

Morphological parameters, heritability, yield component correlation, and multivariate analysis to determine secondary characters in selecting hybrid maize

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Abstract. *Fadhli N, Farid M, Azrai M, Nur A, Efendi R, Priyanto SB, Nasruddin AD, Novianti F. 2023. Morphological parameters, heritability, yield component correlation, and multivariate analysis to determine secondary characters in selecting hybrid maize. Biodiversitas 24: 3750-3757.* Direct selection for grain yield traits in maize (*Zea mays* L.) is often inefficient under specific conditions, necessitating the accurate determination of secondary traits to facilitate implementation and enhance selection precision. This study aimed to examine the morphological parameters, heritability, yield component correlations, and multivariate analysis of hybrid maize for determining potential secondary traits through indirect selection. The experimental design employed a randomized complete block design (RCBD) comprising 17 genotypes, including 15 hybrid maize lines and 2 hybrid maize varieties (RK 457 and RK 57). The results revealed that weight of harvested cob character and yield traits demonstrated significant correlations with production. Correlation values were further analyzed using biplot analysis and path analysis to identify potential secondary traits. The principal component biplot analysis results indicated four characters as effective secondary traits for selection, namely weight of harvested cob, yield, weight of 1000 seeds, and moisture content. MSM53/BCY as a parent of JHD 05 displayed superior performance compared to the two commercial hybrid varieties. Based on path analysis results, the weight of harvested cob character exhibited the highest direct effect on production with a value of 0.93, indicating that weight of harvested cob is the best secondary trait for selection.

Keywords: Correlation, heritability, multivariate analysis, secondary characters, *Zea mays*

INTRODUCTION

Maize (*Zea mays* L.) is a carbohydrate-producing food crop for most of the world's population, widely used for food, feed, and bioethanol productivity for human and animal needs. Population growth and industrial development have a direct impact on the increased demand for maize (Badr et al. 2020; Sah et al. 2020). In Indonesia, national maize demand has reportedly increased annually. Maize demand in 2018 amounted to 14.37 million tons, rising to 23 million tons in 2021 and 23.1 million tons in May 2022 (Rifai et al. 2023). Efforts to increase maize productivity are essential to reduce import quotas in Indonesia. Therefore, efforts to enhance domestic maize productivity are needed. One approach to augment maize production involves utilizing high-quality seeds that can adapt well (El-Latif et al. 2023).

Plant breeding aims to improve and enhance the genetic potential of plants, resulting in new varieties better than their parents (Razzaq et al. 2021; Sanchez et al. 2023). Maize has a significant impact on food crop productivity, playing a crucial role in global food security (Rahman and

Connor 2022). The efficiency of a breeding program can be improved by considering genetic and phenotypic diversity, heritability, and trait correlations at each stage (Nzuve et al. 2014; Kuswantoro 2017). The introduction of hybrid varieties has facilitated productivity and quality improvements in maize cultivation (Hossain et al. 2022).

A critical factor in plant breeding is determining genetic diversity. A base population with high diversity can increase the likelihood of desired trait combinations (Begna 2021). Genetic diversity is crucial for plant improvement, providing a foundation for analyzing combining ability and genotype inbred heterosis (Li et al. 2021; Madobe et al. 2021). The level of genetic diversity among available breeding materials determines the potential success of a breeding program, offering opportunities to develop new plants with desired characteristics that are preferred by farmers (Terfa and Gurmu 2020; Zawadi et al. 2021). Character improvement through direct selection can be implemented for traits with high genetic diversity marked through heritability values (Gesteiro et al. 2023).

Heritability degree is an essential component to consider in plant breeding, providing an overview of the

genetic variance proportion to the phenotypic variance inherited by offspring (Bartaula et al. 2019). Heritability and genetic selection are prerequisites for initiating breeding programs to develop high-yielding hybrid maize varieties (Schmidt et al. 2019; Muliadi et al. 2021). Heritability estimation is useful in breeding quantitative traits because it can be used to determine effective selection strategies and breeding methods for use in breeding programs and to predict selection progress (Priyanto et al. 2023).

The coefficient of correlation values between traits is crucial in selection. Correlation coefficients provide an overview of the relationship between traits and offer valuable information about the level and direction of selection (Aman et al. 2020). Correlation coefficients give an insight into the simple relationship between traits (Anshori et al. 2019). Knowing the correlation between traits is essential in breeding to identify superior genotypes with higher yields through indirect selection, which can be achieved through secondary trait selection (Meseka et al. 2013).

The effectiveness of selection methods in maize is also determined by selection criteria, and determining secondary traits requires equally precise statistical approaches (Suwanti et al. 2022). Multivariate analysis can simplify, reduce, and predict complex data (Matjik and Sumertajaya 2011). Principal components have been utilized as an essential multivariate analysis tool for evaluating various relationships among combinations of test plant characters (Walubita et al. 2022). Therefore, this study aimed to investigate the morphological parameters, heritability, yield component correlations, and multivariate analysis of hybrid maize for determining potential secondary traits through indirect selection.

MATERIALS AND METHODS

Research site

The study was conducted in the Tompobulu District, Maros Regency, South Sulawesi, Indonesia. from February to May 2022. The study area was at an altitude of 115 m above sea level with coordinates 5°08'10"S - 119°38'36"E, and the type of rainfall was C1 according to the Oldeman climatic classification. Rainfall at the time of the study in the field was in the range of 310-758 mm per month (BMKG 2022).

Plant materials

The genetic materials utilized in this study consisted of 17 genotypes (15 hybrid maize lines and 2 commercial hybrid maize varieties (RK 457 and RK 57) (Table 1). These genotypes exhibited characteristics of the dent and semi-dent seed types, and possessing large sizes. Consequently, they were regarded as having high starch quality, making them suitable for application in the food industry. Observed was performed on 10 maize plants for each genotype. The maize lines from the Cereals Plant Instrument Standard Testing Center, Maros, South Sulawesi, Indonesia.

Procedures

The experimental design used a randomized block design consisting of 17 genotypes and was repeated three times, resulting in a total of 51 experimental units. Maize seeds were planted in plots measuring 5 x 3 m with a spacing of 75 x 20 cm. Each planting hole consisted of one seed adjusted to the genotype label. Maintenance in this study included irrigation, fertilization, and weeding. The applied fertilizer used urea at a dose of 150 kg ha⁻¹ and NPK at 15:15:15 at a dose of 300 kg ha⁻¹ at 10 days after planting and urea at a dose of 200 kg ha⁻¹ at 30 days after planting.

Observed variables included length of cob, diameter of cob, number of rows per cob, number of grains per cob row, weight of harvested cob, moisture content, weight of 1000 seeds, seed weight, yield, and productivity. Observation technique refers to the technical guidelines for observing maize adaptation trials (CIMMYT 1994).

Data analysis

The data observed were subsequently analyzed through a series of analytical stages. Initially, variance analysis was conducted using the analysis of variance (ANOVA) method, with a standard error of 5%. Furthermore, the data analysis results are used to find heritability (h²) values. The calculated h² value was broad-sense heritability, according to Jain and Allard (1960) as follows:

$$\text{Heritability (h}^2\text{)} = \sigma^2g/\sigma^2p$$

Where: σ^2g is genetic variance and σ^2p is phenotypic variance.

Table 1. Pedigree of the 17 evaluated hybrid crosses

Rank	Genotypes	Pedigree
	Hybrids	
1	JHD 01	BCY/G102612D
2	JHD 02	GLT226/G1102612D
3	JHD 03	GLT226/ERC24
4	JHD 04	P2/G102612D
5	JHD 05	MSM53/BCY
6	JHD 06	MSM53/P2
7	JHD 07	MSM53/ERC24
8	JHD 08	P2/BCY
9	JHD 09	P2/ERC24
10	JHD 10	ERC24/G102612D
11	JHD 11	MSM53/G102612D
12	JHD 12	GLT226/BCY
13	JHD 13	ERC24/BCY
14	JHD 14	GLT226/MSM 53
15	JHD 15	GLT226/P2
	The commercial hybrid maize	
16	RK 457	PASL14/PASL21
17	RK 57	PASL2531/PASL2524

Subsequently, the h^2 values were grouped according to Stansfield and Hansen (1983) as follows: $h^2 > 0.50$ with high heritability, $0.20 \leq h^2 \leq 0.50$ with moderate heritability, and $h^2 < 0.20$ with low heritability. All yield component traits were then correlated using Pearson correlation, followed by principal component biplot analysis. Traits in the same group as productivity were further analyzed using path analysis to identify the character with the highest direct influence to be selected as the best secondary trait. If the secondary character has a significant correlation, the analysis is continued with the selection of the best genotype using the Tukey test at the 5% level. ANOVA, biplot of principal component analysis, and Tukey tests were performed using STAR 2.0.1 (IRRI 2014). Meanwhile, correlation coefficients and path analysis were performed using Excel (Akintunde 2012).

RESULTS AND DISCUSSION

Morphological parameters

The analysis of variance results show that almost all characters are significantly influenced by genotype, except for seed weight (Table 2). The greater the ratio between genotypic variance and error variance, the more evident the character's diversity. Genotypic variance has a significant effect on 1% (**) on length of cob, diameter of cob, number of rows per cob, number of grains per cob row, moisture content, weight of 1000 seeds, yield, and productivity. Meanwhile, weight of harvested cob has a significant effect on 5% (*). However, the observed diversity needs to be further studied to determine the diversity value caused by genetic or environmental factors.

The environment has a strong influence on the expected diversity, which will become more common with the emergence of climate change (Jackson et al. 2022). The coefficient of variance (CV) values for the observed traits ranged from 1.79% to 10.47%. The CV value provides an overview of the diversity within the population (Kumar et al. 2022). The smaller the CV value, the stronger the character selection in predicting plant populations at different growth stages (Nardino et al. 2020). The CV value is often used by maize plant breeders as an alternative method in the selection process, providing an overview of diversity in a population (Patel et al. 2023). Variance interaction indicates differences in response between each genotype (Alharbi et al. 2019), which forms the basis for character selection (Akbar et al. 2019; Fikri et al. 2023). Therefore, characters significant in the analysis of variance are continued for further analysis.

Heritability

The heritability values are in the range of 0.30 (WHC) - 0.82 (NRC), with almost all yield component heritability values falling within the high category (Table 3). Characters with moderate heritability criteria are weight of harvested cob and productivity with values of 0.30 and 0.38, respectively. Meanwhile, the highest heritability

value is manifested for the character of the number of rows per cob with a value of 0.82, followed by length of cob with a value of 0.76. High heritability values allow plant breeders to decide the direction of selection (Bartaula et al. 2019), which will be used as a guide in selection (Tessema et al. 2022).

Traits with high heritability have a high probability of being inherited (Marwan et al. 2022). Meanwhile, if the heritability value is low, selection can be done in advanced generations using pedigree, single seed descent, and progeny test methods (Kanbar et al. 2011). The low heritability value obtained for the observed characters indicates the influence of the environment rather than genetic factors on the character (Dochtermann et al. 2019; Mustakim et al. 2019).

Heritability estimation helps plant breeders in genotype selection from genetic diversity (Terfa and Gurmu 2020). Breeders can develop more suitable cultivars more quickly when they have access to information about heritability, genetic progress, and the influence of the environment on the expression of displayed characters (Al-Daej 2022). This heritability estimation has been proven by previous studies, such as Merrick et al. (2022) reported heritability estimation in plant breeding programs, and Egeland (2023) stated heritability estimation can provide relevant information. Therefore, heritability estimation of yield component traits can be the basis for further analysis in selecting genotypes according to the desired character.

Correlation coefficient analysis

The correlation coefficient in plant breeding programs can provide an overview of the simple relationship between characters, both in the same direction (positive correlation) and in the opposite direction (negative correlation) (Kuswantoro 2017). The weight of harvested cob (WHC) and yield (Y) have a significant correlation with productivity, indicating that these characters have a high relationship with productivity with values of 0.72 and 0.48, respectively (Table 4). Therefore, these characters should be prioritized when selecting for increased productivity (Devasree et al. 2020; Nithya et al. 2020).

Table 2. Analysis of variance and morphological parameters of observed characters

Characters	MS genotype	MS error	CV (%)
Length of cob	3.73 **	0.37	3.96
Diameter of cob	7.27 **	0.74	1.79
Number of rows per cob	2.63 **	0.18	2.87
Number of grains per cob row	14.38 **	2.60	4.81
Weight of harvested cob	0.64 *	0.28	6.64
Moisture content	17.01 **	1.90	3.76
Weight of 1000 seeds	17.33 **	3.30	4.44
Seed weight	0.06 ns	0.04	10.47
Yield	13.30 **	3.18	2.28
Productivity	0.57 **	0.20	6.77

Note: **significant effect on 1%, *significant effect on 5%, NS: non-significant, MS: mean square, CV: coefficient of variance

Table 3. Estimates of genetic variance, phenotypic variance, environmental variance, and heritability of maize yield component traits

Characters	LC	DC	NRC	NGR	WHC	MC	W1000	Y	P
Genetic variance	1.12	2.18	0.82	3.93	0.12	5.04	4.68	3.37	0.12
Phenotypic variance	1.49	2.92	1.00	6.53	0.40	6.94	7.98	6.55	0.32
Environmental variance	0.37	0.74	0.18	2.60	0.28	1.90	3.30	3.18	0.20
Heritability	0.76 (H)	0.75 (H)	0.82 (H)	0.60 (H)	0.30 (M)	0.73 (H)	0.59 (H)	0.51 (H)	0.38 (M)

Note: LC: length of cob, DC: diameter of cob, NRC: number of rows per cob, NGR: number of grains per cob row, WHC: weight of harvested cob, MC: moisture content, W1000: weight of 1000 seeds, Y: yield, P: productivity, H: high, M: moderate

Table 4. Pearson correlation coefficients among maize yield components

Characters	LC	DC	NRC	NGR	WHC	MC	W1000	Y	P
LC	1.00								
DC	-0.44	1.00							
NRC	-0.07	0.71**	1.00						
NGR	0.72**	-0.41	-0.06	1.00					
WHC	0.04	0.24	-0.13	-0.02	1.00				
MC	0.18	-0.13	-0.09	0.06	0.38	1.00			
W1000	0.24	-0.22	-0.27	-0.31	0.18	0.29	1.00		
Y	0.14	-0.30	-0.31	0.03	0.03	-0.08	0.14	1.00	
P	-0.01	0.17	-0.21	-0.03	0.72**	-0.24	0.05	0.48*	1.00

Note: **significant effect on 1%, *significant effect on 5%, LC: length of cob, DC: diameter of cob, NRC: number of rows per cob, NGR: number of grains per cob row, WHC: weight of harvested cob, MC: moisture content, W1000: weight of 1000 seeds, Y: yield, P: productivity

Correlation coefficient analysis is often used to measure the degree and direction of the relationship between characters, including productivity. The correlation coefficient can measure how strong the relationship is between two variables (Sadeghi 2022). This is very useful for designing, evaluating, and developing selection criteria for the desired traits (Khan et al. 2022). Correlation between characters is essential for helping identify superior genotypes with high production through secondary character selection (Amegbor et al. 2022). The use of correlation coefficient analysis has also been reported in several studies, such as Epule et al. (2022) in maize yield and harvest area, and Akfindarwan et al. (2023) in selection criteria for the S2 maize.

Principal component analysis

Based on the principal component analysis (PCA), the proportion for Principal Component 1 (PC1) is 0.27, and for Principal Component 2 (PC2) is 0.22. PC1, accounting for 27.00% of the observed variability, is primarily responsible for the observed variability (Table 5). According to Mattjik and Sumertajaya (2011), PC1 and PC2 are well-suited dimensions for constructing a selection index, based on the principle that their eigenvalues, which are greater than 1, with values of 2.46 and 2.02, respectively, can explain the cumulative factor and diversity between characters. This concept is also endorsed by Maulana et al. (2023) in the selection of maize mutants under different cropping systems, and Tessema et al. (2022) in the study of genetic variability in potato plants.

Thus, the magnitude of the eigenvalue can estimate the accuracy of the PCA (Anshori et al. 2022). Kaviriri et al. (2023) suggest that an eigenvalue of 1 is the effective limit of dimensionality in aggregating diversity between

characters. Therefore, the eigenvalue can be utilized as a fundamental metric in the selection process.

Multivariate analysis used to identify the best secondary traits is principal component biplot analysis and path analysis. Principal component-based biplot analysis is an analysis that can be used to analyze or integrate large variable data into simpler two-dimensional data (Oyedele 2020). Principal component analysis (PCA) can simplify, reduce, and predict relationships among multiple variables (Wang et al. 2022). This analysis has been widely reported by several researchers in determining secondary traits, as reported by Anshori et al. (2019) in rice under salinity stress, Fadhlí et al. (2020) in maize tolerance to drought stress, and Leite et al. (2022) in selection popcorn genotype. This makes it easier to identify traits with the same character variation as the main traits (Kose et al. 2018; Femenias et al. 2022).

Based on the results of principal component biplot analysis, weight of harvested cob, yield, weight of 1000 seeds, and moisture content have the same clustering with productivity (Figure 1). These four characters can be used as effective secondary traits in selection. Based on the interpretation of principal component biplot analysis, weight of harvested cob, yield, weight of 1000 seeds, and moisture content can be used for path analysis. The application of multivariate analysis such as correlation, principal component biplot analysis, and path analysis is an effective evaluation package for selecting secondary characters. This method has been applied in hydroponic wheat (Farid et al. 2021) and maize (Sinana et al. 2023). Based on both studies, the use of path analysis as a selection index is considered quite effective in determining the desired best secondary characteristics.

Table 5. Principal component analysis of maize yield component

Variable	PC1	PC2
Eigenvalue	2.46	2.02
Proportion	0.27	0.22
Cumulative	0.27	0.50

Note: PC: principal component

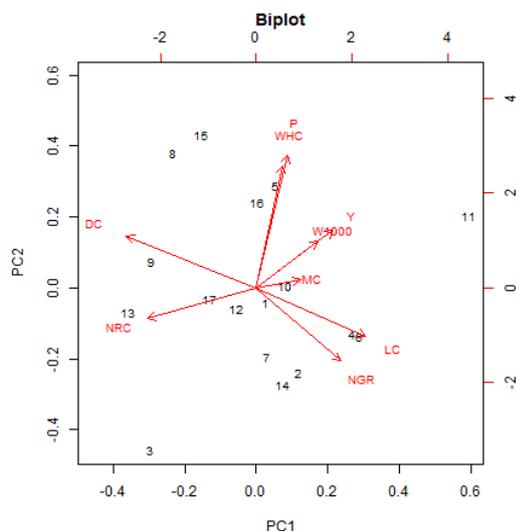


Figure 1. Principal component-based biplot analysis of maize yield component traits. LC: length of cob, DC: diameter of cob, NRC: number of rows per cob, NGR: number of grains per cob row, WHC: weight of harvested cob, MC: moisture content, W1000: weight of 1000 seeds, Y: yield, P: productivity.

Path analysis

Based on the path analysis, the moisture content and weight of 1000 seeds have a negative correlation with productivity, with values of -0.56 and -0.01, respectively (Table 6). This result shows that moisture content and weight of 1000 seeds have an opposite response to weight of harvested cob and yield. Maize production requires low seed moisture content at harvest. However, as a complex quantitative trait, understanding the genetic mechanism of seed moisture content remains a critical gap, especially in hybrids (Dong et al. 2023). The weight of 1000 seeds is

determined by the shape and size of seeds. Seed size is one of the most important traits determining crop yield (Duan et al. 2022). Seed characteristics have different dimensions, causing each seed type to have a different weight (Loon et al. 2020). In these results, weight of harvested cob and yield show the largest significant direct effects on productivity, with values of 0.93 and 0.41, respectively. The response of these two characters is in line with each other. If a character has a direct influence value on the main character that is almost the same, then selection through that character is effective and efficient to carry out (Jakhar et al. 2017; Yahaya et al. 2021). An increasing weight of harvested cob is related to increased productivity, meaning this character can be used as the best secondary character in selecting hybrid maize genotypes.

Path analysis is a multivariate analysis that can analyze and test in more detail the relationships between a set of observed characters. This analysis is effective for partitioning correlation coefficients into direct and indirect effects (Baye et al. 2020). Path analysis provides information about cause and effect in understanding the causes of relationships between two variables (Rajput 2019). This is very useful for determining the best secondary characters, as it is considered a more complex technique compared to ordinary regression, especially for direct effect variables (Faot et al. 2019; Leite et al. 2022). Direct effects are variable indicators of the magnitude of the variation of a character directly influencing the main character's variation (Manjunatha et al. 2018; Al-Amin et al. 2019; Guo et al. 2023).

Selected yield component

Based on the recapitulation of selected yield components, several hybrids from each line show results that meet or exceed the current commercial hybrid varieties (Table 7). MSM53/BCY performs better than both commercial maize hybrid varieties, providing a value of 8.06 kg for weight of harvested cob, 31.00% for moisture content, 40.90 g for the weight of 1000 seeds, and 81.18% for yield. Genotype response to the environment determines hybrid yield superiority in testing (Jackson et al. 2022; Yue et al. 2022). MSM53/BCY has a productivity potential with a value of 7.59 t ha⁻¹, exceeding both current commercial varieties (RK 457 and RK 57) with values of 6.78 t ha⁻¹ and 6.63 t ha⁻¹, respectively, and can be recommended as a candidate variety with high productivity.

Table 6. Path analysis of maize yield component traits in determining the best secondary traits

Characters	DE	WHC	MC	W1000	Y	Residual
WHC	0.93		-0.22	-0.00	0.01	0.23
MC	-0.56	0.36		-0.00	0.03	0.23
W1000	-0.01	0.17	-0.16		0.06	0.23
Y	0.41	0.03	0.04	-0.00		0.23

Note: DE: direct effect, WHC: weight of harvested cob, MC: moisture content, W1000: weight of 1000 seeds, Y: yield

Table 7. Selected yield component characters based on PCA and Path Analysis interpretation

Genotype	WHC (kg)		MC (%)		W1000 (g)		Y (%)		P (t ha ⁻¹)	
BCY/G102612D	7.57	ab	38.87	a	42.15	ab	78.71	abcd	6.15	b
GLT226/G1102612D	7.75	ab	37.67	abcd	43.76	a	74.81	cd	6.07	b
GLT226/ERC24	6.92	b	33.73	cde	38.75	abc	77.37	abcd	5.99	b
P2/G102612D	7.81	ab	39.27	a	41.43	ab	79.71	abc	6.38	ab
MSM53/BCY	8.06	ab	31.00	e	40.90	abc	81.18	ab	7.59	a
MSM53/P2	7.72	ab	37.40	abcd	39.24	abc	78.75	abcd	6.37	ab
MSM53/ERC24	7.87	ab	38.23	ab	37.80	bc	76.59	bcd	6.34	ab
P2/BCY	8.33	ab	36.73	abcd	41.92	ab	77.92	abcd	6.82	ab
P2/ERC24	8.10	ab	33.53	de	35.47	c	77.70	abcd	6.92	ab
ERC24/G102612D	8.16	ab	38.80	a	41.40	ab	77.72	abcd	6.52	ab
MSM53/G102612D	8.44	ab	37.40	abcd	43.80	a	82.20	a	7.31	ab
GLT226/BCY	7.93	ab	34.53	bcde	43.63	a	74.17	d	6.38	ab
ERC24/BCY	8.12	ab	37.53	abcd	41.17	ab	77.56	abcd	6.70	ab
GLT226/MSM 53	6.93	b	33.80	cde	41.02	abc	80.10	abc	6.25	ab
GLT226/P2	8.54	a	37.87	abc	42.83	ab	78.36	abcd	6.99	ab
RK 457	8.29	ab	38.80	a	42.74	ab	79.69	abc	6.78	ab
RK 57	8.25	ab	37.00	abcd	37.50	bc	75.86	bcd	6.63	ab

Note: Numbers followed by the same letter in a column indicate no significant difference from Tukey tests level of 5%. WHC: weight of harvested cob, MC: moisture content, W1000: weight of 1000 seeds, Y: yield, P: productivity

In conclusion, path analysis and principal component analysis have proven to be valuable tools for identifying the morphological parameters and yield component correlations of hybrid maize. The weight of harvested cob trait has been identified as the best secondary trait for selection, as it has the highest significant direct effect on production. Environmental factors, such as climate change, will continue to influence the diversity of these traits, making the selection of suitable secondary traits even more critical. The hybrid MSM53/BCY has demonstrated superior performance compared to other hybrids' current commercial varieties under study and can be recommended as a candidate variety with high productivity potential.

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