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Genetic variability, heritability, and path analysis for agronomic characters in hybrid maize

Abstract. Genetic parameters, which include genetic variability, heritability, and correlation between characters, are essential factors in the selection process. This study aims to: 1) determine the genetic variability and heritability for agronomic characters in hybrid maize and 2) determine the characteristics that directly affect hybrid maize yield. The experiment was conducted at Indonesian Cereal Research Institute (ICERI) Maros from June to October 2021. Fourteen maize hybrids genotypes were arranged in a randomized block design (RBD) with four replications. The observed traits were plant height, ear height, stalk diameter, leaf angle, leaf length, leaf width, days to anthesis, days to silking, days to maturity, number of harvested plants, number of harvested ears, fresh ear weight, shelling percentage, moisture content, ear length, ear diameter, number of rows per ear, number of seeds per row, 1000 seeds weight and yield. The results showed that agronomic characters with high heritability and broad genetic variability were plant height, ear height, leaf angle, leaf length, ear diameter, and 1000 seeds weight. The characters that most influence final yield were fresh ear weight and shelling percentage

Keywords: Genetic variability · Heritability · Maize · Path analysis

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Introduction

Selection is the crucial point in a plant breeding program. Selection effectivity can be increased by noticing genetic and phenotypic variability, heritability, and the correlation between traits in every stage (Nzuve et al., 2014). Variability is the primary capital for plant breeders in improving plant characteristics. The variability in a population was due to genetics, environment, and interaction between genetic and environmental factors. The variability used in plant breeding is variability due to genetic factors (Azrai, 2013). A genetic variability is number that measures the appearance variation due to genetic factors. Genetic variability can describe individual variation in a population(Barmawi et al., 2013; Kristamtini et al., 2014). The higher trait genetic variability gives the greater desired good traits combination chance so the plant breeding program success will be increased (Hapsari, 2016).

One of the things to consider in the selection is heritability. Heritability is the proportion of genetic variance to a trait's total variance, expressed in phenotypic performance, and can be inherited by subsequent generations (Qosim, 2018). Heritability values ranged from 0-1. Higher heritability values indicate more significant genetic and small environmental influences on traits and vice versa. Selection can be made in the early generations for traits with high heritability values, while traits with low heritability values are selected for advanced generations (Rini et al., 2018). A selection guided by heritability can increase the selection program's success in obtaining better results.

There are two ways to select a character. Selection can be made by direct selection and indirect selection through characters that correlate with the desired character. The correlation value will make indirect selection easier. The correlation coefficient provides a relationship between characters and valuable information about the level and direction of selection (Bechere et al., 2014; Maftuchah et al., 2015). The correlation coefficient between traits has an essential meaning in selection. Selection will be effective if there is a close relationship between the estimating character and the desired character.

Yield selection can be based on the correlation between yield and agronomic character. Occasionally, there is bias in the selection because the agronomic character was correlated with each other, so it is necessary to spell the correlation out into the direct and indirect effects. Path analysis can solve that problem by spelling out the character correlated to yield (Manggoel et al., 2012). Path analysis besides being used for food crops including soybeans (Saputra et al., 2016), rice (Kartina et al., 2016), maize (Kmail et al., 2017)) is also commonly used for pineapple (Donazzolo et al., 2017), chilli (Sa'diyah et al., 2020) even on plantations such as cocoa (Sari and Susilo, 2013), sugarcane (Baffa et al., 2014) and jatropha (Hartati et al., 2012).

Studies regarding genetic parameters commonly carried out in crop plant breeders include mung bean (Hapsari, 2016), soybean (Karyawati et al., 2019), rice (Kristamtini et al., 2014) and maize (Mhoswa et al., 2016). Even though maize heritability for character agronomic (Maphumulo et al., 2015) dan shelling percentage (Adriani et al., 2015) have been researched; however, it is done separately so that information on variability, heritability, and correlation still needs. This is the reason behind the need to study hybrid maize genetic parameters. This research was conducted to determine the genetic variability, heritability, and characters that directly affect hybrid maize yield. The information obtained can help a selection program designed for hybrid maize breeding.

Method

This experiment was conducted at Indonesian Cereal Research Institute (ICERI) Maros from June to October 2021. Fourteen maize hybrids genotypes (Table 1) were arranged in a randomized block design (RBD) with four replications.

The experimental dimension plot was 1.4 m x 5 m, with a spacing of 50 cm x 20 cm, with one plant per hole, so there were 25 plants per row. The first fertilization was done seven days after planting (DAP) with 200 kg of urea and 300 kg of Phonska per ha. Second fertilization at 30 DAP with 200 kg of urea per ha. Plant maintenance includes weeding, irrigation, and control pest management. Harvesting was done in the middle two rows of the experimental plot.

Table 1. Hybrid maize in present study

No	Hybrid	Crossing
1	NGN 1	P4 X P8
2	NGN 2	P8 X P7
3	NGN 3	P8 X P2
4	NGN 4	P7 X P2
5	NGN 5	P10 X P2
6	NGN 6	P8 X P6
7	NGN 7	P7 X P5
8	NGN 8	P7 X P3
9	NGN 9	P10 X P8
10	NGN 10	P4 X P2
11	NGN 11	MAL 03 X P7
12	JHANA 1	MAL 03 x CY 15
13	BISI 18	FS46 x FS17
14	NK 7328	NP5150 x NP5139

The observed character are plant height (PH), ear height (EH), stalk diameter (SD), leaf angle (LA), leaf length (LL), leaf width (LW), days to anthesis (DA), days to silking (DS), days to maturity (DM), number of harvested plants (NHP), number of harvested ears (NHE), fresh ear weight (FEW), shelling percentage (SP), moisture content (MC), ear length (EL), ear diameter (ED), number of rows per ear (NRE), number of seeds per row (NSR), 1000 seeds weight (1000 SW) and yield (Y) which was corrected to 15% moisture that converted to units per hectare using the formula (Sujiprihati et al., 2006):

$$\text{Yield (t /ha)} = \frac{10.000}{\text{HA}} \text{ X } \frac{100\text{-GM}}{85} \text{ X FEW x SP} \div 1.000$$

HA = Harvested area (m^2)
GM = Grain moisture (%)
EHW = fresh ear weight (kg)
SP = Shelling percentage (%)

Observed data were analyzed based on Gomez and Gomez (1983) method. Genotypic and phenotypic variability was computed from an analysis of variance (Hallauer *et al.* 2010), presented in Table 2.

Table 2. Analysis of variance with Expected Mean Square

Source of variation	Degree of freedom (df)	Mean Square (MS)	Expected Mean Square (EMS)
Replication	r-1	MSr	$\sigma^2\varepsilon + g\sigma^2 r$
Genotype	g-1	MSg	$\sigma^2\varepsilon + r\sigma^2 g$
Error	(g-1)(r-1)	MSε	$\sigma^2\varepsilon$

According to Table 2, then genotypic and phenotypic variance can be computed as follows: $\sigma^2 g = \frac{MS_g - MS_\varepsilon}{r}$, $\sigma^2 p = MS_g + \varepsilon$

Broad-sense heritability (H^2) was estimated according to the procedure suggested by Allard (1960):

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

H^2 value was grouped according to Stansfield (1983) as follows:

$H^2 > 0,5$ high, $0,2 \leq H^2 \leq 0,5$ medium, $H^2 < 0,2$ low.

Standard deviation of genotypic variance:

$$\sigma_{\sigma_g^2} = \sqrt{\frac{2}{r^2}\left(\frac{{MS_g}^2}{\text{Genotype's df+2}} + \frac{{MS_\varepsilon}^2}{\text{Error's df+2}}\right)}$$

Genetic variability was categorized as low when $\sigma^2_g < 2\sigma_\sigma{}^2_g$ and high when $\sigma^2_g \geq 2\sigma_\sigma{}^2_g$ (Pinaria et al., 1995).

Pearson correlation was used to define the correlation between characters using the formula:

$$r_{xy} = \frac{Cov_{xy}}{\sqrt{Var_x . Var_y}}$$

Where:

r_{xy} = Correlation between x character and y character,
Cov_{xy} = Covariance between x character and y character,
Var_x = Variance of x character
Var_y = Variance of y character

The direct and indirect effect of a character agronomic to yield was determined by conducted path analysis. Path analysis was only carried out on characters that influence yield. The characters that influence yield are decided by stepwise regression analysis. Path analysis was conducted according to Singh and Chaudhary (1979):

$$\underset{R_x}{\begin{bmatrix} r_{11} & r_{21} & \cdots & r_{1p} \\ r_{12} & r_{22} & \cdots & r_{2p} \\ \cdots & \cdots & \cdots & \cdots \\ \cdots & \cdots & \cdots & \cdots \\ r_{1p} & r_{2p} & \cdots & r_{pp} \end{bmatrix}} \underset{C_i}{\begin{bmatrix} C_1 \\ C_2 \\ \cdots \\ \cdots \\ C_p \end{bmatrix}} = \underset{R_y}{\begin{bmatrix} r_{1y} \\ r_{2y} \\ \cdots \\ \cdots \\ r_{py} \end{bmatrix}}$$

Ci (direct effects) were calculated by the formula: $C_i = R_x^{-1} . Ry$

Effects that a model cannot define were classified as the residual effect calculated by the formula:

$$C_s = \sqrt{C_s^2}\ ;\ C_s^2 = C_i' R_x$$

Whereas:

R_x = Correlation matrix of the dependent variable
R_x^{-1} = Inverse matrix of Rx.
C_i = Path coefficient vector that shows the direct effect of each independent variable on the dependent variable
R_y = Correlation coefficient vector between independent variable X_i (i=1, 2…, p) and dependent variable Y
C_s = residual effect or error

C_i' = Transpose matrix of C_i

Data analysis was performed using Statistical Tool for Agricultural Research (STAR) Version: 2.0.1 dan Microsoft Excel software.

Result and Discussion

Analysis of variance for observer variable. The results showed genotype character variability except for stalk diameter, days to silking, days to maturity, number of harvested plants, number of harvested ears, moisture content, and number of seeds per row (Table 3). Characters that do not show significant differences besides having low variance also show a narrow range of values. The difference shown in the analysis of variance is a phenotypic variability. Furthermore, it is necessary to carry out further studies to find out how much the genetic factors influence each character's variability (Nur *et al*. 2013).

The coefficient of variability (CV) in this research is between 1.4% (days to maturity) to 24.9% (yield). CV value represents the variability population in a study. CV shows precision values of research. Karuniawan et al., (2017) mention that higher CV values mean lower precision study and vice versa. Almost all characters show CV values below 20% except fresh ear weight and yield. This means that this study has high precision. CV values between 20-25% in agriculture study is reasonable. Prayudha et al. (2019) say that factors affecting CV values are experimental design, plant characteristics, observed variables, and the experimental environment.

Table 3. Analysis of variance and values range of observed variable

Character	Mean Square (MS)				CV (%)	Values range
	Replication	Genotype		Error		
Plant height	2199.82	866.57	**	83.84	4.30	184.90-237.75
Ear height	1336.29	480.84	**	91.04	8.30	98.13-133.44
Stalk diameter	8.44	2.24		1.52	6.30	18.30-21.05
Leaf angle	0.33	42.85	**	2.90	6.80	20.35-33.30
Leaf length	54.45	121.65	**	30.44	6.20	80.1-98.95
Leaf width	1.61	1.17	*	0.57	9.30	7.13-9.32
Days to anthesis	0.35	2.94	*	1.15	2.00	52.25-55.50
Days to silking	1.78	3.24		1.86	2.50	53.75-57
Days to maturity	3.19	2.55		2.38	1.40	107.50-110.25
Number of harvested plants	5.45	4.16		3.37	5.80	30.00-33.5
Number of harvested ears	5.29	3.49		2.91	5.40	30.25-33.25
Fresh ear weight	8.53	3.35	*	1.46	22.30	3.91-6.76
Shelling percentage	23.72	92.61	*	39.09	8.00	0.65-0.86
Moisture content	23.21	30.39		17.10	14.90	22.00-31.9
Ear length	3.11	5.13	*	2.30	8.80	14.62-18.83
Ear diameter	1.94	45.51	**	11.21	8.10	31.80-45.71
Number of rows per ear	2.66	1.33	**	0.36	4.20	13.55-15.8
Number of seeds per row	10.90	12.90		8.39	8.60	29.15-35.95
1000 seeds weight	1069.18	3743.91	**	834.14	11.70	201.3-297.72
Yield	7.75	4.24	*	1.65	24.90	3.45-6.67

**= significant at P<0.01, *= significant at P<0.05, CV= coefficient of variability

Heritability and genetic variability. The estimated heritability explained in this study is broad sense heritability. The broad sense heritability only describes genetic factors. Table 4 reveals that the observed character heritability values are varied. Low estimated heritability value is shown by days to maturity, number of harvested plants, and number of harvested ears. Low estimated heritability values indicate that these characters have low genetic potential and high environmental influences. Mathew et al. (2018) stated that minor genes usually influence characters with low heritability values The character with low heritability values is selected at advanced generations using pedigree, single seed descent, and progeny test method (Effendy et al., 2018).

Moderate estimated heritability values were displayed by stalk diameter, days to silking, moisture content and number of seeds per row (Table 4). The moderate estimated heritability values mean that additive gen influenced the character. According to Sesay et al (2016) phenotypic selection will be more effective for selection characters with moderate heritability.

Character plant height, ear height, leaf angle, leaf length, leaf width, days to anthesis, fresh ear weight, shelling percentage, ear length, ear diameter, number of rows per ear, 1000 seeds weight, and yield (Table 4) Taneva et al. (2019) mention that high estimated heritability values indicated a low environmental effect on observed character. Mass selection, backcross, and pedigree with the recurrent selection at early generation are the most suitable selection method for the character with high estimated heritability values (Yudilastari et al., 2018).

Table 4 shows that most characters observed have low genetic variability except for plant height, ear height, leaf angle, leaf length, ear diameter, and 1000 seeds weight. It means the variability among individuals in the population is low. This population's low genetic variability due to a narrow genetic background is due to the small number of origin parents. Fourteen hybrids only arranged from seven female parental lines viz P4, P7, P8, P10, MAL 03, FS46 and NP5150 and nine male parentals viz. P2, P3, P5, P6, P7, P8 CY 15, FS17 and NP5139. On another side, there were two lines (P7 and P8) as female and male parents in these hybrids. Line P7 is as female parents for three hybrids (NGN 4; NGN 7, NGN 8) and two hybrids (NGN 2 and NGN 11). Line P8 is the female parent for three hybrids (NGN 2; NGN 3, and NGN 6) and the male parent for two hybrids (NGN 1 and NGN 9). Lines P4, P10, and MAL 03 are female parents for two hybrids. Meanwhile, line P2 become the male parent for four hybrids (Table 1).

Table 4. Genotypic variance and phenotypic variance, heritability and standard deviation of genotypic variance of observed character

Character	σ^2g	$\sigma^2\varepsilon$	σ^2p	H^2	$\sigma_{\sigma_g^2}$
Plant height	195.68	83.84	216.64	0.90 (High)	79.25 (High)
Ear height	97.45	91.04	120.21	0.81 (High)	44.20 (High)
Stalk diameter	0.18	1.52	0.56	0.32 (Moderate)	0.22 (Low)
Leaf angle	9.99	2.90	10.71	0.93 (High)	3.92 (High)
Leaf length	22.80	30.44	30.41	0.75 (High)	11.24 (High)
Leaf width	0.15	0.57	0.29	0.51 (High)	0.11 (Low)
Days to anthesis	0.45	1.15	0.74	0.61 (High)	0.28 (Low)
Days to silking	0.35	1.86	0.81	0.43 (Moderate)	0.31 (Low)
Days to maturity	0.04	2.38	0.64	0.07 (Low)	0.27 (Low)
Number of harvested plants	0.20	3.37	1.04	0.19 (Low)	0.43 (Low)
Number of harvested ears	0.14	2.91	0.87	0.16 (Low)	0.36 (Low)
Fresh ear weight	0.47	1.46	0.84	0.56 (High)	0.32 (Low)
Shelling percentage	13.38	39.09	23.15	0.58 (High)	8.74 (Low)
Moisture content	3.32	17.10	7.60	0.44 (Moderate)	2.94 (Low)
Ear length	0.71	2.30	1.28	0.55 (High)	0.49 (Low)
Ear diameter	8.58	11.21	11.38	0.75 (High)	4.20 (High)
Number of rows per ear	0.24	0.36	0.33	0.73 (High)	0.12 (Low)
Number of seeds per row	1.13	8.39	3.22	0.35 (Moderate)	1.27 (Low)
1000 seeds weight	727.44	834.14	935.98	0.78 (High)	345.02 (High)
Yield	0.65	1.65	1.06	0.61 (High)	0.40 (Low)

Rosminah *et al.*, (2019) mentioned that heritability is not always linear to genetic variability. This study shows that fourteen characters have high heritability and low genetic variability. Six characters have a high heritability and genetic variability. Furthermore, all the character with low and moderate heritability has low genetic variability.

A character with high heritability but a low genetic variability shows that character in the population is homogeneous. Genetic factors strongly influence performance. Characters with high heritability and genetic variability indicate that the character has a high diversity. Genetic factors have a significant influence on character. Characters with high genetic variabilty and low heritability values are marked by characters that show great variability, but the environment influences the character variability. A character with a homogenous performance is more influenced by environmental factors, which indicates a character with low heritability and variability. Selection of characters with high heritability and variability will be more efficient and effective because it will inherit great genetic advances in the future (Effendy et al., 2018; Karyawati et al., 2019). Whereas for characters with low variability, it is necessary to do a genetic induction to make selection more effective. Variabilty induction can be conducted through introduction, hybridization, and mutation (Ahsan et al., 2015).

Coefficient correlation and path analysis. Correlation is only carried out on characters that are directly related to yield. Determination of characters that are directly related to yield is carried out by stepwise regression analysis. Stepwise regression is a method that can help the analysis process get a model that highly contributes to the dependent variable (Andayani et al., 2016; Wohon et al., 2017). The stepwise regression analysis result is shown in Table 5.

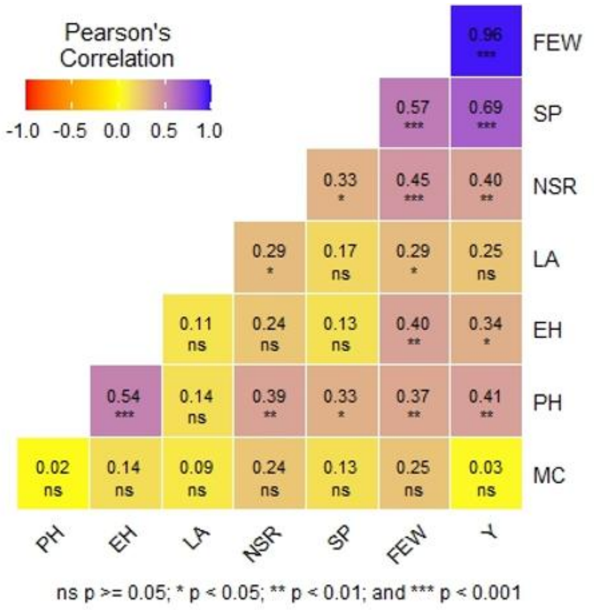
Agronomic characters with a linear relationship to yield are plant height, ear height, leaf angle, fresh ear weight, shelling percentage, moisture content and number of seeds per row (Table 5). The model that can be arranged according to that character is as follows: Y =-1.09-0.01 leaf angle+0.97 fresh ear weight+4.59 shelling percentage-0.08 moisture content-0.02 number of seeds per row. The determination coefficient value (R^2) is 0.994. This means the linear regression equation can explain 99.4% yield variation.

Table 5. Stepwise regression analysis for yield

Character	Regression	SE
PH	0	0
EH	0	0
LA	-0.01	0.01
FEW	0.97	0.02
SP	4.59	0.31
MC	-0.08	0
NSR	-0.02	0.01
intercept	-1.09	0.32

R2=0,994, PH=Plant Height, EH=Ear Height, LA=Leaf Angle, FEW=Fresh Ear Weight, SP=Shelling Percentage, MC=Moisture Content And NSR=Number of Seeds per Row

Figure 1 reveals that five characters have a significant correlation, and two characters do not have a significant correlation to yield. Plant height, ear height, fresh ear weight, shelling percentage and number of seeds per row have significant correlations. Meanwhile, leaf angle and moisture content were not significant.

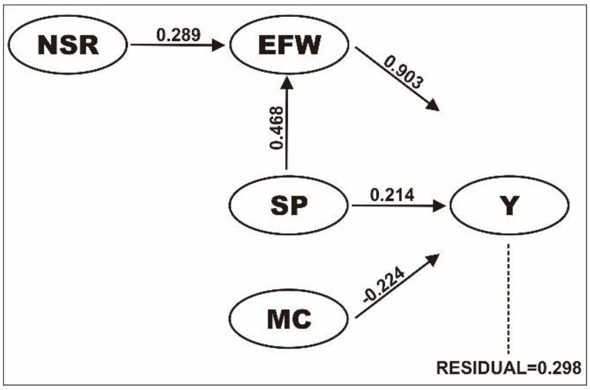


PH=Plant Height, EH=Ear Height, LA=Leaf Angle, FEW=Fresh Ear Weight, SP=Shelling Percentage, MC=Moisture Content And NSR=Number of Seeds per Row

Figure 1. Pearson correlation of maize hybrid character

All of the characters with significant correlation show a positive coefficient. Positive coefficient correlation informs that if there is a change in yield component character will follow yield change in the same direction. This means an increase in the yield component character will be followed by a yield increase and vice versa (Bewick et al., 2003). Fresh ear weight has a very strong correlation to yield (r=0.96) correlation between shelling percentage and yield is categorized as strong (r=0.69). A medium correlation was found in plant height (0.41) Silva et al., (2016) and (Raut et al., 2017) found a moderate positive correlation between plant height and yield. A weak positive correlation was found in ear height (0.34) and number of seeds per row (0.40). Idris et al. (2018) also reported a weak correlation between ear height and number of seeds per row on yield in lokal lebo maize cultivar.

The agronomic characters that correlated to yield also correlate with the other characters. that correlation makes the bias for deciding the actual yield component character effect to yield. The correlation coefficient only illustrates the close relationship between the two characters. However, it cannot explain the magnitude and direction of change because the correlation coefficient does not describe the causal relationship (Gomez and Gomez, 1983). Path analysis can solve this problem by measuring the actual effects by breaking them down into direct and indirect effects (Singh et al., 2017).



PH=Plant Height, EH=Ear Height, LA=Leaf Angle, FEW=Fresh Ear Weight, SP=Shelling Percentage, MC=Moisture Content And NSR=Number of Seeds per Row

Figure 2. Path analysis of agronomic character to yield

Characters that display a direct effect to yield are fresh ear weight, shelling percentage, and moisture content (Figure 2). Fresh ear weight and shelling percentage have a positive direct effect, while moisture content has a negative direct effect. The fresh ear weights direct effect is the highest among all characters. Mhoswa et al. (2016) and Priyanto et al. (2018), in their research also reported that fresh ear weight was a character with the highest direct effect to yield.

The relationship between number of seeds per row and yield is a mediation model. In the path analysis mediation, there is an intermediate variable between variables X and Z (Sudaryono, 2011). that variable can change the direction and magnitude of variable X's effect on variable Z. The total effect of variable X on Z in a mediation model, according to (Noviyanti et al., 2016), is the product of the X-Y and Y-Z pathways. This research reveals that the number of seeds per row affects yield through fresh ear weight. Figure 2 shows that the number of seeds per row’s indirect effect to yield is 0.298, and the total effect of number of seeds per row to yield is 0.269.

Character shelling percentage shows an exciting finding. The relationship between shelling percentage and yield is the combination of multiple regression and mediation regression models (Sarwono, 2011). Character shelling percentage, besides having a direct effect to yield, also has an indirect effect through fresh ear weights. Figure 2 explains that the shelling percentage direct and indirect effect to yield is 0.214 and 0.468, respectively. Shelling percentage total effect to yield is 0.637.

It is effective to implement indirect selection for high-yield maize hybrid through shelling percentage and fresh ear weight. It can be inferred from coefficient correlation and direct effect value of shelling percentage and fresh ear weight to yield is almost equal. The direct effect and correlation coefficient of shelling percentage to yield is 0.637 dan 0.687. It is similar to Efendi et al. (2016) that state shelling percentage can be used in the maize yield indirect selection during drought conditions. The high-value direct effect and coefficient correlation of fresh ear weight to yield (0.903 dan 0.955) indicate that character is effective at the indirect selection. In indirect selection, selection will be effective when the coefficient correlation and direct effect of targeted selection are almost equal.

Conclusion

Agronomic characteristics with high heritability genetic variability are plant height, ear height, leaf angle, leaf length, ear diameter, and 1000 seeds weight. The characteristics with the highest yield effect are fresh ear weight and shelling percentage

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