Gunung Djati Conference Series, Volume 66 (2026)
Proceedings of the International Conference on Perennial Crops
ISSN : 2774-6585
Website : https://conferences.uinsgd.ac.id/

GENETIC DIVERSITY, HERITABILITY, TRAIT CORRELATION OF HYBRID MAIZE EVALUATED IN TWO CONTRASTING TOPOLOGIES

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ABSTRACT

Genetic diversity, heritability, and trait relationships are essential parameters for identifying selection criteria and improving maize productivity across diverse growing environments. This study aimed to evaluate genetic diversity, broad-sense heritability, and correlations among agronomic and yield-related traits of hybrid maize cultivated under two contrasting topologies. Field experiments were conducted using hybrid maize genotypes, and data were analyzed through variance component estimation, heritability analysis, and Pearson correlation coefficients. The results showed that phenotypic variance was generally greater than genotypic variance for most traits, indicating a considerable contribution of environmental factors to trait expression. High heritability values were observed for ear height, leaf width, number of kernels per ear, ear length, ear diameter, and shelling percentage, whereas leaf length, moisture content, kernel row number, and thousand-kernel weight exhibited moderate heritability. All observed traits displayed narrow genetic variability, suggesting limited genetic divergence among the evaluated hybrids. Grain yield was positively associated with fresh ear weight, ear length, ear diameter, number of kernels per ear, leaf length, and stem diameter, while flowering time and several vegetative traits tended to show negative associations with yield. Fresh ear weight showed the strongest relationship with grain yield, indicating its importance as a yield-related trait. These findings demonstrate that ear-related characters can be used as reliable indirect selection criteria for yield improvement in hybrid maize.

Key words: Genetic diversity, Maize, Trait correlation.

INTRODUCTION

Maize (*Zea mays* L.) stands as a vital cereal crop worldwide, playing a decisive role in food security, livestock feed, and industrial production. In Indonesia, maize demand is rising rapidly due to population growth, the expansion of the feed industry, and increased diversification of maize-based products. To address this, boosting maize productivity by developing high-yielding, adaptable cultivars is imperative. Expanding maize cultivation into underutilized dryland areas, especially in medium- and highland regions outside Java, is essential, given their considerable potential to drive sustainable maize production. The successful use of these environments depends largely on the availability of maize cultivars that maintain stable performance across diverse environmental conditions. However, environmental heterogeneity often causes differences in genotype performance, resulting in genotype × environment (G×E)

interactions. Such interactions complicate the selection process because superior genotypes in one environment may not necessarily perform well in another. Therefore, evaluating hybrid maize across contrasting topologies is essential to identify genotypes with broad adaptability and stable agronomic performance.

Plant breeding programs rely heavily on the availability of genetic variation within breeding materials. Genetic diversity provides the foundation for selection and determines the potential for genetic improvement. Populations with greater genetic diversity offer wider opportunities to identify superior genotypes and achieve breeding objectives. In contrast, limited genetic diversity reduces selection efficiency and the likelihood of achieving desirable genetic gains. Consequently, assessing the extent of genetic variability among hybrid maize genotypes is an important step in determining their breeding value and improvement potential. In addition to genetic diversity, heritability is an important parameter that reflects the proportion of phenotypic variation attributable to genetic factors. High heritability indicates that phenotypic performance is largely governed by genetic effects and can be reliably transmitted to subsequent generations. Information on heritability is therefore useful for identifying traits that can serve as effective selection criteria in breeding programs. Furthermore, understanding the relationships among agronomic traits through correlation analysis can improve selection efficiency, particularly for grain yield, which is a complex quantitative trait influenced by multiple genes and environmental factors. Traits strongly associated with grain yield may be used as indirect selection criteria to accelerate breeding progress.

Although numerous studies have investigated genetic variability, heritability, and yield-related traits in maize, little is known about whether trait associations and heritability estimates remain consistent across medium land and highland dryland environments, which may differ substantially in climatic and edaphic conditions. Moreover, the extent to which agronomic traits contribute to grain yield across different topologies remains unclear. Such information is essential for developing effective breeding strategies to improve yield stability and environmental adaptability. Therefore, this study was conducted to evaluate genetic diversity, estimate broad-sense heritability, analyze trait correlations, and assess genotype × environment interactions of hybrid maize grown under two contrasting topologies. The findings are expected to provide valuable insights into identifying promising selection criteria and to support the development of high-yielding, stable, and widely adaptable maize cultivars for diverse agroecological conditions.

MATERIALS AND METHODS

The study was conducted from July to September 2025 in two contrasting dryland environments. One was a mediumland area in Sinoa District, Bantaeng Regency, South Sulawesi (5°28’49.3” S, 119°56’11.2” E, 512 m alt., C3 climate). The other was a highland area in Tomohon District, Tomohon City, North Sulawesi (1°18’86” N, 124°50’42.3” E, 1,006 m alt., C2 climate, Ultisol soil). Eight maize genotypes, consisting of five experimental hybrids (Hyb 80-01, Hyb 47-01, Hyb 35-01, Hyb 56-01, and Hyb 38-01) and three commercial check varieties (P32, NK 306, and NK 212), were evaluated using a Randomized Complete Block Design (RCBD)

with four replications at each location. Data were collected from eight randomly selected plants in each experimental unit.

The evaluated traits included phenological traits (days to tasseling and days to silking), vegetative traits (plant height, ear height, stem diameter, leaf length, leaf width, and leaf area), and yield-related traits (number of ears per plant, number of harvested ears, fresh ear weight, moisture content, number of kernel rows per ear, number of kernels per ear, ear length, ear diameter, thousand-kernel weight, shelling percentage, and grain yield). Subsequently, grain yield was estimated at 15% grain moisture content using fresh ear weight and adjusted according to the standard yield conversion formula:

$$\text{Grain yield}\left(\frac{\text{kg}}{\text{ha}}\right) = \frac{\text{F.W.}\left(\frac{\text{kg}}{\text{plot}}\right) \times (100 - \text{HMP}) \times \text{S} \times 10000}{(100 - \text{DMP}) \times \text{NPA}}$$

Where,

F.W. = Fresh weight of ear in kg per plot at harvest

HMP = Grain moisture percentage at harvest

DMP = Desired moisture percentage, i.e. 15%

NPA = Net harvest plot area, m^2

S = Shelling coefficient, i.e. 0.8

This formula was also adopted by Carangal *et al*. (1971) and Shrestha *et al*. (2015) to adjust the grain yield (kg ha^{-1}) at 15% moisture content. This adjusted grain yield (kg ha^{-1}) was again converted to grain yield (t ha^{-1}).

Table 1. Mean square values for various traits of eight maize genotypes.

	Mean Square					
Variabel	Environment (E)	E/Replication	Genotipe (G)	GxE	Eror	CV (%)
NEP	5166.02	151.86	49.60	49.37	100.89	8.69
DT	232.56	0.26	4.85	4.63	2.14	3.34
DS	390.06	2.39	5.78	3.63	1.90	4.06
PH	18360.25	425.89	169.51	159.62	116.49	8.12
EH	473.61	33.94	96.88	23.24	43.32	4.48
SD	142.51	0.16	1.04	0.98	1.43	8.24
LL	1042.48	6.20	17.83	9.40	10.57	5.17
LW	56.19	0.02	0.95	0.29	0.14	10.74
LA	17.12	6.52	24.15	20.03	3.68	10.08
DM	147.02	8.32	19.57	11.41	5.85	1.82
NHE	135.14	2.65	19.96	19.96	13.36	5.11
FEW	198.86	1.53	6.78	5.48	1.48	18.08
MC	799.40	1.02	7.86	4.66	2.63	10.34
NKR	53.88	0.21	2.60	1.47	1.94	6.01
NRE	187.01	1.11	16.73	4.42	1.97	8.49
EL	7.20	0.46	5.09	0.33	0.46	6.87
ED	244.77	2.63	36.94	12.03	3.42	4.89
TKW	7869.97	284.76	1081.67	717.67	532.89	6.15
SP	0.00	0.00	0.00	0.00	0.00	3.21
YLD	57.02	0.89	2.78	4.27	0.96	13.26

Abbreviations: NEP = Number of Ears per Plant, DT = Days to Tasseling, DS = Days to Silking, PH = Plant Height, EH = Ear Height, SD = Stem Diameter, LL = Leaf Length, LW = Leaf Width, LA =

Leaf Area, DM = Days Maturity, NHE = Number of Harvested Ears, FEW = Fresh Ear Weight, MC = Moisture Content, NKR = Number of Kernel Rows per Ear, NRE = Number of Kernels per Ear, EL = Ear Length, ED = Ear Diameter, TKW = Thousand-Kernel Weight, SP = Shelling Percentage, and YLD = Grain Yield.

Based on Table 1, the genetic variance and phenotypic variance were estimated using the following formulas:

$$\sigma^2\varepsilon = MS\ error$$

$$\sigma^2 gl = \frac{MS\ GxE - MS\ error}{r}$$

$$\sigma^2 g = \frac{MS\ G - MS\ GxE}{re}$$

Where $\sigma^2\varepsilon$ is the error variance, $\sigma^2 gl$ is the genotype x environmrnt interaction variance, $\sigma^2 g$ is the genetic variance, MS_G is the mean square of genotype, MS_{GxE} is the mean square of genotype x environment interaction, MS_{error} is mean square of error, r is the number of replications and *e* is the number of envuronments.

Broad-sense heritability (h^2) was estimated according to Allard (1960) using the following formula:

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

where the phenotypic variance ($\sigma^2 p$) was calculated as:

$$\sigma^2 p = \sigma^2 g + \frac{\sigma^2 ge}{e} + \frac{\sigma^2 e}{re}$$

The heritability estimates were classified according to Stansfield (1983) as follows:

High ($h^2 > 0{,}5$), moderate ($0{,}2 \leq h^2 \leq 0{,}5h^2$) and low ($h^2 < 0{,}20$).

The standard deviation of genetic variance was calculated using the following formula:

$$\sigma_{\sigma^2 g} = \sqrt{\frac{2}{(re)^2}\left(\frac{MS_G{}^2}{dfg+2} + \frac{MS_{GxE}{}^2}{dfge+2}\right)}$$

Where MS_G represents the genotype mean square, MS_{GxE} represents the genotype × environment interaction mean square, df*g* is the degree of freedom for genotype and df*ge* is the degree of freedom for genotype × environment interaction.

Genetic variability was classified according to Pinaria *et al*. (1995) as follows:

$\sigma^2 g < 2\sigma_{\sigma}{}^2 g$: narrow genetic variability

$\sigma^2 g \geq 2\sigma_{\sigma}{}^2 g$: broad genetic variability.

RESULTS AND DISCUSSION

This study was conducted as a multi-environment trial. The trial was carried out across different locations and growing seasons. The combination of locations and seasons generated distinct environmental conditions, resulting in specific environmental characteristics that varied from one environment to another. Such environmental specificity may lead to differences in the performance of the tested hybrids across environments. These differences in hybrid

responses to environmental conditions are referred to as genotype × environment (G × E) interactions.

The estimation of genetic variance based on data from a single environment is often biased because it does not account for the effects of genotype × environment interactions. As a result, the observed phenotypic variation may not accurately reflect the true genetic potential of the genotypes. Therefore, multi-environment trials are essential for obtaining more reliable estimates of genetic parameters by incorporating the influence of genotype × environment interactions into the analysis.

Table 2. Estimates of genetic variance (σ^2g), genotype × environment variance (σ^2ge), phenotypic variance (σ^2p), environmental variance (σ^2e), heritability (h^2), and genetic variability for growth and yield-related traits in eight maize genotypes.

Variabel	σ^2g	σ^2ge	σ^2p	σ^2e	h^2	Heritability Class	σg	Genetic variability Class
NEP	0.03	-12.88	6.20	100.89	0.005	Low	16.72	Narrow
DT	0.03	0.62	0.61	2.14	0.044	Low	1.57	Narrow
DS	0.27	0.43	0.72	1.90	0.371	Low	1.26	Narrow
PH	1.24	10.78	21.19	116.49	0.058	Low	54.14	Narrow
EH	9.20	-5.02	12.11	43.32	0.760	High	9.62	Narrow
SD	0.01	-0.11	0.13	1.43	0.064	Low	0.33	Narrow
LL	1.05	-0.29	2.23	10.57	0.473	Moderate	3.30	Narrow
LW	0.08	0.04	0.12	0.14	0.696	High	0.11	Narrow
LA	0.52	4.09	3.02	3.68	0.171	Low	6.83	Narrow
HPN	0.00	0.00	0.00	0.00	0.000	Low	0.00	Narrow
DM	1.02	1.39	2.45	5.85	0.147	Moderate	3.97	Narrow
NHE	0.00	1.65	2.50	13.36	0.000	Low	6.76	Narrow
FEW	0.16	1.00	0.85	1.48	0.191	Low	1.87	Narrow
MC	0.40	0.51	0.98	2.63	0.407	Moderate	1.62	Narrow
NKR	0.14	-0.12	0.33	1.94	0.434	Moderate	0.51	Narrow
NoK	1.54	0.61	2.09	1.97	0.736	High	1.77	Narrow
EL	0.59	-0.03	0.64	0.46	0.935	High	0.32	Narrow
ED	3.11	2.15	4.62	3.42	0.674	High	4.56	Narrow
TKW	45.50	46.20	135.21	532.89	0.337	Moderate	247.57	Narrow
SP	0.00	0.00	0.00	0.00	0.875	High	0.00	Narrow
YLD	-0.19	0.83	0.35	0.96	-0.533	Low	1.43	Narrow

Negative heritability estimates were considered as zero because environmental variance exceeded genetic variance.

Abbreviations: σ^2g = genetic variance; σ^2ge = genotype × environment interaction variance; σ^2p = phenotypic variance; σ^2e = environmental variance; h^2 = broad-sense heritability.

Days to tasseling (DT) and days to silking (DS) showed limited variation among the evaluated genotypes. Heritability was low for days to tasseling (h^2 = 0.044) and moderate for days to silking (h^2 = 0.371), indicating that silking time was more strongly influenced by genetic factors than tasseling time. Consequently, selection for days to silking is expected to be more effective than selection for days to tasseling. Similar findings were reported by Makmur *et al*. (2024), who demonstrated that silking-related traits generally exhibit greater responsiveness to selection because of their higher heritability and stronger genetic contribution to phenotypic expression. Likewise, Leng *et al*. (2022) reported that silking-related traits were under greater genetic control than tasseling traits under different environmental conditions, resulting in a

more consistent response to selection. The low heritability observed for days to tasseling in the present study suggests that environmental factors substantially influenced trait expression, thereby reducing the efficiency of phenotypic selection.

Plant height (PH) exhibited low heritability (h^2 = 0.058), whereas ear height (EH) showed high heritability (h^2 = 0.760). The high heritability of ear height indicates that phenotypic variation in this trait is largely controlled by genetic factors, making it a reliable target for selection in maize breeding programs. Ear height is an important agronomic trait because it influences plant stability, lodging resistance, and harvestability. Similar findings were reported by Ndou *et al*. (2021), who demonstrated that ear height is predominantly governed by genetic factors and can be effectively improved through selection, whereas plant height is more strongly influenced by environmental conditions. Therefore, the low heritability observed for plant height in the present study suggests that phenotypic selection for this trait may be less efficient and less predictable.

Leaf length (LL) and width (LW) had moderately high heritability (0.473 and 0.696), while leaf area (LA) was low (h^2 = 0.171). Leaf length (LL) and leaf width (LW) exhibited moderate to high heritability values of 0.473 and 0.696, respectively, whereas leaf area (LA) showed low heritability (h^2 = 0.171). These findings indicate that leaf length and width are more genetically stable than leaf area. Leaf morphological traits play important roles in canopy architecture, light interception, and photosynthetic performance, making them valuable targets for improving plant growth and biomass accumulation. Similar findings were reported by Rodríguez *et al* (2016), eaf length (LL) and leaf width (LW) exhibited moderate to high heritability values of 0.473 and 0.696, respectively, whereas leaf area (LA) showed low heritability (h^2 = 0.171). These findings indicate that leaf length and width are more genetically stable than leaf area. Leaf morphological traits play important roles in canopy architecture, light interception, and photosynthetic performance, making them valuable targets for improving plant growth and biomass accumulation. Similar findings were reported by Rodríguez and Maiti (2016), who demonstrated that leaf length and width generally exhibit greater genetic stability than leaf area and are closely associated with canopy development and photosynthetic efficiency. The relatively low heritability of leaf area observed in the present study may be attributed to the strong influence of environmental conditions on leaf expansion and development. This interpretation is supported by Gompert *et al*. (2019), who reported that leaf length and width exhibit strong genetic correlations with each other and with leaf area; however, leaf area is more strongly influenced by environmental factors and is therefore less stable as a selection criterion.

Yield components, such as number of kernels per ear (NER), ear length (EL), and ear diameter (ED), showed high heritability (0.736, 0.935, and 0.674, respectively). These traits are under strong genetic control and are good targets for selection. Ear length, with the highest heritability, is a reliable indirect criterion for boosting grain yield, as it relates to sink capacity and kernel development. In contrast, several economically important traits, including ear weight (EW), ear aspect (EA), thousand-kernel weight (TKW), and grain yield (YLD), exhibited low to moderate heritability estimates. Grain yield showed a negative heritability estimate (h^2 = −0.533), indicating that environmental variance greatly exceeded genetic variance. Negative heritability estimates lack biological meaning and are conventionally set to zero, suggesting a minimal detectable genetic contribution to phenotypic variation. Grain yield is a complex quantitative trait controlled by numerous genes and strongly influenced by environmental conditions and genotype-by-environment interactions. Consequently, direct selection for grain yield in early generations may be inefficient. Instead, indirect selection through highly heritable yield components, such as ear length, ear diameter, and number of kernels per ear, may yield greater breeding progress and more stable selection responses.

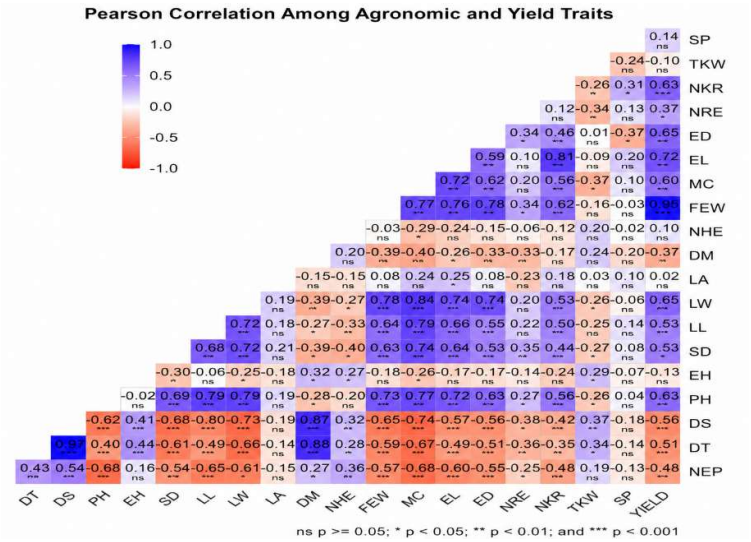

Figure 1. Pearson correlation among agronomic and yield traits

Correlation analysis revealed both positive and negative associations among agronomic and yield-related traits, indicating complex physiological and genetic relationships among the evaluated characters. Harvest ear weight (FEW) exhibited the strongest positive correlation with grain yield ($r = 0.95$, $p < 0.001$), suggesting that increased ear biomass directly contributes to higher grain production. Yield also showed significant positive correlations with ear length (EL), ear diameter (ED), number of kernel rows (NKR), leaf length (LL), and leaf width (LW). These relationships indicate that genotypes with larger ears and greater leaf development tend to produce higher grain yield. Ear-related traits are directly associated with sink capacity and kernel formation, whereas leaf traits contribute to photosynthetic activity and assimilate production. Therefore, these characters may serve as useful indirect selection criteria for improving grain yield in maize breeding programs.

The positive associations observed between yield and several agronomic traits, particularly harvest ear weight, ear length, ear diameter, and leaf-related traits, suggest that these characters contribute collectively to grain production. The strong correlations observed among growth traits and yield components indicate that these characteristics may be regulated by interconnected physiological mechanisms, including photosynthetic efficiency, biomass allocation, and assimilate translocation within the plant. In this context, the relationships among traits provide an important basis for implementing indirect selection strategies in plant breeding programs. However, the presence of negative correlations among certain trait pairs indicates potential biological trade-offs, where improvement in one trait may occur at the expense of another. Such trade-offs are common in plants, particularly between vegetative growth and reproductive development, which often compete for limited assimilates and resources. Furthermore, the complex correlation patterns observed suggest that selection based on a single trait may lead to biased outcomes or the loss of valuable genetic potential associated with other important characteristics. Therefore, a multivariate approach is

considered more appropriate for comprehensively evaluating genotype performance and supporting more effective selection decisions (Olivoto *et al*., 2017).

CONCLUSION

1. Heritability values varied from low to high among the evaluated traits. High heritability was observed for ear height (EH), leaf width (LW), number of kernels (NoK), ear length (EL), and ear diameter (ED), indicating that these traits are predominantly controlled by genetic factors and are promising targets for selection. Moderate heritability was found for PA, LL, RDI, SGrn, DH, NKR, and TKW, whereas the remaining traits showed low heritability, suggesting a greater influence of environmental factors.
2. Correlation analysis, grain yield (YLD) showed significant positive correlations with several agronomic and yield-component traits, particularly ear weight (EW), ear diameter (ED), ear length (EL), number of rows per ear (NRE), leaf length (LL), and plant height (PH), indicating that improvements in these traits are likely to contribute to increased yield. Strong positive correlations were also observed among yield-component traits, suggesting that these characteristics are closely related and collectively contribute to grain production. Conversely, days to tasseling (DT) and days to silking (DS) tended to show negative correlations with several yield-related traits, indicating that later flowering may be associated with lower yield performance.

ACKNOWLEDGMENTS

The authors sincerely thank Mr. Demax and Mr. Bendhard for their support, assistance, and valuable contributions during the conduct of this research. Their help and encouragement were greatly appreciated and contributed significantly to the successful completion of this study.

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