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Estimation of Genetic Variance and Heritability of F_2 Populations of Corn Plants in Dry Land

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Abstract: This study was aimed to determine the genetic variance of several F_2 population traits of maize, broad heritability values and phenotypic correlations between yields and other quantitative traits. The method used is the experimental method. The experiment was designed in a randomized block design, with 6 replications. The number of treatments was 4 populations, namely population F_2, Sinta Unram, hybrid NK212 and NK7328. Each population was planted in 4 rows, each consisted of 40 plants. The observed characteristics included plant height, leaf number per plant, leaf angle, ear length, ear diameter, weight of dry ear harvested per plant and yield (dry seed weight per plant). The data were analyzed by simple statistical analysis and analysis of variance at the 5 percent level of significance. The results showed that the genetic variance of plant height, leaf angle, and dry cob weight at harvest per plant population of F_2 was higher than that of Sinta Unram's genetic diversity with relatively wide genetic diversity. The genetic variance of leaf number per plant, ear length and ear diameter were also higher than that of Sinta Unram; but the genetic diversity is quite narrow. The genetic diversity of the F_2 population's traits is the same as that of Sinta Unram with a broad category. The heritability value of broad meaning classified as high (> 50 %) was obtained on plant height, leave number per plant, ear length, ear diameter, weight of dry ear harvested per plant and yield; while the leaf angle is classified as moderate. Harvested dry cobs weight per plant showed strong phenotypic correlation with yield (0.827); while other properties are classified as very weak to moderate. Improving the yield of the F_2 population can be done by indirect mass selection using the weight of harvested dry cobs per plant as the selected trait

Keywords: Heritability; phenotypic correlation; genetic variance; phenotypic variance

Introduction

Hybridization between P_8IS (Sinta Unram) and NK212 and NK7328 was carried out and the F_1 line was obtained. Sinta Unram is a population based on the eighth cycle of basic index selection and as a candidate for superior varieties for dry land. Some of these F_1 lines have smaller leaf angles than Sinta Unram's leaf angles. The yield strength of most of the F_1 lines tends to increase compared to Sinta Unram (Sudika and Dwi Ratna, 2021). The results of testing the F_2 lines showed that several lines had super early maturity, small leaf angles and higher yields than Sinta Unram (Sudika et al., 2021). These F_2 strains have been genetically recombined and the resulting F_2 recombined populations have been produced. Genetic hybridization and recombination are steps to increase genetic diversity (Sain, 2016).

Genetic diversity is very important in selection activities. Traits that have wide genetic diversity are easier to carry out selection. Julianto, et al. (2016) found that among 10 maize inbred lines had low genetic diversity for most traits; while cob length and seed weight are relatively low. The research results of Adriani, et al. (2015) found that the genetic diversity of the two sets of peak cross hybrids was broad for the character of the seed yield, the weight of the harvested cobs, the yield of the seeds, the number of rows of seeds per cob and the appearance of the cobs. In addition to genetic diversity, heritability values are also

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important in determining selection methods and selection responses (Jain, 1982).

Heritability is the ratio of the magnitude of the genetic variance to the phenotypic variance. Heritability values can be used to determine the traits selected and the selection method. For traits that have a high heritability value, the mass selection method can be used to improve these traits (Basuki, 2005; Ujianto et al, 2020). Several researchers have studied heritability in maize. Wannows, et al. (2010); Shahrokhi, et al. (2013); Azrai, et al. (2016); Kandel et al. (2018); Lubis, et al. (2014) found that the character of ASI (Anthesis Silk Interval), cob dry weight, seed dry weight, and cob weight/plot had broad genetic diversity values, followed by high heritability. Traits that have wide genetic diversity and high heritability can be selected directly. In addition, selection can also be carried out indirectly through traits that are strongly correlated with improved traits (Basuki, 2005). Therefore, it is very important to know the value of the correlation coefficient between traits.

The breadth and narrowness of genetic diversity, can be measured from the genetic variety. Estimation of genetic variance can be done by using hybrid varieties. Hybrids are the first generation (F1) of crossing two or more pure lines and the F1 genotype is uniform (Takdir et al., 2010). Therefore, the variety of phenotypes found in hybrids is an predictor for the variety of environments. Based on the large environmental variance, the genetic variance of the F2 and Sinta Unram populations can be estimated. A model for estimating genetic variance like this has been carried out to determine changes in genetic variance due to selection by Sudika et al. (2019). The study in this study aimed to determine the genetic variance of several quantitative traits of the F2 population of maize plants, broad meaning heritability values and determine the value of the phenotypic correlation coefficient between yields and other quantitative traits.

Method

This research was carried out with activity stages as stated in the following scheme

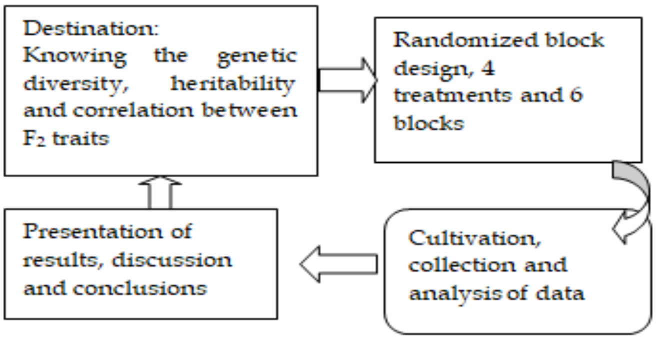

Figure 1. Research flow

Research Methods and Experimental Design

Experimental method has been used in this research. The experiment was carried out on dry land in Amor-Amor hamlet, Gumantar village, North Lombok district. The trial started in May and will continue until August 2022. The materials used included seeds from 4 different populations, Saromyl 35 SD, Furadan 3 G, Calaris 550 SC, Proclaim 5 SG. The tools used were a pair of cows for tillage, a hoe, an analytical balance, caliper, ruler measuring 1 m and 30 cm and a protractor. The experiment was designed with a randomized block design. The treatments consisted of 4 different populations, namely populations F_2, Sinta Unram, hybrids NK212 and NK7328. Each treatment was repeated 6 times, so there were 24 experimental plots.

Experimental Implementation

Soil preparation is done by plowing and harrowing once each. Land that has been processed, then leveled. The trial plot was then divided into 6 blocks and each block was divided into 4 plots with the size of each plot being 2.8 x 8 m.

Planting is done by making planting holes and each hole is filled with two seeds. The planting hole that already contains the seeds is covered with Petroganik fertilizer at a dose of 600 kg/ha. To the left of the planting hole, make a hole for fertilizer with arrack about 10 cm. In the hole, a mixture of Phonska and Urea fertilizers was added. Phonska fertilizer dosage is 150 kg/ha and Urea, 100 kg/ha. The next fertilizer hole is covered with soil. Thinning was done at the age of 10 days by leaving one plant per hole; which is growing better.

Plant maintenance includes irrigation, additional fertilization and control of weeds, pests and diseases. Watering was done 5 times, ie the day before planting, at 21 days, 35, 55, and 65 days after planting. Irrigation is done by dileb using water from pump wells. Weed control was carried out by spraying the insecticide Calaris 550 SC with a concentration of 5 cc/l of water at the age of 14 days. Hilling is done at the age of 25 days by hoeing the soil between the rows of plants, then the soil is used to pile up the plants in the rows to the left and right. Shortly before planting, follow-up fertilization was carried out using 150 kg of Phonska and 100 kg of Urea. Fertilization is done tugal between plants in rows. Control of caterpillar pests that attack corn plants at the age of 35 days, is done by spraying Proclaim 5 G insecticide, with a concentration of 3 grams/16 l of water.

Harvesting is done when 85 percent of the plants in each plot have met the criteria for harvesting. The criteria for harvesting corn were that the cob husk and hair were dry, the seeds were hard, shiny and a black layer had formed on the part of the seed that was attached to the cob.

Variables and Data Analysis

Observations were made on growth variables and yield and yield component variables. Growth variables, namely plant height, number of leaves per plant and leaf angle. Yield and yield component variables included cob length, cob diameter, harvested dry cob weight per plant and yield (chiseled dry seed weight per plant). The sample plants were determined by systematic random sampling of 10 plants per treatment for each block.

Data analysis was performed to calculate genetic variance and heritability values in broad terms. The steps for estimating genetic variance using hybrid variance are as follows:

1) Calculating the phenotypic variance (σ^2_F) for each population using simple statistics, with the formula (Farabi, 2021):

$$\sigma^2_F = \Sigma(Xi - X)^2/n \quad (1)$$

2) Calculating the average phenotypic variance of two hybrids, as an estimate for environmental variance:

$$(\sigma^2_E) = (\sigma^2_F \text{ NK212} + \sigma^2_F \text{ NK7328})/2 \quad (2)$$

3) Calculating the genetic variance of the F_2 population and the genetic variance of Sinta Unram:

$$(\sigma^2_G)\ F_2 = (\sigma^2_F\ F_2) - (\sigma^2_E) \quad (3)$$

$$(\sigma^2_G) \text{ Sinta Unram} = (\sigma^2_F \text{ Sinta Unram}) - (\sigma^2_E) \quad (4)$$

Genetic diversity is said to be wide when σ2G > 2 (σG) and narrow when σ2G < 2 (σG) (Pinaria et al., 1995).

4) Test the genetic variance of the two populations (Nugroho, 2008), namely the F_2 population with the genetic variance of Sinta Unram using the F test at the 5% significance level with the following formula:

$$F_{count} = (\sigma^2_G)\ F_2/(\sigma^2_G) \quad (5)$$

The results of calculating F_{count}, then compared with $F_{0.05}$ (59, 59), with the provisions: If $F_{count} > F_{0.05}$ (59, 59); means that the genetic diversity of F_2 is wider than the genetic diversity of Sinta Unram. Conversely, if $F_{count} < F_{0.05}$ (59, 59); means that the genetic diversity of F_2 is the same as that of Sinta Unram.

Broad meaning heritability is calculated by first analyzing the variance of the observed data. Based on the analysis of variance, the genetic variance and phenotypic variance for the entire population were calculated. The results of calculating genetic variance and phenotypic variance are used to calculate heritability values in the broad sense of Ujianto et al., 2020) as follows:

$$H^2 = (\sigma^2_G/\sigma^2_F) \times 100\ \% \quad (6)$$

with H^2 = broad meaning heritability; σ^2_G, is the genetic variance and σ^2_F is the phenotypic variance. The heritability value is categorized according to the opinion of Syukur et al. (2012), namely low, < 20%; moderate, 20 – 50% and high, > 50%.

The value of the phenotypic correlation coefficient is calculated by the formula (Paiman, 2019), as follows:

$$r = \frac{N\sum XY - (\sum X)(\sum Y)}{\sqrt{N\sum X^2 - (\sum X)^2}\sqrt{N\sum Y^2 - (\sum Y)^2}} \quad (7)$$

Testing whether or not the correlation coefficient is real is done by comparing the correlation coefficient value with the r table value at the 5% level of significance. The correlation is real, if the value of r count is greater than r table and vice versa is not real if $r_{count} < r_{table}$. The level of closeness of the relationship between variables was determined by following the Guilford Criteria (1956 cit. Somantri & Muhidin, 2006) as shown in Table 1.

Table 1. The degree of closeness of the relationship between variables based on the value of the correlation coefficient (r)

Correlation Coefficient Value Range (r)		Closeness category between variables
Positive sign	Negative sign	
0.00 < r < 0.20	- 0.20 < r ≤ 0.00	Very weak
0.20 ≤ r < 0.40	- 0.40 < r ≤ - 0.20	Weak
0.40 ≤ r < 0.70	- 0.70 < r ≤ - 0.40	Middle
0.70 ≤ r < 0.90	- 0.90 < r ≤ - 0.70	Strong
0.90 ≤ r < 1.00	- 1.00 < r ≤ - 0.90	Very strong

Result and Discussion

Some photos during the implementation of the research are presented below.


a b

Figure 1. (a) Inspection of corn fields; (b) Corn plant inspection

The F_2 population of corn plants was the result of hybridization of Sinta Unram with two hybrids, namely NK212 and NK7328. The aim of hybridization is to increase genetic diversity for several quantitative traits of maize plants. The F_2 population is a segregated population and it is expected that some traits will have wide genetic diversity. Estimation of the genotype variance of the F_2 and Sinta Unram populations was carried out using the average of the phenotypic variances of the two hybrids (NK212 and NK7328). The phenotypic variance obtained in the two hybrids is an predictor of environmental variance. In Table 2, the phenotype variance and standard deviation of the growth variables are presented, and in Table 4, the yield and yield component variables are presented.

In Table 2 it can be seen that the plant height and leaf angles of the four populations of maize plants have a variety of phenotypes. The number of leaves per plant is only the F_2 population which has a variety of phenotypes; while Sinta Unram, a hybrid of NK212 and NK7328, has the same characteristics. Phenotypic diversity is caused by genetic variation and environmental variation as well as the interaction of the two variations. In this study, the interaction of genetic variation and environmental variety cannot be calculated because there is only one location, so that the phenotypic variety is the sum of the genetic variety and environmental variety. Therefore, the genetic variety can be obtained from the large phenotypic variety minus the environmental variety. The environmental variance was estimated from the average phenotypic variance of the two hybrids, namely NK212 and NK7328. Based on this, the genetic variance of the F2 and Unram populations can be calculated and the calculation results are presented in Table 3 for the growth variables and Table 5 for the yield and yield component variables.

Table 2. Variation of phenotypes (σ^2_F) and standard deviation (SD) of growth variables in several populations of maize plants

Population	Plant height		Number of leaves per plant		Leaf corner	
	(σ^2F)	SD	(σ^2F)	SD	(σ^2_F)	SD
F_2	634.22 s	25.18	4.15 s	2.04	114.65 s	10.71
Sinta Unram	386.77 s	19.67	1.80 ns	1.34	59.67 s	7.72
NK212 hybrid	224.42 s	14.98	0.76 ns	0.87	25.82 s	5.08
NK7328 hybrid	351.64 s	18.75	0.82 ns	0.90	35.13 s	5.93
Hybrid average	288.03		0.79		30.47	

Note: s is significantly different on the basis of the standard deviation value and ns is not significantly different.

Table 3. Genetic variance (σ^2_G) of growth variables for several maize plant populations

Population	Plant height				Number of leaves per plant				Leaf corner				$F_{tab\ 0.05}$
	σ^2_G	SD	Criteria	F_{count}	σ^2_G	SD	Criteria	F_{count}	σ^2_G	SD	Criteria	F_{count}	
F_2	346.19 s	18.61	Large	3.506	3.36 s	1.83	Narrow	3.321	84.18 s	9.17	Large	2.883	1.533
Sinta Unram	98.74				1.01				29.20				

Note: s, significantly different from Sinta Unram at the 5% level of significance.

In Table 3 it can be seen that the genetic variation of plant height, number of leaves per plant and leaf angle of the F2 population is greater than the genetic variety of Sinta Unram. The genetic diversity of plant height and leaf angle is wide; while the number of leaves per plant is relatively narrow.

Table 4. Variation of phenotypes (σ^2_F) and standard deviation (SD) of yield and yield components of several populations of maize plants

Population	Cob length		Cob diameter		Dry cob weight harvested per plant		Yield (shelled dry seed weight per plant)	
	(σ^2_F)	SD	(σ^2_F)	SD	(σ^2_F)	SD	(σ^2_F)	SD
F_2	6.69 s	2.59	0.12 ns	0.34	1707.68 s	41.32	479.89 s	21.91
Sinta Unram	5.34 s	2.31	0.10 ns	0.31	1473.90 s	38.39	443.56 s	21.06
NK212 hybrid	3.21 ns	1.79	0.06 ns	0.25	1154.51 s	33.98	312.65 s	17.68
NK7328 hybrid	4.86 s	2.20	0.07 ns	0.26	1621.97 s	40.27	418.75 s	20.46
Hybrid average	4.04		0.06		1388.24		365.70	

Note: s, significantly different on the basis of standard deviation values and ns, not significantly different.

In Table 4 it can be seen that cob length, harvested dry cob weight per plant and yield (fine dry seed weight per plant) had a variety of phenotypes, except for cob length of the NK212 hybrid, the phenotype did not vary. The cob diameter of the entire population, the phenotype did not vary.

Table 5. Genetic variation of yield component variables and yield of F_2 and Sinta Unram populations of corn plants

Population	Cob length				Cob diameter			
	σ^2_G	SD	Criteria	F_{count}	σ^2_G	SD	Criteria	F_{count}
F_2	2.66 s	1.63	Narrow	2.044	0.05 s	0.22	Narrow	1.577
Sinta Unram	1.30				0.03			

Continuation of Table 5

Population	Harvest dry cob weight				Yield (shelled dry seed weight per plant)				$F_{tab0.05}$
	σ^2_G	SD	Criteria	F_{count}	σ^2_G	SD	Criteria	F_{count}	
F_2	319.44 s	17.87	Large	3.729	114.19 ns	10.69	Large	1.467	1.533
Sinta Unram	85.66				77.86				

Note: s, significantly different from Sinta Unram at the 5% significance level and ns, not significantly different from Sinta Unram.

Table 5 shows that the genetic variance of cob length, cob diameter and dry cob weight harvested per plant in the F_2 population was greater than the genetic variance of Sinta Unram; while the genetic variance of the results of the two populations is the same. The genetic diversity categories of cob length and cob diameter are narrow; while the dry cob weight harvested per plant and the yield (shell dry seed weight per plant) were broad.

In general, the F_2 population is a population that has wide genetic diversity. Genetic diversity is very important in a breeding program, especially when using selection methods to improve these traits. Wide genetic diversity indicates a greater selection response than narrow genetic diversity. Traits that have wide genetic diversity and are followed by high heritability, then these traits can be selected directly (Basuki, 2005). Plant height, leaf angle, dry cob weight harvested and yield (pill dry seed weight per plant, had wide genetic diversity. Plant height heritability, dry cob weight harvested per plant and yields were high with values ranging from 72.90 – 80.67 % The same thing was obtained by Adriani, et al. (2015), that the genetic diversity of peak cross hybrids was broad for the character of seed yields and harvested cob weight.Therefore, a direct increase in yield can be done through selection, using dry seed weight per plant. Leaf angle is a trait that we also want to reduce in this population, but the genetic diversity is narrow and the heritability is moderate, so it cannot be directly corrected through selection. The genetic diversity of cob length and cob diameter is narrow, making it difficult to obtain a large selection response. The same was obtained by Julianto, et al. (2016), that between 10 maize inbred lines had genetic diversity rather low (narrow) for cob length.

Table 6 shows that plant height has a heritability of 72.90%; number of leaves per plant, 96.05; cob length 55.73; cob diameter, 58.26; harvested dry cob weight per plant, 80.67 and yield (flat dry seed weight per plant) of 73.22%; all are high. Leaf angle heritability of 47.66% is classified as moderate. High heritability for yield and harvested dry cob weight per plant was 60.27% and 59.01%, respectively, also obtained by Sudika and Soemeinaboedhy (2020).

Table 6. Broad meaning heritability values (H^2) of all traits observed in corn plants

Observed properties	Value of H^2	Criteria
Plant height	72.90	Tall
Number of leaves per plant	96.05	Tall
Leaf corner	47.66	Middle
Cob length	55.73	Tall
Cob diameter	58.26	Tall
Dry cob weight harvested per plant	80.67	Tall
Yield (shelled dry seed weight per plant)	73.22	Tall

Kandel et al. (2018), obtained a high heritability of 85%. High heritability indicates that most of the phenotypic variation is due to genetic variation; while moderate heritability means that the phenotypic variation is partly due to genetic variation and partly due to environmental variation. Heritability values are useful for determining selection methods and influencing selection responses (Jain, 1982 and Basuki, 2005). The higher the heritability value, the higher the selection response (Ujianto et al., 2020). Harvested dry cob weight per plant had higher heritability than yield. The genetic variance of harvested dry cob weight was wider than the yield genetic variance of 319.44 and 114.19 respectively (Table 5). On the basis of heritability values and genetic variance, it is probable that the response to selection for dry cob weight harvested per plant will be higher than the response to selection for yield.

Plant height, number of leaves per plant have a weak correlation with yield; leaf corners, very weak; cob length and cob diameter classified as medium. The phenotypic correlation was strong and positive with yields obtained at harvested dry cob weight per plant of 0.827 (Table 7). The value of the phenotypic correlation coefficient is very important if the selection is done indirectly (Basuki, 2005). This means that the increase in maize yields was carried out using another trait selection criterion, namely the dry cob weight harvested per plant. This is due to the highest phenotypic correlation coefficient with a significantly positive strong category. The higher the weight of the cobs selected in the selection, the higher the yield. This is in accordance with the opinion of Paiman (2019), that a real positive correlation means that the higher the value of variable X, the higher the value of variable Y. The use of harvested dry cob weight per plant, has been carried out on mass selection with a basic index by Sudika et al. (2022) and obtained a correlation value of 0.87 with the results. The same thing was obtained by Sudika et al. (2019), of 0.85. Abdalla et al. (2010) also obtained a significant positive correlation between harvested dry cob weight and yield 0.99; Kusnarta and Sudika (2018) of 0.94 and Oktarina (2016) of 0.74. A strong correlation of yield with yield components was also obtained by Al-Naggar et al. (2016).

Table 7. Value of the phenotypic correlation coefficient between the observed traits and the yield (shelled dry seed weight per plant)

Observed properties	r_f value with result	Category
Plant height	0.208 s	Weak
Number of leaves per plant	0.351 s	Weak
Leaf corner	-0.124 ns	Very weak
Cob length	0.680 s	Middle
Cob diameter	0.564 s	Middle
Dry cob weight harvested per plant	0.827 s	Strong

Description: $r_{0.05}$ (178) = 0.146; s, significantly different at the 5% level of significance and ns, not significantly different.

Conclusion

Conclusions and suggestions that can be put forward from the results of the study, that the genetic variation of plant height, leaf angle, and harvested dry cob weight per plant in the F_2 population was higher than that of Sinta Unram with wide genetic diversity. Genetic variance in number of leaves per plant, cob length and cob diameter were also higher than SintaUnram; but the genetic diversity is relatively narrow. The genetic variance of the results was the same between the F_2 and Sinta Unram populations with wide genetic diversity. Broadly speaking heritability values were high (> 50%) obtained on plant height, number of leaves per plant, cob length, cob diameter, dry cob weight harvested per plant and yield; while the leaf angle is moderate. Strong phenotypic correlation with yield was obtained on the weight of harvested dry cobs per plant; while other properties are classified as very weak to moderate. Improving the yield of the F_2 population can be done by indirect mass selection using the harvested dry cob weight per plant as the selected trait

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