

GENETIC VARIABILITY, HERITABILITY AND EXPECTED GENETIC ADVANCES OF QUANTITATIVE CHARACTERS IN F2 PROGENIES OF SOYBEAN CROSSES

Keragaman Genetik, Heritabilitas dan Harapan Kemajuan Genetik Karakter Kuantitatif Populasi Galur F2 Kedelai Hasil Persilangan

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Submitted 28 November 2013; Revised 21 March 2014; Accepted 28 March 2014

ABSTRACT

The F2 progenies of crosses among three soybean varieties were evaluated with their parents at Ngale Experimental Farm, Ngawi, East Java during the dry season of 2011. The experiment was conducted in a randomized block design with three replications. The seeds of each F2 progenies and parents were planted in two rows of 4.5 m long. Plant spacing was 40 cm x 15 cm and each hill contained one plant. Among the characters studied, seed weight per plant, number of pods per plant and days to maturity had the highest coefficient of variability with the means of 52.6%, 48.2% and 41.9%, respectively. Whereas seed size, plant height and number of reproductive nodes had moderate values of 36.9%, 35.5% and 37.4%, respectively. Number of branches and days to flowering had the lowest variability of 11.7% and 15.3%, respectively. Number of pods per plant, days to maturity, plant height and seed size had high mean estimates of heritability coupled with high genetic advance. The genetic progress of these characters that would be obtained for one generation of selection was estimated 47.2%, 45.7%, 40.9% and 40.3%, respectively. Among the agronomic characters, plant height, number of pods per plant, seed size and days to maturity had the highest coefficient of variability associated with high heritability and genetic advance. Therefore, selection for high yielding with early maturity soybean genotypes based on plant height, number of pods per plant and seed size might be possible.

[**Keywords:** Soybean, genetic variability, heritability, genetic advances, quantitative characters]

ABSTRAK

Populasi galur F2 keturunan dari tiga kombinasi persilangan dan empat tetua kedelai dievaluasi di Kebun Percobaan Ngale, Ngawi, Jawa Timur pada musim kemarau 2011. Percobaan menggunakan rancangan acak kelompok dengan tiga ulangan. Setiap galur F2 dan varietas tetua ditanam dua baris dengan panjang barisan 4,5 m. Jarak tanam 40 cm x 15 cm dan setiap lubang ditanam satu benih. Dari delapan karakter kuantitatif yang diamati, bobot biji per tanaman, jumlah polong per tanaman, dan umur polong

masak menunjukkan koefisien keragaman genetik paling tinggi, masing-masing 52,6%, 48,2%, dan 41,9%. Ukuran biji, tinggi tanaman, dan jumlah buku subur mempunyai koefisien keragaman sedang (36,9%, 35,5%, dan 37,4%), sedangkan jumlah cabang dan umur berbunga mempunyai koefisien keragaman paling rendah (11,7% dan 15,3%). Jumlah polong per tanaman, umur polong masak, tinggi tanaman, dan ukuran biji mempunyai dugaan heritabilitas dan kemajuan genetik yang tinggi. Kemajuan genetik yang dapat diperoleh dalam seleksi untuk satu generasi dari jumlah polong per tanaman, umur polong masak, tinggi tanaman, dan ukuran biji diperkirakan masing-masing 47,2%, 45,7%, 40,9%, dan 40,3%. Di antara karakter agronomi yang diamati, tinggi tanaman, jumlah polong per tanaman, ukuran biji, dan umur polong masak mempunyai koefisien keragaman genetik yang tinggi disertai dengan dugaan heritabilitas dan harapan kemajuan genetik yang tinggi. Oleh karena itu, seleksi untuk memperoleh genotipe kedelai yang berdaya hasil tinggi dan berumur genjah berdasarkan karakter tinggi tanaman, jumlah polong per tanaman, dan ukuran biji relatif mudah diperoleh.

[**Kata kunci:** Kedelai, keragaman genetik, heritabilitas, kemajuan genetik, karakter kuantitatif]

INTRODUCTION

Soybean breeding techniques generally exploit the availability of plant genetic variability in population from crosses of two or more parents and to be followed by selection of individual plants. Estimates of genetic variability, heritability and correlation among characters are useful in planning and evaluating the breeding program. Utilization of yield component approach in breeding program should be most effective if the components are highly heritable, genetically independent, and not associated physiologically (Kang 1983). The heritability of the characters determines the extent to which it is transmitted from one generation to the next and it is

most valuable tool when used in conjunction with other parameters in predicting genetic gain that follows the selection for the character (Mohamed and El Shafi 2013). Uzun *et al.* (2013) stated that studies on heritability estimates could also be helpful to know the performance of parents in hybrids.

A knowledge of heritability and genetic advance that exist among important characters may provide a basis for more efficient planning in the breeding program for soybean. However, Kang *et al.* (1983) and Zafar *et al.* (2010) reported that correlation studies alone might not clearly disclose a reliable information for selection, and an inadequate knowledge of interrelationship among heritable traits may lead to negative results. Gravois and Mc. New (1993) stated that increasing grain yield would be most effective if the components involved were highly heritable and genetically independent or positively correlated or physiologically related in positive manner.

Chand *et al.* (2008) and Kumar and Kamendra (2009) reported that genetic improvement of crops for quantitative characters requires reliable estimates of genetic diversity, heritability and genetic advance. Sabu *et al.* (2009) stated that if the heritability for the characters is higher, then selection progress becomes easier and thus response to selection will be greater.

In soybean breeding, considerable emphasis currently is being placed on the development of high yielding cultivar. Fehr (1987) stated that selection for high yielding genotypes would not be effective if the components involved were not heritable. Jansen (1983) reported estimates of heritability in the F2 segregate populations for yield and plant height on soybean and found heritability of 43% for yield and 41% for plant height. Abady *et al.* (2013) reported that the broad sense heritability estimates were high for pods per plant, followed by plant height, number of branches and seed yield per plant.

Gravois and Mc. New (1993) reported that selection to increase yield through improvement of yield components would be most effective if the components were highly heritable. Akhter and Sneller (1996) reported that in F3 progenies of two cross combinations among three soybean varieties, seed yield per plant, plant height and days to maturity had the mean estimates of heritability of 39.4%, 63.0% and 67.0%, respectively. While Kang *et al.* (1983) reported that in F3 population, days to flowering, days to maturity and plant height had the highest mean estimates of heritability of 56.0%, 71.1%, and 70.2%, respectively, whereas the heritability estimates for seed weight per plant was low, only 27.4%. Aditya *et al.* (2011) reported that among eight quantitative characters

studied, plant height and number of pods per plant had the highest heritability estimates of 78.0% and 81.0% coupled with high genetic advances of 23.3% and 45.4%, respectively. Similar observations were found by Abady *et al.* (2013). They reported heritability estimates for plant height of 46.17% and number of pods per plant of 70.57%. The genetic advances of selection to these characters were predicted 67.40% and 20.98%, respectively.

The objectives of this study were to determine the magnitude of genetic variability, heritability and expected genetic advance that could be realized through selection from segregation progenies. The information obtained from this study would be helpful to specify certain traits that could be used as selection indices for identifications of potentially high yielding soybean genotypes.

MATERIALS AND METHODS

Hybridization of three cross combinations among four soybean varieties (Grobogan x Wilis, Rajabasa x Grobogan and Malabar x Rajabasa) was conducted in 2010 at green house of Indonesian Legume and Tuber Crops Research Institute (ILETRI), Malang, East Java. The aims of crosses were to obtain high yielding soybean lines with early maturity (< 80 days) and large seed size (> 14 g per 100 seeds). The F1 seeds were planted at Kendalpayak Experimental Farm, Malang during the wet season of 2010. The F1 populations were harvested through bulk method. The F2 progenies derived from three crosses were evaluated together with their parents (Grobogan, Wilis, Rajabasa and Malabar) at Ngale Experimental Farm, Ngawi, East Java during the dry season of 2011. In case of expected genetic advance, the F2 populations were selected based on selection intensity of 10%.

The experiment was arranged in a randomized block design with three replications. Seeds of each F2 progenies and their parents were sown in four rows of 4.5 m length in each plot. Plant spacing was 40 cm x 15 cm and each hill contained one plant. Plant populations of each F2 progeny and their parents were 120 plants in each replication. The variability among F2 plants within a cross was taken as a measure of genetic variance, whereas the mean of the variability of the parents was used to estimate environmental variance.

The genetic coefficient of variation (Vg) was estimated using formula suggested by Empig *et al.* (1970): $(Vg/X) \times 100$, where $VF2 - [(VP1)(VP2)]^{1/2}$.

Basal fertilizer was applied at the rate of 50 kg urea, 100 kg SP-36 and 50 kg NPK per hectare. Agronomic practices such as irrigation, weeding and insect pests control were carried out as needed.

The agronomic characters were recorded based on individual plant, including days to flowering, days to maturity, plant height, number of branches per plant, number of reproductive nodes per plant, number of pods per plant, seed weight (g per 100 seeds) and grain yield per plot. A list of parental varieties and their characteristics used in crosses is presented in Table 1.

Heritability (H) for all characters in the F2 was estimated using formula suggested by Empig *et al.* (1970) as follows

$$H = \frac{VF2 - [(VP1)(VP2)]^{1/2}}{VP2} \times 100$$

where:

VF2 = variance among F2 plants

VP1 = variance within female parents

VP2 = variance within male parents

Table 1. Characteristics of parental varieties of soybean used in crosses.

Variety	Days to flowering	Days to maturity	Plant height (cm)	Seed weight (g 100 ⁻¹ seeds)	Yield (t ha ⁻¹)
Grobogan	32	73	63	17	2.3
Wilis	39	90	51	10	1.6
Rajabasa	35	82	54	15	2.0
Malabar	31	70	57	12	1.3

Source: Indonesian Legumes and Tuber Crops Research Institute, Malang.

To estimate the variances were calculated from 120 F2 progeny plants and 120 plants of each parent. Expected genetic advance (GA) was calculated using formula suggested by Empig *et al.* (1970) as follows

$$GA = K(VF2)^{1/2} \times \frac{H}{X}$$

where:

K = 2.06, based on selection intensity of 10%

X = mean of the F2 population

RESULTS AND DISCUSSION

Genetic Variability

The genetic variability of eight characters in the F2 population is shown in Table 2. The mean variability of eight characters in the F2 population ranged from 11.7% to 52.6%. Among the characters studied, seed weight per plant, number of pods per plant and days to maturity had the highest coefficient of variability, with the means of 52.6%, 48.2% and 41.9%, respectively. Number of branches and days to flowering had the lowest variability and the means were only 11.7% and 15.3%, respectively. Plant height, seed size and number of reproductive nodes per plant had a moderate coefficient of variability of 36.9%, 35.5% and 37.4%, respectively (Table 2).

Among the characters studied, seed weight per plant and number of pods per plant showed the highest variability in the three cross combinations. This indicated that selection for identification of high yielding soybean genotypes based on these two

Table 2. Estimates of eight characters variability in the F2 generation of three soybean crosses, Ngawi, East Java, dry season of 2011.

Characters	General variability (%)			Mean (%)
	1	2	3	
Days to flowering	15.4	12.3	18.2	15.3
Days to maturity	47.7	38.6	39.4	41.9
Plant height (cm)	33.5	40.0	37.2	39.9
No of branches per plant	12.3	10.8	12.0	11.7
No of reproductives nodes	41.2	35.0	36.0	37.4
No of pods per plant	44.7	49.5	50.4	48.2
Seed size (g 100 ⁻¹ seeds)	30.5	45.8	30.2	35.5
Seed weight per plant (g)	63.7	54.1	40.0	52.6

1, 2 and 3 are F2 populations of the crosses of Grobogan x Wilis, Rajabasa x Grobogan and Malabar x Grobogan, respectively.

characters are possible. Similarly for days to maturity it had a high genetic variability suggested that selection for early maturing genotypes might be possible.

Hakim and Suyamto (2012) observed the mean genetic variability in F4 plants of two soybean crosses for days to flowering (17.2%), days to maturity (42.9%), plant height (33.6%), number of branches (14.0%), number of reproductive nodes (14.3%), number of pods per plant (47.4%), seed size (23.5%), and seed weight per plant (50.4%). Whereas in the present study, plant height, number of reproductive nodes, number of pods per plant, seed size and seed weight per plant had the mean genetic variability higher than those of previous observation (Table 2). The mean genetic variability for days to flowering and number of branches were lower, while the mean genetic variability for days to maturity had a similar high genetic variability with previous observation.

Heritability and Genetic Advance

Estimates of heritability (broad sense) obtained in the F2 are shown in Table 3. The mean estimates of heritability of eight characters ranged from 18.1% to 56.1%. Number of pods per plant and days to maturity had the highest mean estimate of heritability of 56.1% and 54.3%. Similarly for plant height and seed size it had high mean estimates of heritability of 49.2% and 46.3%, respectively. These results were comparable with those of Ertl and Fehr (1985), that number of pods per plant, days to maturity, seed size and plant height were heritable. The present study suggests that considerable amount of genetic variability is present in the three crosses of soybean and that selection for high yielding with early maturing genotypes based on these characters might be

possible to be conducted in the F3. Parida and Singh (1984) reported that heritability estimates for plant height, number of pods per plant, days to maturity and seed size in mungbean were quite high, namely 56.6%, 65.9, 43.1% and 50.9%, respectively.

Seed weight per plant and number of branches per plant had the lowest heritability, with the means of only 18.7% and 18.1%, respectively. Similar result was reported by Imrie *et al.* (1985). This indicates that the genetic progress of seed weight and number of branches predicted as a substantial gain for one generation of selection was low. Number of reproductive nodes and days to flowering had a moderate heritability estimate, with the means of 36.7% and 31.9%, respectively.

Estimates of genetic advance of eight characters if selection were performed with the intensity of 10% are shown in Table 4. The expected genetic advance at 10% selection intensity ranged from 12.3% for number of branches to 47.2% for number of pods per plant. Number of pods per plant and days to maturity had the highest expected genetic advance due to its high heritability (Table 3 and 4). The genetic advance of these characters was predicted as a substantial gain for one generation of selection obtaining 47.2% and 45.7%, respectively. Rohman and Hussain (2003) reported that high genetic advance associated with high value of heritability indicating additive gene effect in controlling the characters. In the present observation, number of reproductive nodes, plant height and seed size also had a high mean estimate of genetic advances of 42.0%, 40.9% and 40.3%, respectively. Whereas seed weight per plant and days to flowering had a moderate mean estimate of 35.5% and 33.6%, respectively. Among the characters studied, number of branches per plant showed the lowest expected genetic gain (Table 4).

Table 3. Estimates of heritability of eight characters in the F2 generation of three soybean crosses, Ngawi, East Java, dry season of 2011.

Characters	Estimate of heritability (%)			Mean (%)
	1	2	3	
Days to flowering	33.5	32.2	30.0	31.9
Days to maturity	58.0	54.4	50.5	54.3
Plant height (cm)	53.6	49.3	44.7	49.2
No of branches per plant	17.5	19.4	17.4	18.1
No of reproductives nodes	33.3	36.8	40.0	36.7
No of pods per plant	58.3	55.9	54.1	56.1
Seed size (g 100 ⁻¹ seeds)	39.4	45.4	54.1	56.1
Seed weight per plant (g)	16.7	19.2	20.2	18.7

1, 2 and 3 are F2 populations of the crosses of Grobogan x Wilis, Rajabasa x Grobogan and Malabar x Grobogan, respectively.

Table 4. Estimates of genetic advance at 10% selection intensity of eight characters in the F2 generation of three soybean crosses, Ngawi, East Java, dry season of 2011.

Characters	Estimate of genetic advance (%)			Mean (%)
	1	2	3	
Days to flowering	33.4	35.1	32.3	33.6
Days to maturity	46.0	49.1	42.0	45.7
Plant height (cm)	44.2	37.9	40.6	40.9
No of branches per plant	10.7	14.4	11.8	12.3
No of reproductives nodes	39.7	46.1	40.2	42.0
No of pods per plant	45.1	49.3	47.2	47.2
Seed size (g 100 ⁻¹ seeds)	38.9	41.8	40.2	40.3
Seed weight per plant (g)	36.6	34.5	35.4	35.5

1, 2 and 3 are F2 populations of the three crosses of Grobogan x Wilis, Rajabasa x Grobogan and Malabar x Grobogan, respectively.

In relation to grain yield, number of pods per plant, plant height and seed size had high mean estimate of heritability (56.1%, 49.2% and 46.3%) and high genetic advance (47.2%, 40.9% and 40.3%) associated with high value of genetic variability (48.2%, 36.9% and 35.5%, respectively). Sumarno and Zuraida (2006) reported that plant height and number of pods per plant had a positive significant correlation with grain yield. While Pandey and Torrie (1973) stated that pods per plant and seed size positively correlated with grain yield. The direct effects of these characters on grain yield were high. Therefore, selection to increase grain yield through improvement of plant height, pods per plant and seed size might be possible.

CONCLUSION

Among quantitative characters studied, number of pods per plant and days to maturity had the highest coefficient of variability, associated with high heritability and high expected genetic advance. This indicates that selection to obtain soybean genotype with high number of pods and early maturity on the next generation is relatively easy.

Number of pods per plant, plant height and seed size had high mean estimates of genetic advance coupled with high values of heritability. The coefficients of variability of these characters were also quite high. Therefore, selection to increase grain yield through improvement of pods per plant, plant height and seed size will be effective.

In relation to grain yield, the mean heritability estimate for seed weight per plant was low. However, considerable high genetic variability and high genetic advance were present for seed weight per plant.

Therefore, inheritance study for seed weight per plant should be conducted to identify the use of this character as a selection indice.

ACKNOWLEDGEMENTS

We deeply thank to Ir. Suyamto, head of Ngale Experimental Station, for his support and to Mr. Sukadi for his assistance during the study.

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