Variability, Heritability, and Genetic progress of Maize Population F2 as a result of crossing BSM0729S3-A with BAP 27799-1

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Abstract— The research aims to see the variability value, heritability and genetic progress of the F2 maize population which is the result of crossing BSM0729S3-A with BAP27799-1. The final goal of this research series is to assemble high yielding composite maize. The study was conducted from April to July 2019 on the community fields, Nagari Sitiung, Sitiung District, Dharmasraya District, West Sumatra. The material used was maize seed population F2 (the result of crossing BSM0729S3-A with BAP27799-1) and the two elders were BSM0729S3-A and BAP27799-1. The observed variables were plant height, age of anthesis, age of hair appearing, cob weight without maize husk, cob length, cob diameter, and seed weight per cob. The results of the analysis of the variability values showed that all the observed variables had a wide variability, whereas based on the results of the analysis of the heritability values showed that (except for the length of the cob) all the observed variables had high heritability values. Based on the results of the analysis of the genetic progress value, the plant height variable, the cob weight without maize husk, the diameter of the cob, and the weight of the cobs of seed have a high genetic progress value, the anthesis age variable and the age of hair appearing have a high genetic progress value, while the length of the cob variable has a value low genetic progress. It can be concluded that the selection activities in the F2 population to get high-yielding maize seeds can be carried out effectively and efficiently.

Keywords— variability, heritability, genetic progress, maize population F2.

I. INTRODUCTION

Maize (*Zea mays*) is one of the economically valuable cereals and has the opportunity to be developed in Indonesia. This commodity is very multipurpose, besides using as food, it is also used for feed, as well as industrial raw materials. In fact, domestic maize production has not been able to meet their needs so they have to import. According to data from the Central Statistics Agency (BPS), the volume of maize imports as of September 2018 is 477 thousand tons [1]. One of the causes of Indonesia's national maize supply shortage is due to low productivity.

One of the efforts to increase maize productivity can be done by focusing on the components of production technology, namely superior varieties both hybrid and free-range. Both types of these varieties have advantages and disadvantages. Hybrid varieties have high yield potential but must be cultivated in fertile areas and more intensive maintenance, meanwhile free extract maize has wider adaptability, cheap seed prices, and the seeds can be used directly in the next planting season, but the level of production lower than hybrid maize. Because the

productivity of composite maize is still low, efforts are needed to improve the population by doing selection in order to get high-yielding composite maize varieties.

Composite maize is maize originating from a population of random crosses (at least 5 times) from mixing seeds of the same amount from several varieties of free-lined, synthetic or hybrid. Selecting the F2 generation period for a number of cross-combination results in the context of the formation of high-yield (seed) composite maize is needed. To ensure a series of activities in the framework of producing composite maize, the calculation of the value of variability, heritability and genetic progress is very necessary. The purpose of this study was to look at the variability value, heritability and genetic progress of maize population F2 which was the result of the crossing of BSM0729S3-A with BAP27799-1.

II. MATERIALS AND METHODS

2.1 Implementation Research

The study was conducted for four months from April to July 2019. The research was carried out in the

community fields in Dharmasraya Regency, the location of the research location is at coordinates 1 ° 00′ 36.78″ LS and 101 ° 37′ 30.57″ Administratively, this area is included in the area of Sitiung Subdistrict, Dharmasraya Regency, West Sumatra Province. The materials used were population F2 maize seeds (crossing results of BSM0729S3-A with BAP27799-1) and the two elders were BSM0729S3-A and BAP27799-1, Urea fertilizer, SP-36, and KCl, Ridomil 35 SD, Furadan, Herbicide, and Insecticide. The tools used were tractors, torches, hoes, gauges, calipers, digital cameras, sickles, permanent markers, digital scales, observation guidelines, and stationery.

2.2 Data analysis

The observed variables were plant height, age of anthesis, age of hair appearing, weight of cob without maize husk, and weight of seeds per cob. Observational data for each variable were analyzed for mean values, genetic variability, heritability, and estimated values of genetic progress. The average can be calculated using the following formula:

$$\mu = \frac{\Sigma X_i}{n} = \frac{X_1 + X_2 + X_3 + \cdots + X_n}{n}$$

Notes:

μ	:	Average
ΣX_i	:	Addition of figures for all data
n	:	Amount of data

Genetic variance and Standard deviation can be calculated using the formula:

$$\sigma^2 = \frac{\Sigma(x_i - \mu)^2}{n - 1}$$

$$\sigma = \sqrt{\frac{\Sigma(x_i - \mu)^2}{n - 1}}$$

Notes:

σ^2	:	Varian
σ	:	Standard deviation
μ	:	Average
x_i	:	1st, 2nd data etc.
n	:	Amount of data

Genetic variability is said to be broad if $\sigma^2 g \geq 2$ standard deviations (sd), and said to be narrow when $\sigma^2 g \leq 2$ standard deviations (sd) [2]. Heritability can be calculated using the formula:

$$h^2{}_{(BS)} = \frac{\sigma^2 F2 - \sqrt{(\sigma^2 p1)(\sigma^2 p2)}}{\sigma^2 F2} \times 100\%$$

Notes:

h^2	:	The value of heritability is broad meaning
$\sigma^2{}_{F2}$	:	Variability values in population F2
$\sigma^2{}_{P1}$	:	The value of variability in the first population
$\sigma^2{}_{P2}$	:	the value of variability in the second population

Criteria for heritability: Low (h2 bs <0.2); Medium (0.2 <h2 bs ≤ 0.5); High (h2 bs> 0.5).

Genetic Progress (KGH) can be calculated using the formula:

$$KGH = i. h^2. \sigma p$$

$$\%KGH = \frac{KHG}{\mu} \times 100\%$$

Notes:

KGH	:	Genetic progress
I	:	The intensity of the selection, 10% = 1.76
h^2	:	Heritability
σp	:	Phenotype standard deviation
μ	:	Average value

Criteria for genetic progress expectations according to [3]: low (0 - 3.3%); rather low (3.31% - 6.6%); quite high (6.61% - 10%); high (> 10%).

III. RESULT AND DISCUSSIONS

3.1 Value of Variability, Heritability and Genetic Progress of Plant Height Variables

Based on the analysis of plant height variables, the population of F2 from the crossing of BSM0729S3-A with BAP27799-1 has wide genetic variability (KG), high heritability, and high genetic progress (Table 1). Wide genetic variability will make effective selection activities in order to get the desired plant criteria. The effectiveness of selection will be more efficient if the estimated value of heritability (hbs2) is high [4]. Heritability is a component in calculating the value of expected genetic progress [5], where a high heritability value is accompanied by high genetic progress, of course, it will be very effective and efficient for the selection activities done

Table 1. Results of analysis of genetic variability, heritability and genetic progress on plant height variables F2 from the crossing between BSM0729S3-A and BAP27799-1

Plant Height (cm)	Analysis results
μ	208.77
$\sigma^2 g$	981.59
$2\sigma g$	62.66
KG	Wide
H_{bs}^2	0.54
H_{bs}^2 criteria	High
%KGH	14.36
KGH criteria	High

Note: μ = average; $\sigma^2 g$ = genetic variability; $2\sigma g$ = standard deviation; KG = genetic variability; H_{bs}^2 = heritability.

Plant height is one of the agronomic characters which is usually the higher a plant means the use of sunlight for photosynthesis will be optimal, so that it will produce optimal fruit as well. In research [6] states that the production is positive correlated significantly with plant height. So the optimal plant height will produce optimal production as well.

3.2 Values of Variability, Heritability and Genetic Progress Variable anthesis and hair age

Based on the analysis of the anthesis age and the age at which hair appeared, the F2 population resulting from crossing of BSM0729S3-A with BAP27799-1 had wide genetic variability (KG), high heritability, and high genetic progress (Table 2 and Table 3).

Table 2. The results of the analysis of the value of genetic variability, heritability and genetic progress on the age anthesis population F2 from the crossing between BSM0729S3-A and BAP27799-1

Age of anthesis	Analysis results
μ	55.82
$\sigma^2 g$	5.59
$2\sigma g$	4.73
KG	Wide
H_{bs}^2	0.91
H_{bs}^2 criteria	High
%KGH	6.81
KGH criteria	High enough

Note: μ = average; $\sigma^2 g$ = genetic variability; $2\sigma g$ = standard deviation; KG = genetic variability; H_{bs}^2 = heritability.

Table 3. The results of the analysis of genetic variability, heritability and genetic progress on the age variables appearing hair F2 population results from crossing BSM0729S3-A with BAP27799-1

Age of hair appears	Analysis results
μ	57.43
$\sigma^2 g$	7.72
$2\sigma g$	5.56
KG	Wide
H_{bs}^2	0.95
H_{bs}^2 criteria	High
%KGH	8.10
KGH criteria	High enough

Note: μ = average; $\sigma^2 g$ = genetic variability; $2\sigma g$ = standard deviation; KG = genetic variability; H_{bs}^2 = heritability.

Usually flowering age is positively correlated with age of harvest. If the age of flowering is fast then the age of harvest will also be fast. As stated by [7] that in rice plants whose flowering age is faster has a faster generative phase too, so that the faster the flowering plants the faster the harvesting time.

3.3 Values of Variability, Heritability and Genetic Progress Variable weight of cob without maize hudk and seed weight per cob.

Based on the analysis of the weightless cob variable and seed weight per cob, the population of F2 from the crossing of BSM0729S3-A with BAP27799-1 has wide genetic variability (KG), high heritability, and high genetic progress (Table 4 and Table 5).

Table 4. Results of analysis of genetic variability, heritability and genetic progress in the weight variable of cob without maize husk population F2 resulting from crossing of BSM0729S3-A with BAP27799-1

cob weights without maizehusk	Analysis results
μ	128.38
$\sigma^2 g$	2343.42
$2\sigma g$	96.82
KG	Wide
H_{bs}^2	0.81
H_{bs}^2 criteria	High
%KGH	53.47
KGH criteria	High

Note: μ = average; $\sigma^2 g$ = genetic variability; $2\sigma g$ = standard deviation; KG = genetic variability; H_{bs}^2 = heritability.

Table 5. The results of the analysis of genetic variability, heritability and genetic progress on seed weight per cob F2 population resulted from crossing BSM0729S3-A with BAP27799-1

Seed weight per cob	Analysis results
μ	85.12
$\sigma^2 g$	1140.48
$2\sigma g$	67.54
KG	Wide
H_{bs}^2	0.75
H_{bs}^2 criteria	High
%KGH	52.29
KGH criteria	High

Note: μ = average; $\sigma^2 g$ = genetic variability; $2\sigma g$ = standard deviation; KG = genetic variability; H_{bs}^2 = heritability.

The wide genetic variability caused by the population used is F2 seed with the highest level of segregation. Wide genetic variability will make the effective selection process in order to get the desired plant criteria, namely maize plants with high yield of seeds. Characters that have wide genetic variability and are accompanied by high heritability values will accelerate the selection process for the characters developed. According to [8] heritability is needed to determine the extent to which the appearance of a plant character is influenced by genetic and environmental factors. If the heritability is high, most of the phenotypic variation is caused by genetic variation, so the selection will get genetic progress [9].

IV. CONCLUSION

Selection activities in the F2 generation resulting from crossing BSM0729S3-A with BAP27799-1 can be effective because the observed variables, generally have wide genetic variability, quite high tilll high heritability and high genetic progress.

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