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Estimation of genetic parameters and path analysis in sweet-waxy corn (*Zea mays* var. *ceratina*)

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Abstract. *Ritonga AW, Mukhlisin, Sutjahjo SH. 2025. Estimation of genetic parameters and path analysis in sweet-waxy corn (*Zea mays *var.* ceratina*). Biodiversitas 26: 879-889.* Waxy corn is commonly consumed as a staple food in Eastern Indonesia. The development of hybrid sweet-waxy corn is crucial for enhancing its quality and productivity. The information about genetic parameters and yield-related traits is essential in plant breeding programs to obtain high-yielding hybrids. This study aimed to determine the genetic variability, heritability, and yield-related traits in sweet-waxy corn hybrids. This research was carried out at two locations, Bogor and Lampung, from September 2023 to February 2024. Fifteen sweet-waxy corn hybrids were sown in a randomized complete block design with three replicates. The recorded data were plant height, ear height, stem diameter, leaf width, leaf length, the number of leaves, the number of kernels per row, the number of rows per ear, ear diameter, ear length, and ear weight without husk. The findings revealed that the G1, G7, and G12 hybrids demonstrated superior yield traits at both locations. All observed traits demonstrated high heritability, with the exception of stem diameter and the number of kernels per row. The phenotypic and genotypic coefficients of variation were within the moderate to high, with percentages ranging from 4.15% to 16.69%. Correlation analysis suggested a positive association between ear weight without husks with the other traits. Ear diameter, ear length, and the number of kernels per row had highly positive direct effects on the ear weight without husks, while leaf width had a strong indirect effect through ear diameter (0.415). Thus, these traits may be utilized as selection criteria in corn breeding programs.

Keywords: Correlation, heritability, path analysis, sweet-waxy corn

Abbreviations: CV: Coefficient of variation; GCV: Genotypic coefficient of variation; G × E: Genotype × environment interaction; Hbs: Heritability broad sense; PCV: Phenotypic coefficient of variation

INTRODUCTION

Waxy corn exhibits distinct characteristics compared to regular corn, primarily due to its high amylopectin content. Amylopectin is a starch that confers a sticky texture to waxy corn upon consumption (Ahmad et al. 2022). Although it is extensively cultivated in several regions of Indonesia, including South Sulawesi, West Nusa Tenggara, and Maluku, sweet-waxy corn breeding remains relatively limited (Fowo et al. 2019). Similar to sweet corn, waxy corn is classified as an early maturing crop, typically reaching harvest maturity 65-70 days after planting (Sahilatua et al. 2019). Waxy corn contains 97% amylopectin and 0-7% amylose, whereas regular corn contains a mixture of 72% amylopectin and 28% amylose (Edy dan Ibrahim 2016). Waxy corn exhibits a recessive wx gene in the homozygous state (*wxwx*), which influences the chemical composition of starch and contributes to its characteristic flavor profile (Edy et al. 2019). Sweet-waxy corn represents a combination of the recessive waxy control gene (*wxwx*) and sweet gene within a single ear. Distinct single recessive genes govern these two types of corn: the *wx* gene for waxy corn and the sweet gene (*su*/*sh2*). The development of hybrid sweet-waxy corn represents a crucial endeavor in augmenting flavor quality and yield, thereby enabling plant breeders to generate superior cultivars that resonate with consumer preferences. The integration of these two genetic characteristics facilitates the development of a hybrid sweet sticky corn variant, which manifests both a tender texture and sweet flavor within individual ears (Lertrat and Thongnarin 2008).

Improvements in maize plant breeding, in addition to hybridization, require genotype × environment (G × E) interaction testing. This interaction can be utilized to ascertain the ranking disparities among genotypes within a specific environment (Begna 2020). The magnitude of the G × E interaction is likely to be substantial when significant environmental variation exists, such as differences in temperature, precipitation, elevation, and solar radiation intensity. A statistically significant G × E value indicates that the environment exerts an influence on the genotype, whereas a non-significant G × E value suggests that the environment does not affect the genotype (Teressa et al. 2021).

The successful improvement of traits in sweet-waxy corn can be achieved through plant breeding methods, particularly by identifying superior traits from the selection results. Estimating genetic parameters, such as variance, coefficient of variation, heritability, and environmental correlation, is crucial for understanding genetic variability within the genetic resources of a plant population. This analysis serves as an important prerequisite for initiating plant improvement programs and for selecting appropriate breeding techniques. Genetic variability provides insight into the level of variation in desirable traits, which can be leveraged to assess the potential benefits of genetic selection (Terfa and Gurmu 2020). Therefore, a deeper understanding of this genetic variability will enable plant breeders to design effective and targeted breeding strategies aimed at enhancing the desired traits in cultivated plants (Bartaula et al. 2019).

Direct and indirect effects analysis is a statistical approach employed in plant breeding to elucidate the cause and effect relationships between genetic or environmental variables and crop outcomes, such as yield, which are crucial selection criteria (Crevelari et al. 2018). Path analysis systematically delineates and quantifies the direct and indirect effects of each causal component on an outcome variable. This methodology facilitates the identification of the most influential components in the selection process. The study of genetic parameters and pathway analysis in waxy sweet corn is of paramount importance, as it provides a comprehensive understanding of trait inheritance, factors influencing yield and quality, and identification of pathways that contribute to the improvement of plant traits. This research aims to determine the genetic diversity, heritability, and yield characteristics of sweet, waxy corn hybrids.

MATERIALS AND METHODS

Study area

This study was conducted from October 2023 to February 2024 at two distinct experimental sites: Bandar Agung Experimental Farm in Lampung (with an altitude of 80 masl 5°17'18.6" S; 105°39'17.9" E) and Pasir Kuda Experimental Farm in Bogor (with an altitude of 263 masl 6°36'36.4" S; 106°47'04.1" E). The climate conditions in Bogor exhibit monthly rainfall ranging from 204.56-832.97 mm, with daily average temperatures ranging from 26.87-27.71°C and relative humidity levels between 73.7-83.70%. In comparison, the climate conditions in Lampung are characterized by monthly rainfall ranging from 100.50-237.90 mm, daily average temperatures ranging from 27.29-28.28°C, and relative humidity levels between 75.63-85.62%.

The use of waxy corn as the female parent and sweet corn as the male parent in the IPB hybridization program is intended to integrate the distinct advantages of both varieties, namely the seed quality and sweetness of sweet corn, along with the high waxy content of waxy corn. This hybridization is expected to produce unique offspring with superior traits, such as increased yield and seeds that exhibit a combination of waxy and sweet characteristics, making them more valuable both agronomically and commercially. The study employed 15 genotypes of sweet-waxy corn, which included 12 hybrid varieties developed by the IPB Plant Breeding Laboratory and 3 commercial varieties (Arumba, Kumala, and Srikandi). Comprehensive details of these genetic materials are provided in Table 1.

Procedures

Land preparation was carried out two weeks prior to planting and involved several critical steps, including soil tillage, the establishment of drainage channels, weed removal, and field mapping. Planting was conducted in single rows with a spacing of 20 × 75 cm, placing one seed per hole according to the specified genotype. Each planting hole was treated with Furadan 3R insecticide to protect the seeds from pest damage and then covered with soil.

Maintenance practices included irrigation, replanting, fertilization, weed control, and pest and disease management. Weeds were removed either manually or with hoes, while hilling was performed to cover exposed roots and ensure plant stability. Replanting was conducted 10 days after planting to replace non-germinated or dead seeds.

Table 1. Genetic material consisted of 15 genotypes of sweet-waxy corn

Code	Genotype	Source
G1	JPS 13.6.1P.10 × JPM 1.6P.7	IPB hybrids
G2	JPS 13.16.12.7 × JPM 1.6P.7	IPB hybrids
G3	JPS 53.10P.15 × JPM 1.2P.3	IPB hybrids
G4	JPS 13.16.12.12 × JPM 1.2P.3	IPB hybrids
G5	JPS 30.2.15.8 × JPM 1.2P.3	IPB hybrids
G6	JPS 13.16.12.12 × JPM 1.6P.3	IPB hybrids
G7	JPS 13.6.1P.15 × JPM 1.6P.7	IPB hybrids
G8	JPS 13.6.1K.1 × JPM 1.2P.3	IPB hybrids
G9	JPS 13.6.1K.1 × JPM 1.2P.6	IPB hybrids
G10	JPS 30.21.5.8 × JPM 1.6P.7	IPB hybrids
G11	JPS 13.16.12.7 × JPM 1.6P.4	IPB hybrids
G12	JPS 13.6.1P.15 × JPM 1.6P.4	IPB hybrids
G13	Arumba	Commercial hybrids (Agri Makmur Pertiwi)
G14	Kumala	Commercial hybrids (East-West Seed Indonesia)
G15	Srikandi	Commercial hybrids (BISI Internasional)

Fertilization was applied in two stages (i) urea fertilizer at 150 kg ha^{-1}, SP-36 at 200 kg ha^{-1}; and (ii) KCL at the rate of 200 kg ha^{-1}; the second fertilization at 35 DAP at the rate of 100 kg N ha^{-1}. Pest and disease control involved the application of *Demorf* 60 WP fungicide and *Sagri-beat* 7/30 WP insecticide. Harvesting of sweet-waxy corn was performed when the ears were still immature, specifically 21 days after pollination.

Quantitative traits were recorded by analyzing 10 sample plants per genotype in each replication, following the procedures specified by UPOV (2009). The study evaluated 13 quantitative traits: plant height, ear height, stem diameter, leaf width, leaf length, number of leaves, ear length, ear diameter, number of kernel rows, number of kernels per row, ear weight without husk, ear weight with husk, and productivity.

Data analysis

Analysis of Variance (ANOVA) was conducted using Microsoft Excel and using PKBT STAT 3.1 (http://pbstat.com/pkbt-stat/), with a significance level set at 5%. The HSD test was applied with a confidence interval of α = 0.05 for assessing quantitative variables. Estimation of genetic parameters and heritability follows the method of Deshmukh et al. (1986). Pearson correlation and path analysis, including both direct and indirect effects, were conducted using RStudio (R version 4.1.2). Cluster analysis was conducted employing "Euclidean distance" and the "Complete linkage clustering method," utilizing Microsoft Excel and Minitab 17 software for the analysis.

RESULTS AND DISCUSSION

Quantitative characterization of sweet-waxy corn genotypes

The results of the combined analysis of variance for 15 genotypes of sweet corn are presented in Table 2. The mean square values indicate that genotypes significantly affect all observed traits. This suggests that the sweet-waxy corn genotypes used in this study exhibit genetic differences. Environmental factors significantly influenced plant height, ear height, leaf width, ear length, ear weight with husk, and ear weight without husk ($p<0.05$). Conversely, other traits demonstrated highly significant effects at ($p<0.01$). The significant environmental effects indicate differing conditions in the two test environments.

The genotype-by-environment (G × E) interaction had a highly significant effect ($p<0.01$) on ear length, ear diameter, number of rows, number of kernels per row, and ear weight without husk. For plant height, stem diameter, and leaf width, the G × E interaction was significant ($p<0.05$). In contrast, the traits of ear height, leaf length, number of leaves, ear weight with husk, and productivity showed no significant G × E interaction. The significant differences in G × E interactions suggest that the performance of genotypes varied across the testing environments, leading to different genotype rankings. Meanwhile, the non-significant G × E interactions indicate that genotype performance was consistent across various environments (Zakir 2018). This is consistent with the study by Özata (2020) on waxy corn, which demonstrated a significant G × E interaction effect on the observed traits. The analysis revealed that the coefficient of variation for 12 traits ranged from 3.12% to 10.28%. This indicates that the coefficients of variation are relatively low, signifying a high accuracy level of the obtained data (Nzuve et al. 2014).

Genotypes that exhibit significant G × E interactions require a selection strategy that takes into account various environmental conditions to ensure that the selected genotypes perform well across different environments. In contrast, genotypes that demonstrate trait stability across environments allow breeders to focus more on the genetic improvement of these traits without concern for potential environmental fluctuations (Adham 2022). Therefore, a thorough understanding of G × E patterns is crucial in the effort to develop more adaptive and superior varieties.

Table 2. Analysis of variance of 15 sweet-waxy corn genotypes in two locations

Traits	Genotype	Environment	G × E	Error	CV (%)
Plant height	2.471.52 **	32.646.75*	691.17*	289.88	7.90
Ear height	2.171.23**	25.541.23*	184.02^{ns}	114.78	9.40
Stem diameter	2.83**	7.286.76**	1.89*	0.07	8.80
Leaf width	1.71**	14.61*	0.25*	0.13	4.59
Leaf length	108.03**	737.19**	9.22^{ns}	9.32	3.12
Number of leaves	5.71**	53.44**	0.44^{ns}	0.65	7.01
Number of rows	35.04**	16.448.97**	27.64**	0.34	10.28
Number of kernels per row	15.08**	11.258.71**	14.10**	8.20	5.44
Ear diameter	73.64**	3.266.45**	21.63**	5.60	6.56
Ear length	10.77**	68.98*	1.46**	0.56	4.37
Ear weight with husk	7.598.56**	21.853.44*	975.03^{ns}	606.04	9.77
Ear weight without husk	4.431.89**	10.628.25*	670.03**	228.53	9.73
Productivity	23.37**	6.11**	3.51^{ns}	2.18	9.77

Notes: G × E: Genotype × environment interaction, CV: Coefficient of variation, *: Significant at α = 5%, **: Significant at α = 1%, ns: Not significant

The average values for plant height and ear height among 15 genotypes of sweet-waxy corn across two locations are presented in Table 3. Plant height and ear height at the Lampung site were significantly higher than those at the Bogor site. The tallest sweet corn genotype G7, measured 266.89 cm in Lampung, while genotype G5 recorded the lowest height at 152.47 cm in Bogor. The average ear height for all tested genotypes at the Lampung site (130.08 cm) exceeded that observed at the Bogor site. Genotype G7 exhibited the best average plant height (247.70 cm) and ear height (145.64 cm) compared to the other genotypes evaluated.

Environmental factors influence the variation in plant height and ear height at each location. Agronomic conditions in each region significantly affect the growth of corn plants. The data indicated considerable differences in sunlight duration, which is a critical factor in plant height. Increased sunlight exposure enhances photosynthesis, promoting taller plants and higher ear placement (Wu et al. 2023). The ideal plant height for sweet-waxy corn, as anticipated by breeders, ranges from 180 to 220 cm (Aman et al. 2020). Excessively tall plants are undesirable as they are prone to lodging, and greater height can result in higher ear placement, complicating the harvesting process. Additionally, taller plants require more nutrients, which can extend the vegetative phase and subsequently impact the generative phase until harvest. This can potentially lead to lower yields of sweet corn, affecting the economic viability of the crop.

The average values for leaf length, leaf width, and number of leaves exhibited notable differences across the two testing locations, as shown in Table 4. Leaf length and number of leaves did not show significant differences among the genotypes at each location; however, the locations themselves displayed significant differences for these traits. Specifically, Lampung showed a higher average for leaf length and number of leaves compared to Bogor. Leaf width, on the other hand, was significantly influenced by genotype. Genotype G7 demonstrated significantly greater leaf width in Lampung, while genotype G12 exhibited higher leaf width in Bogor. Leaf characteristics play a crucial role in photosynthesis, which is essential for storing energy reserves that can be translocated to the kernels on the ear. Photosynthesis heavily relies on sunlight as an energy source, and differences in sunlight exposure between locations can also affect the photosynthetic process, potentially hindering plant growth (Wu et al. 2023).

The analysis results from both locations indicated that the location treatment had no significant effect on stem diameter; however, the genotype displayed a highly significant effect (Table 5). The average values across both locations revealed that genotype G1 had a greater diameter compared to G4, G5, and G13, although it did not differ significantly from other genotypes. Stem diameter correlates with plant height; larger diameters tend to be stronger than smaller diameters, which is crucial for preventing lodging.

The characteristics of ear diameter and ear length at the Bogor location showed greater average values compared to the Lampung location (Table 6). Genotype G7 exhibited the largest average ear diameter at Bogor, measuring 45.90 mm, while genotype G9 displayed the smallest ear diameter in Lampung. Genotype G15 had the largest average ear length at both Bogor (20.56 cm) and Lampung (19.76 cm). Conversely, genotype G3 exhibited the smallest ear length at Bogor (16.52 cm) and Lampung (14.77 cm). Across both locations, genotype G1 (41.01 mm) had the average largest ear diameter, while genotype G5 (29.68 mm) had the smallest. The greatest average ear length was observed in G15 (20.16 cm), while the shortest length was associated with genotype G5 (15.68 cm).

Table 3. Average plant height and ear height of 15 sweet-waxy corn genotypes in two locations

Genotype	Plant height (cm)		Average genotype	Ear height (cm)		Average genotype
	Bogor	Lampung		Bogor	Lampung	
G1	220.73^{a}	212.80^{bc}	216.77^{abcd}	124.63	152.63	138.63^{ab}
G2	203.44^{ab}	241.31^{abc}	222.38^{abcd}	103.93	126.75	115.34^{cdef}
G3	190.20^{abc}	212.14^{bc}	201.17^{cd}	88.27	118.52	103.39^{defgh}
G4	219.30^{a}	233.04^{abc}	226.17^{abc}	104.43	124.33	114.38^{cdefg}
G5	152.47^{c}	236.27^{abc}	194.37^{cd}	70.40	125.33	97.87^{fgh}
G6	219.45^{a}	258.91^{ab}	239.18^{ab}	124.24	143.99	134.11^{abc}
G7	228.50^{a}	266.89^{a}	247.70^{a}	127.60	163.68	145.64^{a}
G8	179.97^{abc}	227.37^{abc}	203.67^{bcd}	73.00	110.51	91.76^{h}
G9	186.43^{abc}	207.68^{c}	197.06^{cd}	81.97	115.79	98.88^{efgh}
G10	202.04^{abc}	239.43^{abc}	220.74^{abcd}	105.40	136.93	121.17^{bcde}
G11	214.13^{a}	259.76^{ab}	236.95^{ab}	110.20	138.73	124.47^{abcd}
G12	229.90^{a}	260.03^{ab}	244.96^{a}	126.17	149.96	138.06^{ab}
G13	159.38^{bc}	214.73^{bc}	187.06^{d}	67.23	118.10	92.67^{gh}
G14	160.98^{bc}	222.37^{abc}	191.68^{cd}	63.05	112.77	87.91^{h}
G15	180.77^{abc}	226.35^{abc}	203.56^{bcd}	86.13	124.02	105.08^{defgh}
Average location	196.51^{B}	234.61^{A}		97.11^{B}	130.80^{A}	

Note: Values followed by the same letter within the same column are not significantly different according to the HSD test at the 5% significance level

Table 4. Average leaf length, leaf width, and number of leaves of 15 sweet-waxy corn genotypes in two locations

Genotype	**Leaf length (cm)**		**Leaf width (cm)**		**Number of leaves**	
	Bogor	**Lampung**	**Bogor**	**Lampung**	**Bogor**	**Lampung**
G1	99.10	105.83	8.56^{abc}	7.23^{bcd}	11.5	13.33
G2	94.31	102.76	8.04^{bcd}	7.18^{bcd}	10.9	12.33
G3	95.98	103.80	8.02^{bcd}	7.22^{bcd}	10	11.33
G4	95.73	98.98	7.33^{d}	6.82^{cd}	10.13	12
G5	87.17	95.80	7.47^{d}	6.40^{d}	8.73	11.33
G6	97.24	105.51	7.78^{cd}	7.66^{bc}	11.12	12.67
G7	101.47	102.85	8.80^{abc}	8.82^{a}	12.7	14.25
G8	88.83	95.38	8.13^{abcd}	7.42^{bcd}	9.97	11.33
G9	94.40	96.02	8.17^{abcd}	7.26^{bcd}	10.47	12
G10	98.15	101.87	7.84^{bcd}	7.23^{bcd}	10.95	12
G11	98.50	104.61	7.98^{bcd}	7.37^{bcd}	11.7	12.93
G12	101.17	105.16	9.17^{a}	7.89^{ab}	12.07	13.33
G13	91.47	100.03	8.27^{abcd}	7.20^{bcd}	9.47	11.33
G14	87.40	92.43	7.23^{d}	6.41^{d}	9.33	11.33
G15	94.30	100.03	8.88^{ab}	7.49^{bc}	11.63	12.27
Average location	95.01^{B}	100.74^{A}	8.11^{A}	7.31^{B}	10.71^{B}	12.25^{A}

Note: Values followed by the same letter within the same column are not significantly different according to the HSD test at the 5% significance level

Table 5. Average stem diameter of 15 sweet-waxy corn genotypes in two locations

Genotype	**Stem diameter (mm)**		**Average genotype**
	Bogor	**Lampung**	
G1	2.84	2.13	2.49^{a}
G2	2.09	2.05	2.07^{ab}
G3	2.04	1.86	1.95^{ab}
G4	1.94	1.87	1.90^{b}
G5	1.76	1.83	1.80^{b}
G6	2.08	2.08	2.08^{ab}
G7	2.23	2.19	2.21^{ab}
G8	1.98	1.09	1.94^{ab}
G9	2.58	1.98	2.28^{ab}
G10	1.99	2.12	2.06^{ab}
G11	2.03	2.13	2.08^{ab}
G12	2.19	2.02	2.10^{ab}
G13	1.99	1.86	1.93^{b}
G14	1.89	2.02	1.96^{ab}
G15	2.29	2.14	2.22^{ab}
Average location	2.12	2.01	

Note: Values followed by the same letter within the same column are not significantly different according to the HSD test at the 5% significance level

Table 6. Average ear diameter and ear length of 15 sweet-waxy corn genotypes in two locations

Genotype	**Ear diameter (mm)**		**Average genotype**	**Ear length (cm)**		**Average genotype**
	Bogor	**Lampung**		**Bogor**	**Lampung**	
G1	44.26^{a}	34.07^{abcd}	39.17^{abc}	19.76^{ab}	17.07^{bcde}	18.41^{b}
G2	43.66^{a}	26.93^{efg}	35.30^{bcd}	17.77^{bc}	14.77^{fg}	16.27^{de}
G3	33.98^{c}	26.00^{fg}	29.99^{e}	16.52^{c}	14.90^{efg}	15.71^{e}
G4	43.28^{a}	25.74^{g}	34.51^{cde}	17.45^{c}	14.59^{g}	16.02^{de}
G5	36.03^{bc}	23.33^{g}	29.68^{e}	16.90^{c}	14.45^{g}	15.68^{e}
G6	42.29^{ab}	27.78^{defg}	35.04^{bcd}	17.17^{c}	15.11^{defg}	16.14^{de}
G7	45.90^{a}	36.12^{ab}	41.01^{a}	19.98^{ab}	17.22^{bcd}	18.60^{ab}
G8	40.00^{abc}	29.05^{cdefg}	34.53^{cde}	17.47^{c}	15.99^{cdefg}	16.73^{cde}
G9	41.80^{ab}	25.58^{g}	33.69^{de}	17.43^{c}	15.40^{defg}	16.42^{de}
G10	44.67^{a}	33.57^{abcde}	39.12^{abc}	18.13^{bc}	17.94^{abc}	18.04^{bc}
G11	45.14^{a}	27.13^{defg}	36.14^{abcd}	17.10^{c}	14.67^{g}	15.88^{e}
G12	44.60^{a}	35.40^{abc}	40.00^{ab}	18.18^{bc}	16.92^{bcdef}	17.55^{bcd}
G13	40.95^{abc}	32.97^{abcdef}	36.96^{abcd}	18.63^{abc}	18.27^{ab}	18.45^{b}
G14	41.18^{ab}	29.20^{bcdefg}	35.19^{bcd}	16.93^{c}	16.67^{bcdefg}	16.80^{cde}
G15	43.65^{a}	37.80^{a}	40.73^{a}	20.56^{a}	19.76^{a}	20.16^{a}
Average location	42.09^{A}	30.04^{B}		18.00^{A}	16.25^{B}	

Note: Values followed by the same letter within the same column are not significantly different according to the HSD test at the 5% significance level

Ear diameter and length in sweet-waxy corn demonstrate a strong positive correlation with harvest weight. These traits significantly influence kernel filling within the ear, as larger ear diameters and greater lengths are associated with an increased number of kernels per ear. This relationship suggests that enhancing these characteristics can potentially augment overall yields in sweet corn production. Consequently, the identification of superior genotypes is not just important but crucial for optimizing final harvest outcomes.

The number of kernel rows per ear of sweet-waxy corn was found to be higher at the Bogor location compared to the Lampung location, with average counts ranging from 10.20 to 13.78 in Bogor and from 9.87 to 13.70 in Lampung (Table 7). Genotype G7 exhibited the highest average number of kernels per row at the Lampung site, with a value of 39.63, while genotype G10 had the lowest at 30.49. In contrast, at the Bogor location, genotype G11 showed the highest number of kernels per row at 45.43, while genotype G3 recorded the lowest at 29.92.

The number of kernel rows per ear and the number of kernels per row significantly influence the yield of sweet-waxy corn. The total number of kernel rows impacts the filling capacity within the ear, as an increase in kernel rows leads to a higher number of kernels developing, which can enhance the total ear weight due to the increased kernel count. Additionally, a greater number of kernels per row increases the potential total kernel count within the ear. Ears with more kernels per row are likely to yield a greater overall number of kernels, subsequently contributing to an increase in total ear weight. In general, the number of kernel rows per ear in this study ranged from 10 to 14, consistent with the typical range of 10 to 16 rows, which is usually an even number (Suriani et al. 2017). Furthermore, the trait of kernel row number in sweet-waxy corn is more strongly influenced by genetic factors than by environmental conditions.

The combined average values for ear weight with husk and without husk are presented in Table 8. The results indicate that the highest yields for both ear weight measurements were observed at the Bogor location. Genotype G12 exhibited the highest average weight for ear with husk at 297.91 g, while genotype G3 recorded the lowest average weight at 181.04 g. The highest weight for ears without husk was obtained from genotype G15, which measured 198.62 g and did not significantly differ from genotype G7. Conversely, genotype G3 had the lowest weight for ears without husk at 102.74 g. Ear weight can be influenced by several other yield-related traits, such as ear length, ear diameter, and the number of kernel rows (Fadhli et al. 2023).

The analysis results revealed that there were no significant differences in productivity among the genotypes at both locations (Table 9). The combined average values indicated that productivity at the Bogor location was higher than that at the Lampung location. Across both locations, genotype G7 exhibited the highest productivity at 17.88 tons per hectare, which did not significantly differ from G1 (17.25 tons per hectare), G12 (17.24 tons per hectare), and the comparison variety G15 (17.22 tons per hectare). In comparison to other corn types, the productivity of sweet-waxy corn is comparable to that of hybrid corn varieties commonly available in the market. Previous studies on sweet-waxy corn hybrids have reported productivity ranging from 10.03 to 16.51 tons per hectare (Aprilianti et al. 2016).

Cluster analysis

Cluster analysis is a statistical method used to classify groups based on the similarity of sample traits, resulting in the formation of clusters that share common characteristics. In this study, cluster analysis was conducted using Euclidean distance, which indicates that smaller Euclidean distances suggest that genotypes have more similar or closer values to one another. Conversely, larger Euclidean distances indicate greater differences or dissimilarities among the measured characteristics.

Table 7. The average number of rows and number of kernels per row of 15 sweet-waxy corn genotypes in two locations

Genotype	Number of rows		Average genotype	Number of kernels per row		Average genotype
	Bogor	Lampung		Bogor	Lampung	
G1	11.59^{cde}	12.67^{abc}	12.13^{cd}	43.80^{ab}	36.52^{ab}	40.16^{ab}
G2	12.00^{bcd}	12.35^{abc}	12.18^{cd}	43.77^{ab}	34.90^{ab}	39.34^{abc}
G3	10.20^{e}	9.87^{d}	10.04^{e}	29.92^{e}	35.13^{ab}	32.53^{d}
G4	12.35^{abcd}	11.66^{c}	12.01^{cd}	31.18^{de}	33.47^{ab}	32.33^{d}
G5	11.73^{bcde}	12.10^{abc}	11.92^{cd}	34.52^{cde}	33.40^{ab}	33.96^{cd}
G6	13.02^{abc}	12.40^{abc}	12.71^{abc}	38.62^{abcd}	31.91^{ab}	35.27^{bcd}
G7	11.78^{bcde}	11.88^{bc}	11.83^{cd}	39.73^{abc}	39.63^{a}	39.68^{abc}
G8	13.13^{abc}	11.67^{c}	12.40^{bcd}	39.50^{abcd}	31.90^{ab}	35.70^{abcd}
G9	13.07^{abc}	12.29^{abc}	12.68^{abc}	41.53^{abc}	31.57^{ab}	36.55^{abcd}
G10	13.32^{ab}	13.58^{ab}	13.45^{ab}	41.56^{abc}	30.49^{b}	36.03^{abcd}
G11	11.80^{bcde}	12.60^{abc}	12.20^{cd}	45.43^{a}	37.40^{ab}	41.41^{a}
G12	11.02^{de}	11.44^{cd}	11.23^{de}	36.64^{bcde}	36.43^{ab}	36.54^{abcd}
G13	11.20^{de}	11.33^{cd}	11.27^{d}	41.85^{abc}	33.63^{ab}	37.74^{abcd}
G14	11.53^{cde}	12.13^{abc}	11.83^{cd}	39.91^{abc}	31.03^{b}	35.47^{abcd}
G15	13.78^{a}	13.70^{a}	13.74^{a}	39.14^{abcd}	39.79^{a}	39.46^{abc}
Average location	12.1	12.11		39.14^{B}	34.48^{A}	

Note: Values followed by the same letter within the same column are not significantly different according to the HSD test at the 5% significance level

Table 8. Average ear weight with husk and ear weight without husk of 15 sweet-waxy corn genotypes in two locations

Genotype	Ear weight with husk (g)		Average genotype	Ear weight without husk (g)		Average genotype
	Bogor	Lampung		Bogor	Lampung	
G1	298.2	276.8	287.50^{ab}	186.67^{ab}	173.33^{ab}	180.00^{abc}
G2	269.51	213.49	241.50^{bcdef}	176.61^{ab}	134.29^{bcde}	155.45^{cde}
G3	204.11	157.97	181.04^{g}	114.46^{d}	91.02^{e}	102.74^{g}
G4	269.37	176.87	223.12^{defg}	166.20^{b}	97.89^{e}	132.04^{efg}
G5	207.36	192.14	199.75^{fg}	114.53^{cd}	110.83^{de}	112.68^{fg}
G6	252.91	234.16	243.54^{bcdef}	149.95^{bcd}	129.39^{bcde}	139.67^{ef}
G7	301.3	273.3	287.30^{ab}	211.11^{a}	167.49^{abc}	189.30^{ab}
G8	274.46	250.9	262.68^{abcde}	148.72^{bcd}	127.54^{cde}	138.13^{ef}
G9	294.44	246.64	270.54^{abcd}	165.10^{b}	129.19^{bcde}	147.15^{de}
G10	276.79	275.8	276.29^{abc}	172.36^{ab}	183.63^{a}	178.00^{abcd}
G11	296.59	248.43	272.51^{abcd}	175.00^{ab}	149.03^{abcd}	162.02^{bcde}
G12	300.79	295.03	297.91^{a}	181.18^{ab}	167.84^{abc}	174.51^{abcd}
G13	236.92	231.53	234.23^{cdef}	156.98^{bcd}	162.27^{abc}	159.63^{bcde}
G14	218.23	213.07	215.65^{efg}	159.35^{bc}	161.13^{abc}	160.24^{bcde}
G15	313.38	260.7	287.04^{ab}	214.96^{a}	182.28^{a}	198.62^{a}
Average location	267.62^{A}	236.46^{B}		166.21^{A}	144.48^{B}	

Note: Values followed by the same letter within the same column are not significantly different according to the HSD test at the 5% significance level

Table 9. The average productivity of 15 sweet-waxy corn genotypes in two locations

Genotype	Productivity (ton ha^{-1})		Average genotype
	Bogor	Lampung	
G1	17.89	16.61	17.25^{ab}
G2	16.17	12.81	14.49^{bcdef}
G3	12.24	9.48	10.86^{g}
G4	16.16	10.61	13.39^{defg}
G5	12.44	11.53	11.99^{fg}
G6	15.17	14.05	14.61^{bcdef}
G7	18.08	17.7	17.88^{a}
G8	16.47	15.05	15.76^{abcde}
G9	17.67	14.8	16.23^{abcd}
G10	16.61	16.55	16.58^{abc}
G11	17.79	14.9	16.35^{abcd}
G12	18.05	16.4	17.24^{ab}
G13	14.22	13.89	14.06^{cdef}
G14	13.09	12.78	12.94^{efg}
G15	18.08	15.64	17.22^{ab}
Average location	16.06^{A}	14.19^{B}	

Note: Values followed by the same letter within the same column are not significantly different according to the HSD test at the 5% significance level

The results of the analysis revealed three clusters that illustrate the similarities among sweet-waxy corn genotypes. Cluster I comprises genotypes G1, G7, G12, G2, G11, and G6, exhibiting a similarity level of 48.16-82.97%. Cluster II includes genotypes G10 and G15, with a similarity level of 66.44%. Meanwhile, Cluster III consists of genotypes G9, G3, G5, G14, and G13, showing a similarity level of 47.36-62.46% (Figure 1). The prominent differences distinguishing the clusters are characterized by traits such as ear weight without husk, ear diameter, number of kernels per row, plant height, and ear height.

A similarity level exceeding 80% suggests that the tested genotypes likely originate from the same lineage. Upon examining the parental lines utilized, it is evident that genotypes G7 and G12 share a common maternal lineage. The observed differences in diversity and genetic clustering may be attributed to variations in the number and types of traits measured, as well as the genetic variability among the genotypes employed in each trial (Heryanto et al. 2022). Such variations can significantly influence the results of cluster analysis or genetic grouping, as distinct traits and diverse genetic backgrounds can lead to different clustering patterns, depending on the analytical methods utilized.

Variance components and heritability

The estimated values for variance components and broad-sense heritability of sweet-waxy corn across two locations are summarized in Table 10. The Genotypic Coefficient Of Variation (GCV) serves as an important parameter for quantifying genetic variability within a population. In comparison, the phenotypic coefficient of variation (PCV) assesses the extent of phenotypic variability. The analysis revealed that for all traits assessed in sweet-waxy corn, the GCV values were consistently lower than the PVC values (Fadhli et al. 2023). This finding indicates that the observed trait variation is predominantly influenced by environmental factors rather than genetic factors, corroborating the results of (Pangestu et al. 2023).

In this study, the GCV and PCV values were classified as low to moderate. Notably, the traits of ear height (15.97% and 16.69%) and ear weight without husk (11.12% and 13.03%) were categorized within the moderate variability range, while other traits exhibited low variability. The low GCV and PCV values suggest that the observed traits demonstrate comparable variability within the population (Sadimantara et al. 2021). Conversely, high GCV and PCV values indicate substantial variability in specific traits, suggesting that traits exhibiting high variability are amenable to effective improvement through selective breeding (Terfa and Gurmu 2020).

Heritability represents the proportion of genetic variance relative to phenotypic variance. The criteria for determining broad-sense heritability values follow the guidelines established by Stansfield (1991), categorizing heritability as high if H²bs>50%, moderate if 20%≤H²bs≤50%, and low if H²bs<20%. The analysis results indicated that the heritability values of the tested traits fall within the low to high range, specifically from 12.87% to 92.29%. Traits classified as having high broad-sense heritability include plant height, ear height, leaf width, leaf length, leaf number, kernel rows per ear, ear diameter, ear length, and ear weight without husk. The stem diameter was categorized as having moderate heritability at 50.00%.

Conversely, the number of kernels per row exhibited low heritability at 12.87%. This is different from other types of corn, as research by Heryanto et al. (2022) indicates that in sweet corn, traits such as plant height, ear height, leaf width, leaf length, and ear weight with husk show high heritability values. Meanwhile, traits such as stem diameter, leaf number, ear diameter, and ear length exhibit low heritability values. In contrast, in waxy corn, high heritability values are found for traits such as plant height, number of leaves, ear length, ear diameter, and productivity (Edy et al. 2020). High or low heritability affects breeding strategies by determining the influence of genetic factors on trait expression and guiding the focus on genetic selection or environmental management.

Table 10. Variance value components, coefficient of diversity, and heritability

Traits	σ^2e	σ^2g	$\sigma^2_{G\times E}$	σ^2p	GCV	PCV	H^2bs
Plant height	289.880	296.725	133.763	411.920	7.99^{L}	9.42^{L}	72.03^{H}
Ear height	114.780	331.202	23.080	361.872	15.97^{M}	16.69^{M}	91.52^{H}
Stem diameter	0.070	0.015	0.007	0.030	5.92^{L}	8.37^{L}	50.00^{M}
Leaf width	0.130	0.243	0.040	0.285	6.40^{L}	6.92^{L}	85.38^{H}
Leaf length	9.320	16.468	0.033	18.005	4.15^{L}	4.34^{L}	91.47^{H}
Number of leaves	0.650	0.878	0.070	0.952	8.16^{L}	8.50^{L}	92.29^{H}
Number of rows	0.340	0.685	0.117	0.800	6.88^{L}	7.43^{L}	85.63^{H}
Number of kernels per row	8.200	0.990	10.670	7.692	2.90^{L}	8.08^{L}	12.87^{L}
Ear diameter	5.600	8.668	5.343	12.273	7.05^{L}	8.39^{L}	70.63^{H}
Ear length	0.560	1.552	0.300	1.795	6.97^{L}	7.49^{L}	86.44^{H}
Ear weight with husk	606.040	1103.922	122.997	1266.427	13.18^{M}	14.12^{M}	87.17^{H}
Ear weight without husk	225.310	298.295	148.240	409.967	11.12^{M}	13.03^{M}	72.76^{H}

Note: σ^2e: Environmental variance; σ^2g: Genotypic variance; $\sigma^2_{G\times E}$: Interaction genotypic and environmental variance, σ^2p: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation, H^2bs: Broad-sense heritability, L: Low; M: Moderate; H: High

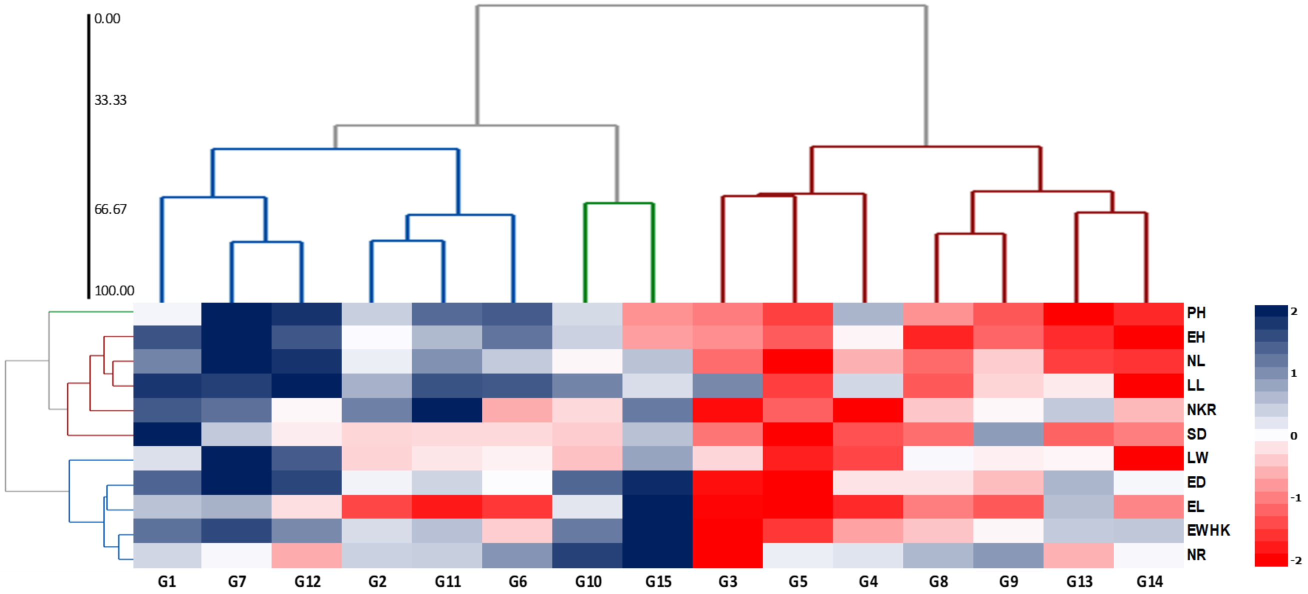

Figure 1. Cluster analysis of 15 sweet-waxy corn genotypes using quantitative traits. PH: Plant height, EH: ear height, SD: Stem diameter, LW: Leaf width, LL: Leaf length, NL: Number of leaves, NR: Number of rows, NKR: Number of kernels per row, ED: Ear diameter, EL: Ear length, EWHK: Ear weight without husk

The high broad-sense heritability values indicate that genetic factors more influence these traits than by environmental factors (Marwan et al. 2022). In contrast, traits with low heritability are predominantly influenced by environmental conditions (Kuswantoro et al. 2021). High heritability values suggest that selection can be effectively conducted early in the breeding process. Furthermore, selection based on high broad-sense heritability is easier compared to traits with low heritability (Sushmitha et al. 2024). This information is particularly valuable as it facilitates breeders' selection of optimal traits for crop improvement. Thus, breeders need to consider heritability when designing breeding programs while also considering environmental factors that could influence selection results and the improvement of traits.

Correlation analysis of sweet-waxy corn

The correlation analysis was conducted to investigate the relationships among various parameters and to identify factors influencing the weight of the ear without husk. The results of the correlation analysis for sweet-waxy corn across two locations are illustrated in Figure 2. The weight of the ear without husk exhibited a significant positive correlation with all observed traits, including plant height (r = 0.31), ear height (r = 0.41), stem diameter (r = 0.46), leaf width (r = 0.52), leaf length (r = 0.31), leaf number (r = 0.57), total kernel count (r = 0.46), kernels per row (r = 0.57), ear diameter (r = 0.88), and ear length (r = 0.78). These results indicate that the increase in the weight of the ear without husk in sweet-waxy corn is attributed to all traits that enhance yield. This finding is consistent with the study conducted by Aman et al. (2020), which also demonstrated that several traits significantly positively influence yield.

Direct and indirect effects on sweet-waxy corn

Path analysis is a multivariate analytical method employed to examine the direct and indirect effects of one trait on another, offering insights that cannot be detailed through correlation analysis alone. This methodology provides accurate information regarding the contributions of various traits and serves as a foundational basis for trait selection aimed at enhancing yield. Its particular value lies in its ability to identify optimal secondary traits, enhancing the practical benefits of trait selection. It is considered a more sophisticated approach compared to regression analysis, as it effectively maps the direct effects of these traits (Fadhli et al. 2023). The results of the path analysis for sweet-waxy corn, specifically regarding the weight of the ear without husk, are summarized in Table 11. According to Lenka and Mishra (1973), the path analysis effect values can be classified into five categories: negligible (0-0.09), low (0.10-0.19), moderate (0.20-0.29), high (0.30-0.99), and very high (≥1.00).

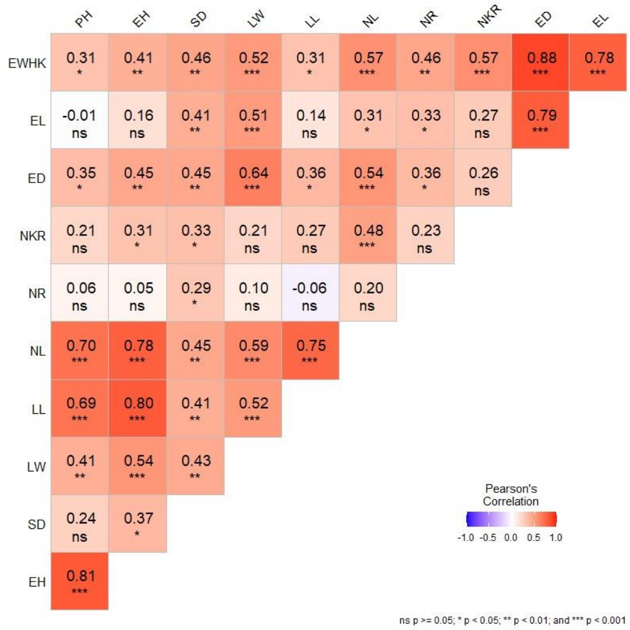

Figure 2. Correlation analysis of 15 sweet-waxy corn genotypes for quantitative traits. PH: Plant height; EH: Ear height; SD: Stem diameter; LW: Leaf width; LL: Leaf length; NL: Number of leaves; NR: Number of rows; NKR: Number of kernels per row; ED: Ear diameter; EL: Ear length; EWHK: Ear weight without husk

Table 11. Direct and indirect effects of sweet-waxy corn on ear weight without husk characters

Traits	Direct effect	Indirect effect										
		PH	EH	SD	LW	LL	NL	NR	NKR	ED	EL	xry
PH	0.066^{ns}	-	-0.013	-0.005	-0.034	-0.034	0.029	0.005	0.071	0.227	-0.002	0.31
EH	-0.016^{ns}	0.054	-	-0.008	-0.045	-0.039	0.033	0.004	0.105	0.292	0.032	0.41
SD	-0.021^{ns}	0.016	-0.006	-	-0.036	-0.020	0.019	0.024	0.111	0.292	0.081	0.46
LW	-0.083^{ns}	0.027	-0.009	-0.009	-	-0.026	0.025	0.008	0.071	0.415	0.101	0.52
LL	-0.049^{ns}	0.046	-0.013	-0.009	-0.043	-	0.031	-0.005	0.091	0.233	0.028	0.31
NL	0.042^{ns}	0.046	-0.013A	-0.009	-0.049	-0.037	-	0.017	0.162	0.350	0.061	0.57
NR	0.084^{ns}	0.004	-0.001	-0.006	-0.008	0.003	0.008	-	0.078	0.233	0.065	0.46
NKR	0.338**	0.014	-0.005	-0.007	-0.017	-0.013	0.020	0.019	-	0.168	0.053	0.57
ED	0.648**	0.023	-0.007	-0.009	-0.053	-0.018	0.023	0.030	0.088	-	0.156	0.88
EL	0.198**	-0.001	-0.003	-0.009	-0.042	-0.007	0.013	0.028	0.091	0.512	-	0.78

Notes: PH: Plant height; EH: Ear height; SD: Stem diameter; LW: Leaf width; LL: Leaf length; NL: Number of leaves, NR: Number of rows; NKR: Number of kernels per row; ED: Ear diameter; EL: Ear length

The analysis results indicate that three traits exert significant direct effects on the weight of the ear without husk. These traits are ear diameter (0.648), kernels per row (0.338), and ear length (0.198). This finding suggests that improvements in these traits can enhance the yield of sweet-waxy corn. Correlation analysis also shows that these direct traits have a high positive correlation, making them suitable references for selecting optimal secondary traits in the best genotypes. This is consistent with the research conducted by Yahaya et al. (2021) on both sweet-waxy corn and waxy corn, which demonstrates that the traits of kernels per row, ear diameter, and ear length have significant direct effects on yield. Path analysis, particularly for sweet-waxy corn, is relatively rare. Thus, further development and research are needed to explore the interactions of traits that are beneficial for selection.

In addition to their direct effects, the traits also exhibit indirect effects on the weight of the ear without husk in sweet-waxy corn. Specifically, kernels per row and ear length demonstrate indirect effects through ear diameter, with coefficients of 0.233 and 0.168, respectively. This indicates that improvements in the weight of the ear without husk may result from the traits of kernels per row and ear length mediated by ear diameter.

Another trait that can be considered for indirect selection is leaf width, which positively influences the weight of the ear without husk through ear diameter, with a coefficient value of 0.415. This indicates that each unit increase in leaf width results in a 0.415 increase in ear diameter, which subsequently contributes to an increase in the weight of the ear without husk in sweet-waxy corn. Efficient selection can be achieved when it is conducted early in the observation process. The results of the study indicate that leaf area has a significant impact on maize yield. An increase in leaf area enhances the plant's photosynthetic capacity, thereby enabling greater energy production. This energy is subsequently allocated to various plant tissues, particularly the ear. As a result, this contributes to higher maize yield, both in terms of the number of kernels per ear and the ear size. Therefore, in maize breeding programs, selecting genotypes with optimal leaf area may serve as an effective strategy to improve yield potential (Yang et al. 2022).

The analysis reveals a residual effect in the path analysis of 0.2742, indicating that 72.58% of the variance in the weight of the ear without husk can be explained by the studied traits. Conversely, 27.42% represents the residual direct effects that have not been accounted for in traits yet to be identified (Aman et al. 2020). The small residual effect value suggests that the traits included in this study explain a significant percentage of the variation in the weight of the ear without husk.

In conclusion, genotypes G1, G7, and G12 exhibit advantages in ear weight without husk and high productivity due to efficient photosynthesis and optimal resource utilization. These genotypes possess morphological and physiological traits that support the formation of larger diameters and more kernels, with good adaptation to environmental conditions. Therefore, G1, G7, and G12 are promising candidates for development in sweet-waxy corn breeding programs. Traits with moderate broad-sense heritability include ear height, ear weight with husk, and ear weight without husk. All observed traits demonstrated high broad-sense heritability, except for stem diameter, which showed moderate heritability, and kernel number per row, which exhibited low heritability. All traits showed significant positive correlations. Traits with a direct and positive impact on ear weight without husk include kernel number per row, ear diameter, and ear length. Leaf width has an indirect effect on ear weight without husk through ear diameter. Therefore, these traits are considered suitable criteria for selection in sweet-waxy corn breeding programs.

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