel	17.16	2.01	2.86	4.87	41.31	8.27	12.86
Ear diameter	46.02	10.62	4.86	15.48	68.61	7.08	8.55
Number row on ear,	32.83	19.6	9.95	29.55	66.33	13.49	16.56
Number kernel of row	14.25	0.96	1.41	2.37	40.59	6.89	10.81
Total Soluble Solids	14.27	0.24	1.63	1.87	12.83	0.03	0.1
Productivity	16.29	8.12	3.88	12	67.68	17.5	21.27

Note: σ2p: Genotypic variance, σ2e: Environmental variance, σ2p: Phenotypic variance, h^2 bs: Broad sense heritability, GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation

Table 7. Diversity description of qualitative characters of anthocyanin leaf, roots of hybrid sweet purple corn

Genotipe	LS	LO	ALS	WLE	AL	ALL	AI
G1	Pointed	Slightly recurved	Medium	Intermediate	Very weak	Very weak	Weak
G2	Pointed	Slightly recurved	Small	Intermediate	Very weak	Very weak	Weak
G3	Pointed	Recurved	Medium	Intermediate	Weak	Weak	Weak
G4	Pointed	Strongly recurved	Medium	Very weak	Very weak	Very weak	Very weak
G5	Pointed	Strongly recurved	Medium	Intermediate	Very weak	Very weak	Medium
G6	Pointed	Recurved	Medium	Intermediate	Very weak	Very weak	Very weak
G7	Pointed	Slightly recurved	Small	Intermediate	Very weak	Very weak	Strong
G8	Pointed	Slightly recurved	Small	Intermediate	Very weak	Very weak	Weak
G9	Pointed	Recurved	Medium	Intermediate	Weak	Weak	Medium
G10	Pointed	Slightly recurved	Medium	Intermediate	Weak	Very weak	Very weak
G11	Pointed	Slightly recurved	Medium	Intermediate	Very weak	Very weak	Very weak
G12	Pointed	Slightly recurved	Medium	Intermediate	Medium	Medium	Very strong
G13	Pointed	Slightly recurved	Medium	Intermediate	Strong	Weak	Very strong
G14	Pointed	Recurved	Medium	Intermediate	Weak	Weak	Medium
G15	Pointed	Recurved	Medium	Intermediate	Weak	Weak	Very strong
G16	Pointed	Slightly recurved	Medium	Intermediate	Strong	Medium	Very strong
G17	Pointed to rounded	Recurved	Medium	Intermediate	Weak	Weak	Strong
G18	Pointed to rounded	Recurved	Medium	Intermediate	Strong	Medium	Strong
G19	Pointed	Slightly recurved	Medium	Intermediate	Strong	Medium	Very strong
G20	Pointed to rounded	Recurved	Medium	Intermediate	Strong	Medium	Very strong
G21	Pointed	Slightly recurved	Medium	Intermediate	Strong	Medium	Very strong
G22	Pointed to rounded	Recurved	Medium	Intermediate	Weak	Weak	Weak

Note: LS: Leaf tip Shape, LO: Leaf Orientation, ALS: Angle between Leaf blade and Stem, WLE: Waving of Leaf blade Edges, AL: Anthoyanins on Leaf, ALL: Anthoyanins on Leaf Leaves, AI: Anthocyanin Internodes

Table 8. Diversity description of qualitative anthocyanin traits in the tassel, silk, and seeds of hybrid purple sweet corn genotypes

Genotype	AH	AA	ASH	GS	AMB	MBN	AHR	AS
G1	Strong	Strong	Strong	Sparse	Medium	Many	Weak	Medium
G2	Strong	Strong	Strong	Medium	Medium	Medium	Weak	Medium
G3	Medium	Medium	Medium	Sparse	Medium	Medium	Medium	Medium
G4	Medium	Medium	Weak	Sparse	Medium	Medium	Weak	Strong
G5	Medium	Strong	Strong	Sparse	Medium	Medium	Medium	Weak
G6	Medium	Medium	Medium	Sparse	Medium	Medium	Medium	Very strong
G7	Medium	Medium	Medium	Sparse	Small	Few	Medium	Medium
G8	Medium	Medium	Medium	Sparse	Medium	Medium	Medium	Very strong
G9	Medium	Medium	Medium	Sparse	Medium	Medium	Medium	Medium
G10	Medium	Medium	Medium	Sparse	Small	Few	Medium	Weak
G11	Weak	Weak	Weak	Sparse	Small	Few	Medium	Weak
G12	Weak	Weak	Weak	Sparse	Small	Few	Strong	Medium
G13	Strong	Strong	Strong	Sparse	Medium	Few	Medium	Medium
G14	Medium	Medium	Medium	Sparse	Small	Few	Medium	Medium
G15	Strong	Strong	Strong	Sparse	Small	Few	Strong	Strong
G16	Medium	Medium	Medium	Sparse	Small	Few	Weak	Weak
G17	Medium	Medium	Medium	Sparse	Small	Few	Strong	Strong
G18	Strong	Strong	Strong	Medium	Medium	Medium	Medium	Very strong
G19	Strong	Strong	Strong	Sparse	Medium	Medium	Strong	Very strong
G20	Strong	Strong	Strong	Medium	Small	Few	Medium	Strong
G21	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium
G22	Medium	Medium	Medium	Sparse	Medium	Medium	Medium	Strong

Note: AH: Anthocyanins of rice Husk, AA: Anthocyanin staining in Anthers, ASH: Anthocyanin staining at the base of the Husk, GS: Grain density, AMB: Angle between Main and lateral Branch, MBN: Main Branch Number, AHR: Anthocyanin on Hair, AS: Anthocyanin on Seeds

Panicle morphology showed variation in terms of grain density, where most genotypes were categorized as sparse (18 genotypes) and a few as moderate (4 genotypes). The angle between the main and lateral branches was observed as small (9 genotypes) or medium (13 genotypes). The number of main branches also varied, with few (10 genotypes), moderate (11 genotypes), and many (1 genotype). The overall variation in panicle architecture is illustrated in Figure 3. Anthocyanin expression in the silks and kernels further demonstrated genotypic variation. In the silks, anthocyanin levels were classified as weak (4 genotypes), moderate (14 genotypes), and strong (4 genotypes). In the kernels, pigmentation ranged from weak (4 genotypes), moderate (9 genotypes), strong (4 genotypes), to very strong (4 genotypes), as shown in Figure 4. The variation in purple pigmentation is partly attributed to the influence of the male parent (pollen donor), as observed in xenia effects. This aligns with the findings of Ishartati et al. (2020), who reported that pollen source significantly affects anthocyanin expression in maize kernels, suggesting that xenia can be visually observed in kernel coloration. Additionally, environmental conditions likely contributed to the variation in anthocyanin expression across genotypes. Purple corn varieties with pigmentation in the pericarp layer accumulate anthocyanins at levels nearly eight times greater than those with aleurone-based coloration, indicating their enhanced value as dietary sources of natural antioxidants (Anirban et al. 2023).

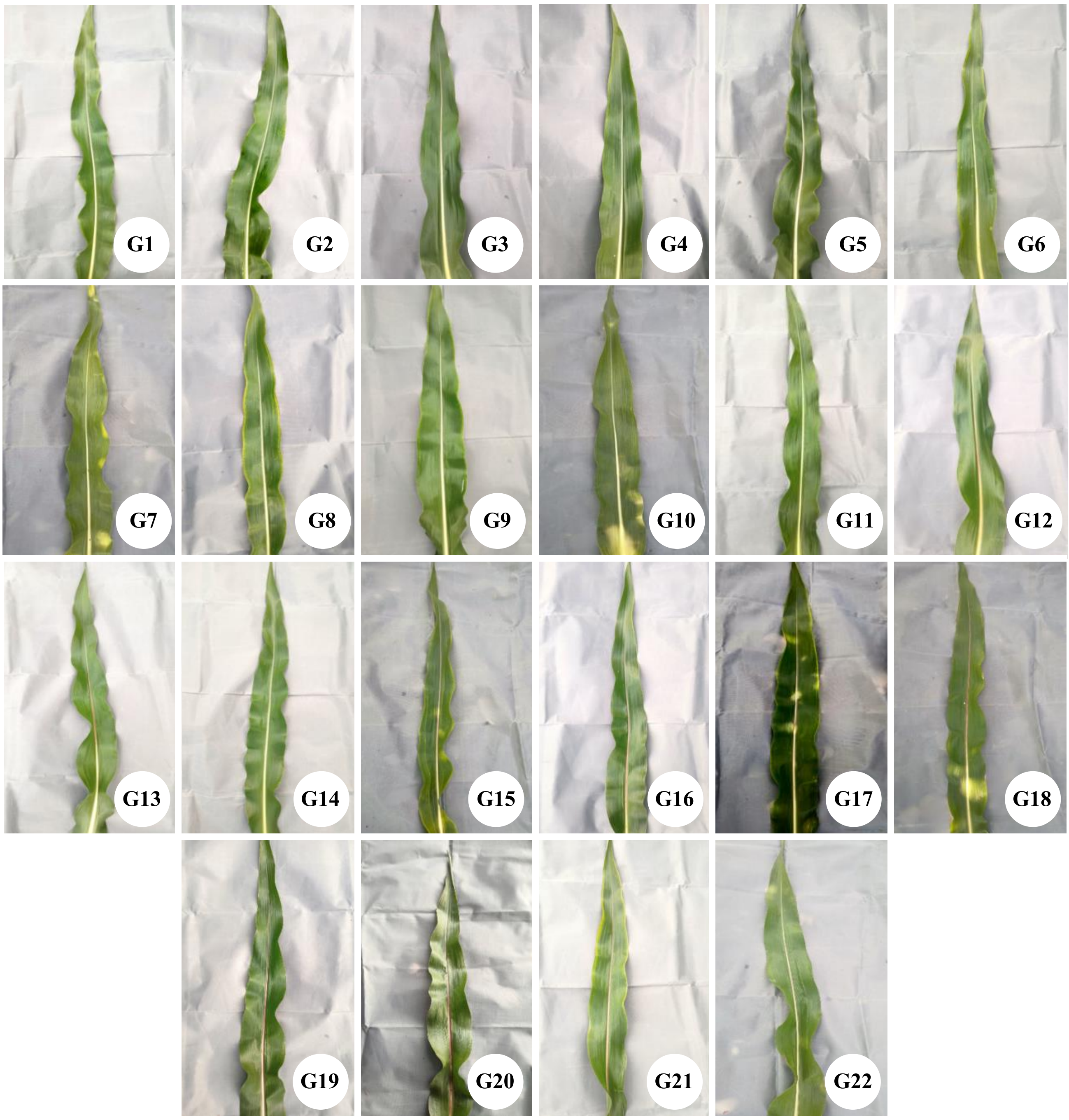


Figure 1. Diversity leaf of anthocyanin and characteristic morphological on leaf

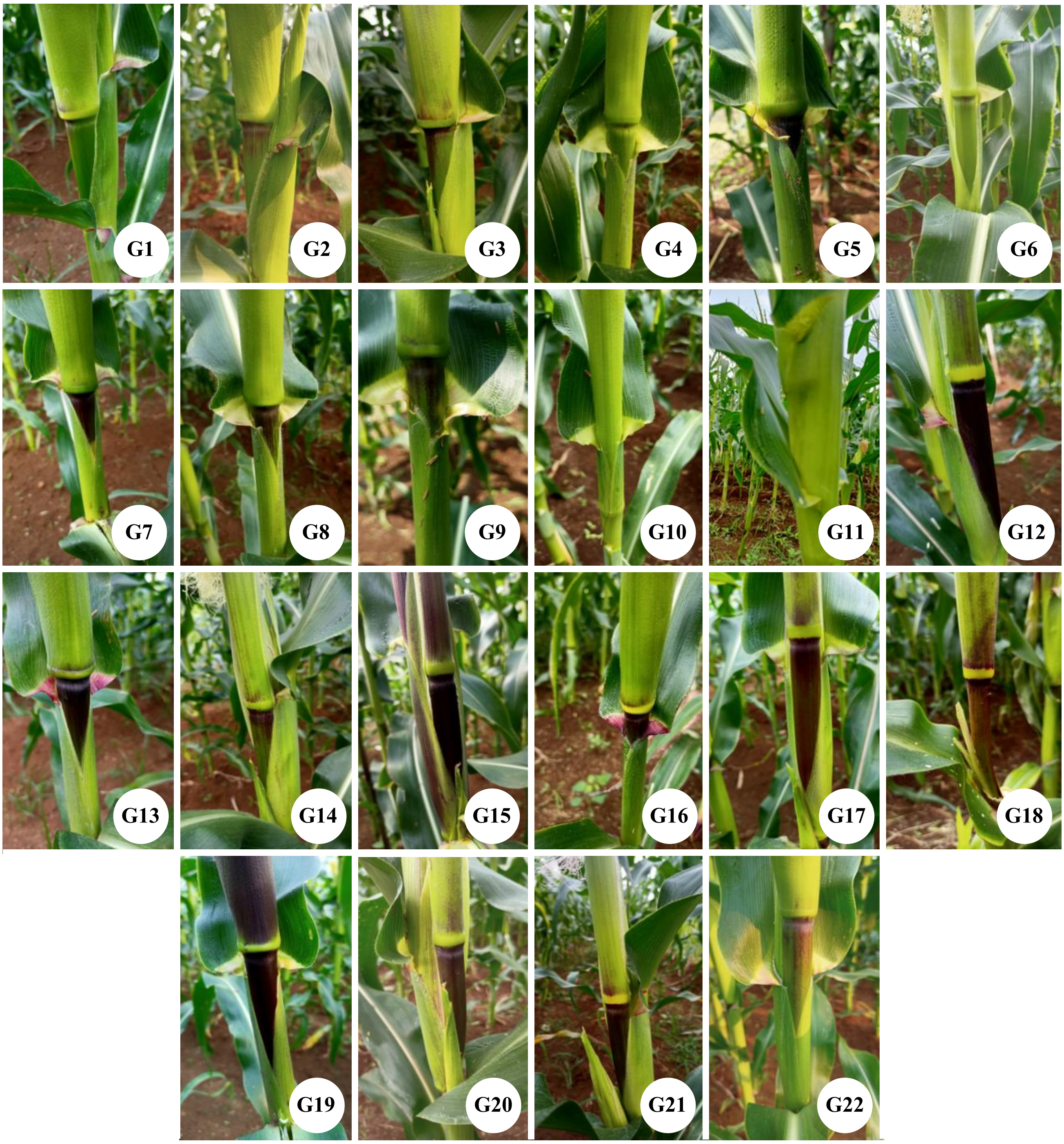


Figure 2. Diversity internode anthocyanin and characteristic morphological on internode

Pearson correlation analysis of agronomic traits in hybrid purple sweet corn

Based on the results of the correlation analysis, this study aimed to assess the relationships among traits closely associated with ear weight without husk. The correlation analysis for purple sweet corn, presented in Figure 5, showed that ear weight without husk was significantly and positively correlated with several traits, including plant height (r = 0.55), ear height (r = 0.58), stem diameter (r = 0.71), number of leaves (r = 0.51), leaf length (r = 0.59), leaf width (r = 0.44), and ear weight with husk (r = 0.68). These findings are in line with the report by Long et al. (2024), who indicated that ear weight, ear diameter, and the number of kernels per row are the most influential traits contributing to yield performance. Therefore, integrating correlation analysis with path coefficient analysis can provide a reliable basis for identifying key traits that contribute to the improvement of complex yield-related characteristics (Islam et al. 2015).

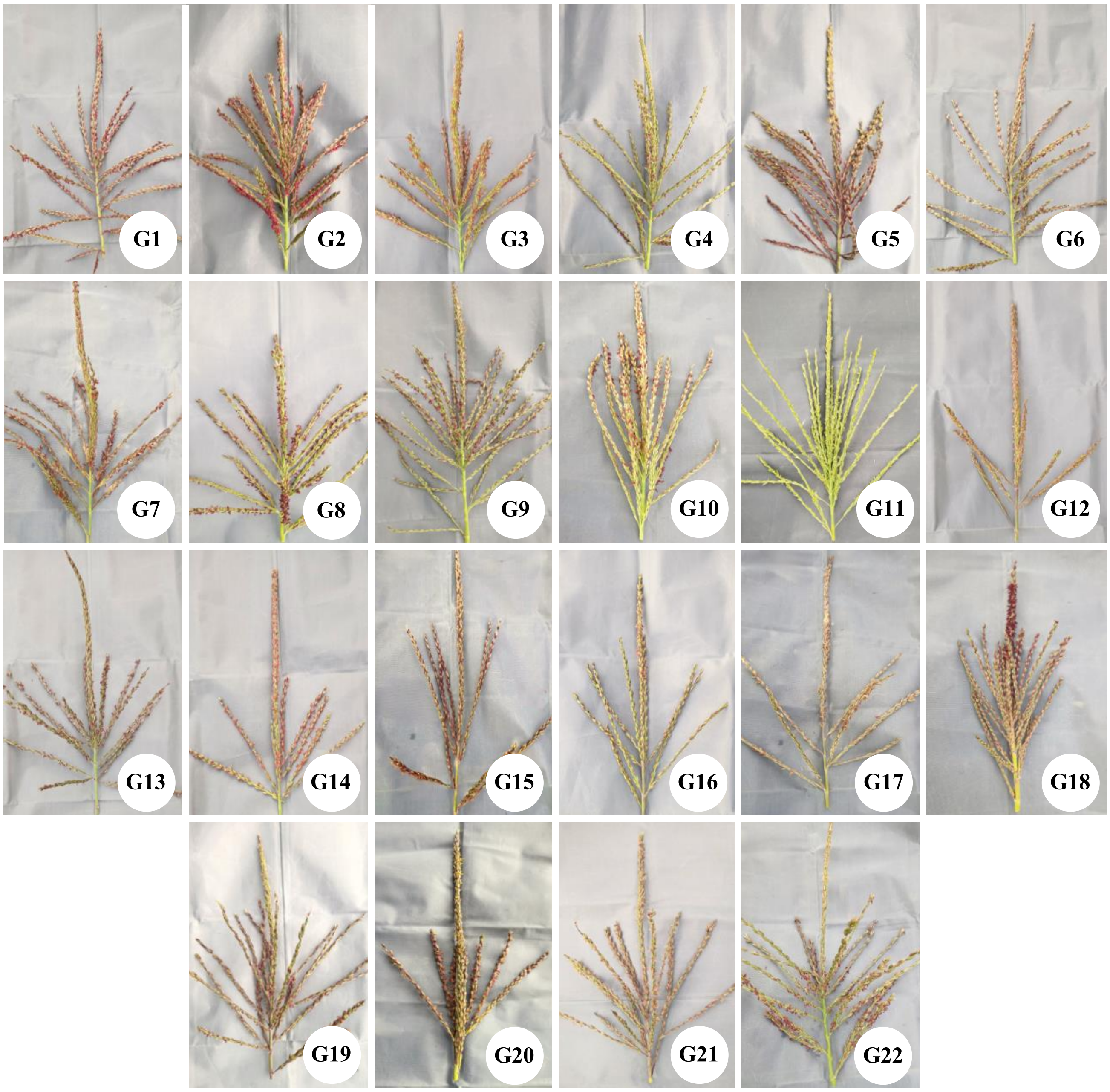


Figure 3. Diversity flowering anthocyanin and characteristic morphological on flower

Cluster analysis of quantitative and qualitative traits in hybrid purple sweet corn

Cluster analysis is a multivariate statistical method used to group individuals or genotypes based on the degree of similarity in observed characteristics. Cluster analysis revealed a high level of genetic diversity among the 22 purple sweet corn hybrids. This was evidenced by a low similarity coefficient of 20.05%, indicating a high genetic dissimilarity of 79.5% among the genotypes. Genetic diversity is a crucial factor influencing the success of plant breeding programs. These hybrids may be recombined with each other or with yellow sweet corn lines to develop superior purple sweet corn genotypes with improved agronomic and yield-related traits.

In this study, 22 purple sweet corn genotypes were classified into three distinct clusters based on both quantitative and qualitative traits. The primary traits differentiating these clusters included ear diameter, ear weight with husk, number of kernels per row, ear height, anthocyanin intensity in the seeds, and anthocyanin accumulation at the base of the husk. Cluster I comprised 14 genotypes (G1, G2, G3, G4, G6, G7, G8, G9, G10, G11, G14, G15, G22), with similarity levels ranging from 40.81% to 65.93%. Genotypes in this group were characterized by the largest ear diameter and the highest ear weight. Cluster II included three genotypes (G12, G16, G21), with a similarity level of 41.22%, and was distinguished by the highest number of kernel rows and the lowest ear height. Cluster III consisted of four genotypes (G13, G18, G19, G20) with a similarity level of 30.80%, characterized by the highest anthocyanin concentration in both the seeds and the base of the husk. This finding is consistent with the approach used by Duangpapeng et al. (2019), who applied cluster analysis to classify maize genotypes based on anthocyanin concentration and agronomic traits, demonstrating the effectiveness of this method in differentiating genetic variability among purple corn lines. Euclidean distance was employed to measure the degree of similarity among genotypes, where smaller values indicate greater resemblance. These results are consistent with the findings of Tan et al. (2022), who emphasized the effectiveness of cluster analysis in distinguishing genotypic variation based on multiple trait combinations.

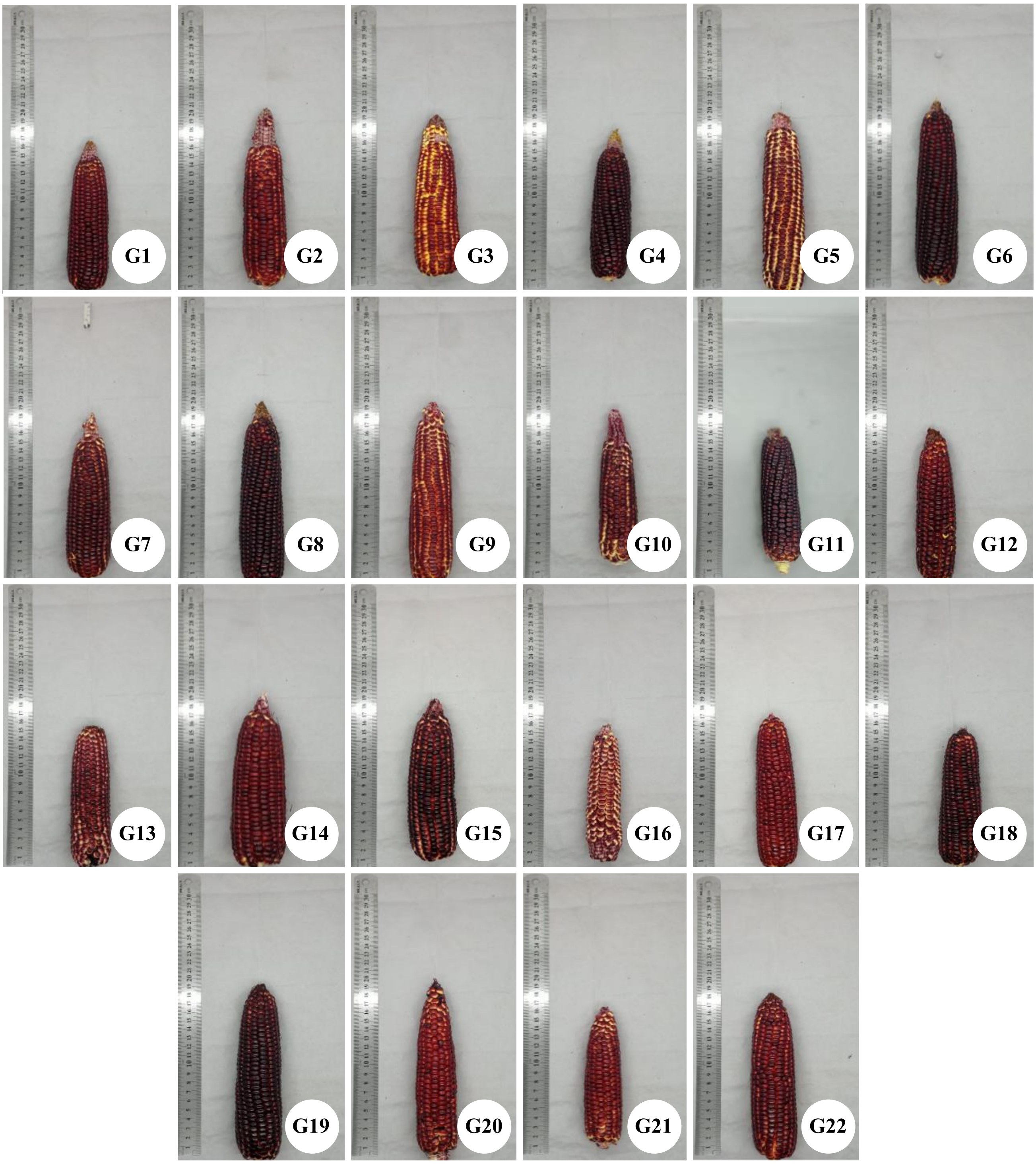
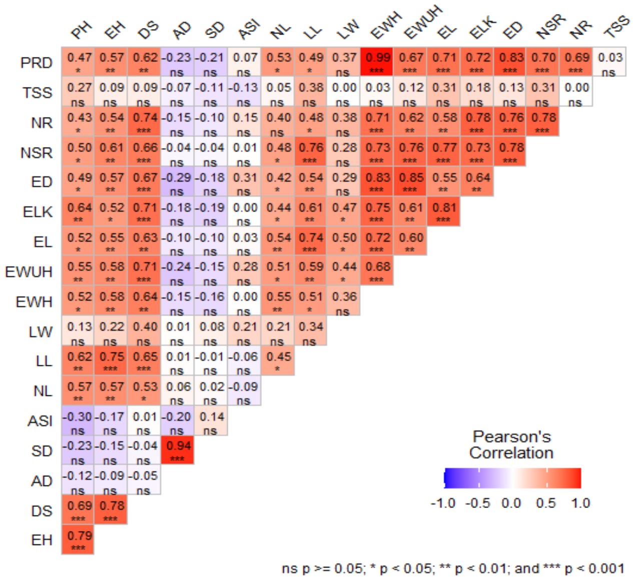


Figure 4. Diversity cob of anthocyanin and characteristic morphological on cob



	PH	EH	DS	AD	SD	ASI	NL	LL	LW	EWH	EWUH	EL	ELK	ED	NSR	NR	TSS
PRD	0.47 *	0.57 **	0.62 **	-0.23 ns	-0.21 ns	0.07 ns	0.53 *	0.49 *	0.37 ns	0.99 ***	0.67 ***	0.71 ***	0.72 ***	0.83 ***	0.70 ***	0.69 ***	0.03 ns
TSS	0.27 ns	0.09 ns	0.09 ns	-0.07 ns	-0.11 ns	-0.13 ns	0.05 ns	0.38 ns	0.00 ns	0.03 ns	0.12 ns	0.31 ns	0.18 ns	0.13 ns	0.31 ns	0.00 ns	
NR	0.43 *	0.54 **	0.74 ***	-0.15 ns	-0.10 ns	0.15 ns	0.40 ns	0.48 *	0.38 ns	0.71 ***	0.62 **	0.58 **	0.78 ***	0.76 ***	0.78 ***		
NSR	0.50 *	0.61 **	0.66 ***	-0.04 ns	-0.04 ns	0.01 ns	0.48 *	0.76 ***	0.28 ns	0.73 ***	0.76 ***	0.77 ***	0.73 ***	0.78 ***			
ED	0.49 *	0.57 **	0.67 ***	-0.29 ns	-0.18 ns	0.31 ns	0.42 *	0.54 **	0.29 ns	0.83 ***	0.85 ***	0.55 **	0.64 **				
ELK	0.64 **	0.52 *	0.71 ***	-0.18 ns	-0.19 ns	0.00 ns	0.44 *	0.61 **	0.47 *	0.75 ***	0.61 **	0.81 ***					
EL	0.52 *	0.55 **	0.63 **	-0.10 ns	-0.10 ns	0.03 ns	0.54 **	0.74 ***	0.50 *	0.72 ***	0.60 **						
EWUH	0.55 **	0.58 **	0.71 ***	-0.24 ns	-0.15 ns	0.28 ns	0.51 *	0.59 **	0.44 *	0.68 ***							
EWH	0.52 *	0.58 **	0.64 **	-0.15 ns	-0.16 ns	0.00 ns	0.55 **	0.51 *	0.36 ns								
LW	0.13 ns	0.22 ns	0.40 ns	0.01 ns	0.08 ns	0.21 ns	0.21 ns	0.34 ns									
LL	0.62 **	0.75 ***	0.65 ***	0.01 ns	-0.01 ns	-0.06 ns	0.45 *										
NL	0.57 **	0.57 **	0.53 *	0.06 ns	0.02 ns	-0.09 ns											
ASI	-0.30 ns	-0.17 ns	0.01 ns	-0.20 ns	0.14 ns												
SD	-0.23 ns	-0.15 ns	-0.04 ns	0.94 ***													
AD	-0.12 ns	-0.09 ns	-0.05 ns														
DS	0.69 ***	0.78 ***															
EH	0.79 ***																

ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001

Figure 5. Correlation characters for quantitative Analysis of 22 Genotypes hybrid Purple sweet corn. Note: PH: Plant Height, EH: Ear Height, DS: Diameter of Stem, AD: Anthesis Date, SD: Silking Date, ASI: Anthesis Silking Interval, NL: Number of Leaf, LL: Leaf Length, LW: Leaf Width, EWH: Ear Weight Husk, EWUH: Ear Weight Unhusked, EL: Ear Length, ELK: Ear Length with Kernel, ED: Ear Diameter, NSR: Number kernel of Row, NR: Number of Row kernel on ear, TSS: Total Soluble Solids, PRD: Productivity

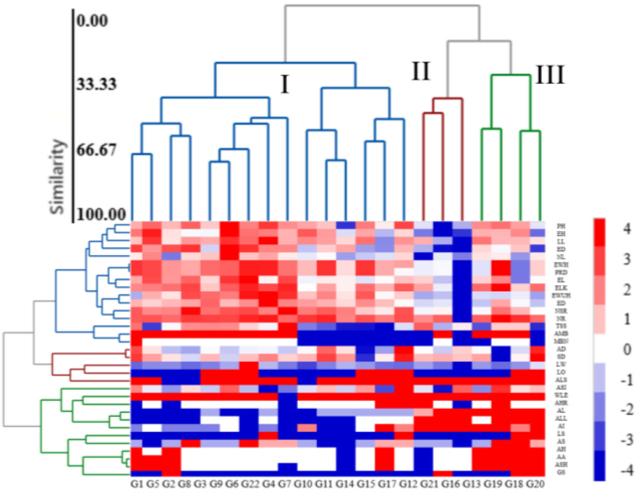


Figure 6. Heatmap clusters analysis with characters quantitative and qualitative 22 hybrid purple sweet corns based on agronomic characters and morphological using a complete linkage method PH: Plant Height, EH: Ear Height, DS: Diameter of Stem, AD: Anthesis Date, SD: Silking Date, ASI: Anthesis Silking Interval, NL: Number of Leaf, LL: Leaf Length, LW: Leaf Width, EWH: Ear Weight Husk, EWUH: Ear Weight Unhusked, EL: Ear Length, ELK: Ear Length with Kernel, ED: Ear Diameter, NSR: Number kernel of Row, NR: Number of Row kernel on ear, TSS: Total Soluble Solids, PRD: Productivity, LS: Lea Tip Shape, LO: Leaf Orientation, ALS: Angle between Leaf blade and Stem, WLE: Waving of Leaf blade Edges, AL: Anthoyanins on Leaf, ALL: Anthoyanins on Leaf Leaves, AI: Anthocyanin Internodes, AH: Anthocyanins of rice Husk, AA: Anthocyanin staining in Anthers, ASH: Anthocyanin Staining at the base of the Husk, GS: Grain Density, AMB: Angle between Main and lateral Branch, MBN: Main Branch Number, AHR: Anthocyanin on Hair, AS: Anthocyanin on Seeds

In conclusion, this study revealed significant genetic variability among 22 hybrid purple sweet corn genotypes, with high heritability in key yield traits such as ear diameter, ear weight with husk, and Productivity. Strong correlations between ear weight traits and yield suggest their value as selection indicators. Cluster analysis grouped genotypes based on morphological and agronomic traits, highlighting G19 as a promising candidate. These findings provide a scientific basis for selecting superior genotypes and can support breeding programs aimed at developing high yielding, anthocyanin rich cultivars suitable for tropical agroecosystems. Further evaluation of promising genotypes across environments is recommended to confirm their performance and nutritional potential.

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