

## GENE ACTION AND HERITABILITY ESTIMATES OF QUANTITATIVE CHARACTERS AMONG LINES DERIVED FROM VARIETAL CROSSES OF SOYBEAN

### Aksi Gen dan Dugaan Heritabilitas Karakter Kuantitatif pada Populasi Galur Kedelai Hasil Persilangan

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#### ABSTRACT

The knowledge of genetic action, heritability and genetic variability is useful and permits plant breeder to design efficient breeding strategies in soybean. The objectives of this study were to determine gene action, genetic variability, heritability and genetic advance of quantitative characters that could be realized through selection of segregation progenies. The F1 population and F2 progenies of six crosses among five soybean varieties were evaluated at Muneng Experimental Station, East Java during the dry season of 2014. The lines were planted in a randomized block design with four replications. The seeds of each F1 and F2 progenies and parents were planted in four rows of 3 m long, 40 cm x 20 cm plant spacing, one plant per hill. The result showed that pod number per plant, seed yield, plant yield and harvest index were found to be predominantly controlled by additive gene effects. Seed size was also controlled by additive gene effects, with small seed dominant to large seed size. Plant height was found to be controlled by both additive and nonadditive gene effects. Similarly, days to maturity was due mainly to additive and nonadditive gene effects, with earliness dominant to lateness. Days to maturity had the highest heritability estimates of 49.3%, followed by seed size (47.0%), harvest index (45.8%), and pod number per plant (45.5%). Therefore, they could be used in the selection of a high yielding soybean genotype in the F3 generation.

[**Keywords:** gene action, heritability, soybean, varietal crosses]

#### ABSTRAK

Dalam pemuliaan kedelai, pengetahuan tentang aksi gen, heritabilitas, dan keragaman genetik sangat diperlukan agar pemulia dapat merencanakan program seleksi yang efektif dan efisien. Penelitian ini bertujuan untuk mempelajari aksi gen, heritabilitas, kemajuan genetik, dan keragaman genetik karakter kuantitatif, galur kedelai hasil persilangan. Tanaman F1 dan galur F2 keturunan dari enam kombinasi persilangan, dan lima varietas tetua dievaluasi di Kebun Percobaan Muneng, Jawa Timur pada musim kemarau 2014. Percobaan menggunakan rancangan acak kelompok dengan empat ulangan. Biji F1 dan F2 dari setiap kombinasi persilangan dan varietas tetua ditanam masing-masing empat baris dengan panjang

barisan 3 m. Jarak tanam 40 cm x 20 cm, satu tanaman per rumpun. Hasil penelitian menunjukkan jumlah polong per tanaman, hasil biji per tanaman, bobot brangkas, dan indeks panen secara dominan dikendalikan oleh gen aditif. Ukuran biji juga dikendalikan oleh gen aditif, dan ukuran biji kecil bersifat dominan terhadap biji besar. Tinggi tanaman dikendalikan oleh gen aditif dan nonaditif, demikian pula umur polong masak secara dominan dikontrol oleh banyak gen (aditif dan nonaditif), dan umur genjah bersifat dominan terhadap umur dalam. Umur polong masak mempunyai dugaan heritabilitas paling tinggi (49,3%), diikuti ukuran biji, indeks panen, dan jumlah polong per tanaman, masing-masing 47,0%, 45,8%, dan 45,5%. Seleksi terhadap umur polong masak, ukuran biji, indeks panen, dan jumlah polong per tanaman mempunyai harapan kemajuan genetik cukup tinggi, masing-masing 41,0%, 38,8%, 33,6%, dan 29,1%. Oleh karena itu, karakter tersebut dapat digunakan sebagai kriteria seleksi untuk memperoleh genotipe kedelai yang berdaya hasil tinggi, berumur genjah, dan berukuran biji besar pada galur F3.

[**Kata kunci:** aksi gen, galur persilangan, heritabilitas, kedelai]

#### INTRODUCTION

In a selection program, knowledge of gene action, heritability and genetic variability is useful and permits plant breeder to design efficient selection strategies. Many traits of soybean are inherited in a quantitative manner. The quantitative characters of soybean have been extensively studied included the seed yield, primary yield components, such as pods per plant, seed weight per plant and seed size as well as the trait related to plant size and development.

Seed yield of soybean is an important trait as it measures the economic productivity of the plant. However, inheritance of this character is extremely complex. Studies on combining ability and types of gene action on soybean by Murty et al. (2009) indicated that both additive and nonadditive gene effects contribute to seed yield with parent cultivars differing in the

relative importance of each. Similarly, Rao et al. (2009) reported that seed yield, harvest index and seed size were predominantly controlled by additive genes effects, while days to maturity was apparently controlled by both additive and nonadditive gene effects and the dominance effects being more evident in F2 generation.

Hakim et al. (2014) reported that in F2 progenies of three cross combinations among three soybean varieties, inheritance for pod number per plant, plant height and seed size in the next generation were high, while that for seed yield per plant was relatively small. Selection for high yielding soybean genotypes by increasing pod number per plant, plant height and seed size should be possible. While selection for increasing grain yield through improvement of seed yield per plant was relatively difficult.

Nonadditive gene action is the most important character in the F1 generation of *Phaseolus aureus* with degree of dominance reduced in the F2 and F3 (Singh and Singh 1987). These data illustrate the complexity of inheritance for seed yield. Imrie et al. (1987) reported that plant yield, seed yield and harvest index of mungbean were predominantly controlled by additive genes effects. Similarly, seed size was controlled by additive gene effects, while days to maturity by both additive and dominant gene effects. Knowledge of heritability and genetic advance of soybean may provide a basis for efficient planning in breeding program for soybean. Uzun et al. (2013) stated that studies on heritability estimates are helpful in knowing parent performance in hybrids of sesame.

Increasing grain yield would be most effective if the components involved were highly heritable and genetically independent of positively correlated of physiologically related in positive manner (Gravois and Mc New 1993). Genetic improvement of crops for quantitative characters requires reliable estimates of genetic diversity, heritability and genetic advance (Chand et al. 2008; Kumar and Kamendra 2009). If the heritability for the characters is higher, then selection progress becomes easier and thus response to selection will be greater.

Abady et al. (2013) 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 heritability estimates of 39.4%, 63.0% and 67.1%, respectively. While Zafar et al. (2010) reported that in F3 population, days to flowering, days to maturity and plant height had the highest heritability estimates of 56.0%, 71.1% and 70.2% respectively. Whereas the heritability estimate for seed weight per plant was low of only 27.4%. Aditya et al. (2013) reported that among

eight quantitative characters studied, plant height and pod number per plant had the highest heritability estimates of 78.0% and 81.0% coupled with high genetic advance of 25.3% and 45.4%, respectively. Similar result was found by Akhter and Sneller (1996) who obtained heritability estimate for plant height of 46.7% and pod number per plant of 70.5%. The genetic progress of selection for these characters was predicted 67.4% and 20.9%, respectively.

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

## MATERIALS AND METHODS

### Genetic Materials and Development of F2 Populations

Genetic materials used and their characteristics are shown in Table 1. Six cross combinations among five soybean varieties (Muria x Grobogan, Muria x Burangrang, Muria x Panderman, Kawi x Grobogan, Kawi x Burangrang, Kawi x Panderman) were conducted in the wet season of 2013 at Screen House, Muneng Experimental Station, Probolinggo, East Java. The main aims of the crosses were to improve grain yield ( $>2 \text{ t.ha}^{-1}$ ), days to maturity (75 days) and seed size ( $> 17 \text{ g.100}^{-1}$  seeds) of variety Muria and Kawi which at present both varieties have low yield, late maturity and small seed size.

The F1 seeds were planted at Muneng Experimental Station, Probolinggo, East Java, during the dry season of 2013. The F1 plants were harvested through a bulk method. A total of twenty four F2 progenies of each cross were developed from each F1 plant.

**Table 1. Characteristics of parental varieties of soybean used in crosses for developing F2 populations.**

Code of parents	Varieties	Days to maturity	Plant height (cm)	Seed size (g.100 <sup>-1</sup> seeds)	Yield (t.ha <sup>-1</sup> )
P1	Muria	90	50	12	1.7
P2	Kawi	95	70	10	1.8
P3	Grobogan	73	65	19	2.7
P4	Burangrang	78	70	17	2.5
P5	Panderman	80	65	19	2.4

Source: Indonesian Legumes and Tuber Crops Research Institute (2005).

## Field Trials of F1 and F2 Progenies

The F2 progenies derived from the six crosses consisted of two hundred and four progenies each were evaluated together with their parents (Muria, Grobogan, Burangrang, Panderman and Kawi) at Muneng Experimental Station, Probolinggo, East Java during the dry season of 2014. In case of expected genetic advance, the F2 populations were selected based on 10% selection intensity.

The experiment was arranged in a randomized block design with four replications. The seeds of each F1 and F2 progenies and their parents were sown in four rows of 3 m long, 40 cm x 20 cm plant spacing, one plant per hill. Population of each F1 plant, F2 progenies and the parents were 60 plants in each plot. Basal fertilizers were applied at the rate of 50 kg urea, 100 kg Phonska and 50 kg SP36 per hectare. Agronomic practices such as weeding and insect pest control were carried out according to recommendation.

Data were collected based on individual plants of sixty plants per plot. Parameters observed included days to maturity (DM), plant height (PH), pod number per plant (PP), seed size (SS), seed yield per plant (SY), plant yield (PY) and harvest index (HI). Collected yield data were then calculated as  $SY/(SY+PY)$ .

## Data Analyses

The genetic variation was estimated using a formula suggested by Stuber (1970): additive variance ( $S^2A$ ) = ( $S^2m + S^2f$ ); nonadditive variance ( $S^2D$ ) =  $S^2mf$ , in the F1 generation and a  $S^2D = 4S^2mf$ , in the F2 generation. Whereas,  $S^2m$  is the variance for male parents,  $S^2f$  is a variance for female parents, and  $S^2mf$  is a male x female interaction variance.

The ratio of additive to nonadditive (dominance) variance was calculated using a formula of  $S^2A/S^2D$ . The heritability (H) was estimated using a formula:  $H = S^2A/(S^2A + S^2D + S^2e)$ . Genetic advance (GA) was estimated using a formula:  $GA = K (VF^2)^{1/2} \times H/X$ , based on 10% selection intensity,  $K = 2.06$ ,  $VF^2$  = variance among F2 plants, H = heritability, X = means of F2 population.

The genetic coefficient of variation (VG) was estimated using a formula suggested by Empig et al. (1970):  $(VG/X) \times 100$ , where  $VG = VF_2 - [(VP_1)(VP_2)]^{1/2}$ ;  $VF_2$  is a variance among F2 plants,  $VP_1$  is a variance within female parents, and  $VP_2$  is a variance within male parents.

## RESULTS AND DISCUSSION

### Gene Action

Estimates of various components based on individual plants in F1 and F2 gene actions are presented in Table 2. Days to maturity was predominantly controlled by both additive and nonadditive (dominant) gene effects. Therefore, inheritance of days to maturity was associated with both additive and nonadditive gene effects and the dominance effects being more evident in F2 generation. This observation is comparable with that reported by Kumar et al. (2009) where days to maturity was mainly controlled by additive and nonadditive gene effects. In mungbean, Wilson et al. (1986) reported that earliness was controlled by additive gene and dominance or partial dominance. In this study the variance analysis indicated that additive effects were significant in F1, while nonadditive effects were significant in F2 generations, with earliness being dominant to lateness (Table 2).

Examination of individual crosses for days to maturity revealed underlying simple segregation ratio of 3:1 in progenies of late maturing parent (Muria) which matured 90 days, where three parts of the tested plants showed early maturity (<82 days) and one part of the tested plants showed late maturity (>82 days). However, the progeny of the other late maturing parent (Kawi) which matured 95 days, segregated in the ratio of 15:1, where fifteen parts of the plants showed early maturity (<82 days) and one part of the plants demonstrated late maturity (>82 days) (Table 3).

Results of variance analysis showed that plant height was predominantly controlled by both additive and nonadditive gene effects (Table 2). Therefore, inheritance of plant height was associated with both additive and nonadditive gene effects. Similar results were observed by Murty et al. (2009) who found significant effects of additive and nonadditive genes for tallness in some parents and dwarfness in other parent. Rao et al. (2009) reported that dominance effects and duplicate epistatic played an important role in expression of plant height. However, Wilson et al. (1986) stated that mode of gene action for plant height was determined by parent genotypes used in crosses.

Pod number per plant was significantly controlled by additive gene effects. This indicated that inheritance of pod number per plant was associated with additive gene effects. Similar results was reported by Singh and Malhotra (2007). They stated that additive gene effects were significant and played an important role in expression of pod number per plant. Luthra et al. (2009) stated that additive effects on pods per plant were larger

**Table 2. Estimates of variance components of seven characters in F1 and F2 soybean progenies, Muneng Experimental Station, dry season of 2014.**

Characters	Generation	Variance components		Male Female interaction variance (S <sup>2</sup> mf)	Ratio (S <sup>2</sup> A/S <sup>2</sup> D)
		Male parents (M)	Female parents (F)		
Days to maturity	F1	0.00	3.11*	2.38	3.25
	F2	0.00	2.24	7.21*	0.16
Plant height (cm)	F1	0.01	3.18	2.01	2.08
	F2	0.03	3.08	6.31	0.20
Pod number per plant	F1	0611	2.75	1305	2.05
	F2	2620	3.80	188	3.03
Seed size (g.100 <sup>-1</sup> seeds)	F1	87.9**	4.11*	1.47	2.27
	F2	46.5*	3.27	6.23**	0.18
Plant yield (g) <sup>a</sup>	F1	7812*	6870	0.0	1.12
	F2	3202**	4218**	0.0	1.39
Seed yield per plant (g)	F1	2225*	1.18	1265	1.87
	F2	1305	371	163	2.57
Harvest index	F1	239**	2337**	0.0	1.89
	F2	438*	1021**	1.90	2.00

\*P<0.05; \*\*P<0.01. <sup>a</sup>Plant yield is a seed yield plus the weight of all other plant parts.

**Table 3. Segregation ratio between earliness and lateness parents in F2 progenies of six soybean cross combinations, Muneng Experimental Station, dry season of 2014.**

Early <sup>a</sup> parents	Late parents <sup>b</sup>					
	P1			P2		
	Ratio <sup>c</sup>	X <sup>2d</sup> (3:1)	Prob.	Ratio <sup>c</sup>	X <sup>2d</sup> (15:1)	Prob.
P3	20:3	1.755	P>0.10	15:1	0.044	P>0.80
P4	10:5	0.636	P>0.30	17:1	0.019	P>0.90
P5	25:6	0.408	P>0.50	24:3	1.035	P>0.20
Total	55:14	1.349	P>0.20	55:5	0.549	P>0.70

<sup>a</sup>Early parents and progenies matured <82 days; <sup>b</sup>Late parents and progenies matured >82 days; <sup>c</sup>Ratio of early to late maturity progenies observed from this study; <sup>d</sup>Chi-square test of the tested ratio; Prob = probability level.

in F2 generation, while in F1 generation the effects were not significant.

Seed size was predominantly controlled by additive gene effects. This means that the additive gene effects were significant and played an important role in expression of inheritance on seed size. Similar results were obtained by Matik et al. (2007), reporting that seed size was apparently controlled by additive gene effects in F1 and F2 generations, with small seeds being dominant to large seeds. Malhotra et al. (2008) on the other hand reported that small seed size was partially dominant over large with predominantly additive gene action.

Examination of individual cross combinations for seed size in F2 generation revealed underlying segregation ratio of 15:1 in each progeny derived from large seed

size parents P3 (Grobogan), P4 (Burangrang) and P5 (Panderman), which had seed size of 19 g, 17 g and 19 g.100<sup>-1</sup> seeds, respectively. Each progeny segregated in the ratio of fifteen progenies demonstrated small seed size (<13 g.100<sup>-1</sup> seeds) and one progeny had large seed size (>13 g.100<sup>-1</sup> seeds) (Table 4).

Seed yield per plant was predominantly controlled by additive gene effects. Similarly plant yield and harvest index were controlled by additive effects (Table 2). This indicated that inheritance of these characters was predominantly controlled by additive gene effects. Analyses of variance indicated that additive gene effects for seed yield and plant yield were greater than those of nonadditive gene effects. Malik et al. (2007) and Rao *et al.* (2009) reported that additive gene effects were important in the expression of inheritance on seed yield per plant. Singh and Singh (1987) reported that nonadditive gene effects (dominant and epistatic) were mostly important in plant seed yield in F1 generation, while degree of dominance reduced in F2 and F3 generations.

Results of variance analysis indicated that additive gene effects for harvest index were greater than nonadditive gene effects (Table 2). Harvest index was less subjected to environmental variation and consequently had a higher heritability (45.8%) (Table 5). Therefore, selection criteria based on this character would be more useful for yield improvement. Similar result was reported by Ahuja and Chowdhury (1981) and Gupta and Singh (1987). They stated that harvest index had a substantially higher additive variance component than that of nonadditive component. This character is mainly governed by additive genes.

**Table 4. Segregation ratio between large seed and small seed parents in F2 progenies of six soybean cross combinations, Muneng Experimental Station, dry season of 2014.**

Large seeds parents <sup>a</sup>	Small seed parents <sup>b</sup>					
	P1			P2		
	Ratio <sup>c</sup>	X <sup>2d</sup> (15:1)	Prob.	Ratio <sup>c</sup>	X <sup>2d</sup> (15:1)	Prob.
P3	21:4	1.445	P>0.20	20:3	1.022	P>0.30
P4	12:6	0.612	P>0.30	16:1	0.16	P>0.70
P5	27:9	0.403	P>0.30	23:3	1.032	P>0.40
Total	60:19	1.127	P>0.20	P>0.20	0.878	P>0.50

<sup>a</sup>Large seeds of parents and progenies >13 g.100<sup>-1</sup> seeds; <sup>b</sup>Small seeds of parents and progenies < 13 g.100<sup>-1</sup> seeds, <sup>c</sup>Ratio of small to large seed size progenies observed from this study; <sup>d</sup>Chi-square test of the tested ratio, Prob = probability level.

### Heritability and Genetic Advance

Heritability estimates (broad sense) obtained in the F2 are shown in Table 5. The means of heritability estimates of seven characters ranged from 13.0% to 49.3%. Days to maturity had the highest heritability estimate of 49.3% followed by seed size of 47.0%. This indicates that inheritance of days to maturity and seed size in the next generation (F3) are high, and selection to obtain soybean genotypes with early maturity and large seed size in the F3 is relatively easy. Similar results were reported by Abady et al. (2013), who obtained heritability estimates of 46.6% for days to maturity and 43.0% for seed size. Aditya et al. (2013) pointed out that days to maturity and seed size were heritable and they suggested that selection to increase grain yield through days to maturity and seed size should consider plant height and pod number per plant.

Harvest index also demonstrated high heritability estimates with mean value of 45.8% across the six F2 populations used in this study (Table 5). Ahuja and Chowdhury (1981) reported heritability estimates for harvest index of 56.7%. They stated that inheritance of harvest index was quite high, and genotypes showing higher harvest index could produce higher grain yield. Harvest index, therefore, is an important character and this character can be used as a selection criterion in soybean yield improvement program.

Plant height, on the other hand, showed moderate heritability estimate of 33.2% (Table 5). This indicates that inheritance of plant height in the F3 is relatively low. This result is comparable to that observed by Zafar et al (2010), reporting the mean heritability estimates for plant height of 35.0% in the F2 and 37.6% in the F3 plants, while Karasu (2009) observed mean heritability estimate for plant height of only 19.7%. Variation of heritability

**Table 5. Estimates of broad sense heritability of seven quantitative characters in the F2 generation of six soybean crosses, Muneng Experimental Station, dry season of 2014.**

Characters	Broad sense heritability estimates among six F2 populations (%) <sup>a</sup>						Means (%)
	1	2	3	4	5	6	
Days to maturity	43.0	47.1	59.4	50.2	45.0	51.1	49.3
Plant height	29.8	36.5	40.3	33.9	21.7	37.0	33.2
Pod number per plant	42.2	39.2	47.1	50.0	40.3	54.2	45.5
Seed size	46.5	49.0	38.6	51.3	43.6	53.0	47.0
Plant yield	11.2	16.8	13.0	9.1	12.3	15.6	13.0
Seed yield per plant	16.4	21.6	11.9	20.1	24.5	15.3	18.3
Harvest index	42.8	39.2	47.5	50.6	40.4	54.3	45.8

<sup>a</sup>1, 2, 3, 4, 5, 6 are six F2 populations developed from six independent cross combinations.

estimates in those studies might be mostly due to high differences in environmental conditions affecting high variation among the study results.

Pod number per plant also had a high heritability estimate of 45.5%. This result is comparable with that reported by Arsyad et al. (2006). They found that in F3 progenies of two cross combinations among three soybean varieties, pod number per plant, seed yield per plant and plant height had high heritability estimates of 57.2%, 53.0% and 39.4%, respectively. While Faisal et al. (2007) found heritability estimate of 45.6% for pod number per plant in the F2 segregating population. Abady et al. (2013) stated that pod number per plant had a high mean heritability estimate, then selection for this character in the next generation (F3) became easier and thus showing a greater response to selection.

In this study, seed yield per plant had a low heritability estimate of only 18.3% (Table 5). This indicates that inheritance of seed yield per plant in the next generation (F3) is relatively small. Therefore, selection for high yielding genotypes based on seed yield per plant in the F3 generation is relatively difficult. Karasu et al. (2009) found heritability estimate for seed yield per plant in F2 plants of only 19.7% with expected genetic advance of 27.4%. They stated that selection to increase grain yield based on seed yield per plant in the early generation (F2-F3) would not be effective. Selection based on this character should be done in a later generation (F6-F7).

Among seven characters studied in the F2 progenies, plant yield showed the lowest heritability estimate of only 13% (Table 5). This indicates that inheritance of plant yield in the next generation (F3) is small. Sabu

et al. (2009) observed heritability estimate for plant yield in the F3 of only 11.6%, thus selection based on this character would not be effective. Uzun et al. (2013) reported that genotypes which had a high plant yield may not always produce high seed yield.

Estimates of genetic advance of seven characters at 10% selection intensity are shown in Table 6. Genetic advances expected at 10% selection intensity of the seven characters observed in this study ranged from 14.9% to 41.0%. Days to maturity and seed size had the highest expected genetic advances of 41.0% and 38.8%, respectively (Table 6). The genetic advances of these characters were predicted as a substantial gain for one generation of selection obtaining 41% for days to maturity and 38.8% for seed size. This result is comparable to that found by Akhter and Sneller (1996) who obtained genetic advance of 39.7% for days to maturity and 43.1% for seed size. Seed yield per plant and harvest index also showed high expected genetic advance of 35% and 33.6%, respectively. The genetic advance of these characters that would be obtained for one generation of selection was estimated to be 35% for seed yield per plant and 33.6% for harvest index. A similar result was reported by Aditya et al. (2013) who found genetic advance of 45.4% for seed yield per plant and 45.1% for harvest index. This means that genetic progress for seed yield per plant and harvest index were predicted as a substantial gain for one generation of selection obtaining 45.4% and 45.14%, respectively. Parida et al. (2007) reported that genetic advance for seed yield per plant in F2 generation of mungbean was 37.2% and for harvest index was 40.3%. This indicates that genetic progress for seed yield per plant obtained for

one generation of selection was estimated to be 37.2%, while for harvest index was 40.3%.

Pod number per plant and plant height had moderate expected genetic advances of 29.1% and 25.7%, respectively (Table 6). This indicates that genetic progress of pods per plant and plant height was predicted as a substantial gain for one generation of selection obtaining 29.1% and 25.7%, respectively. These results were comparable with the genetic advance of pods per plant and plant height that were considered as moderate.

Among the characters studied, plant yield showed the lowest expected genetic advance of 14.9% (Table 6). This observation was comparable with that reported by Rohman and Husain (2003) who found genetic progress for plant yield of only 11.7%. The lowest expected genetic advance for plant yield was due to its low heritability.

### Genetic Variability

Genetic variability of seven quantitative characters observed in the F2 population is shown in Table 7. The mean variability of the seven characters observed in F2 population ranged from 15.6% to 53.5%. Among the characters studied, seed weight per plant, plant height and pod number per plant showed the highest coefficient of variability with the mean values of 53.5%, 49.0%, and 43.2%, respectively. Days to maturity, harvest index, and seed size showed moderate coefficient of variability of 36.5%, 33.6% and 33.0%, respectively, whereas plant yield demonstrated the lowest variability with the mean value of 15.6% (Table 7).

Results of this study showed that days to maturity, seed size, harvest index and pod number per plant had

**Table 6.** Estimates of genetic advance by using 10% selection intensity of seven quantitative characters observed in F2 generation of six soybean crosses, Muneng Experimental Station, dry season of 2014.

Characters	Estimates of genetic advance (%) <sup>a</sup>						Means (%)
	1	2	3	4	5	6	
Days to maturity	42.0	48.1	44.5	39.4	32.0	40.0	41.0
Plant height	24.7	25.4	25.3	28.9	23.6	26.3	25.7
Pod number per plant	22.7	38.0	25.1	24.3	38.7	25.8	29.1
Seed size	37.4	40.1	35.5	39.0	36.4	44.4	38.8
Plant yield	19.1	14.0	10.0	19.8	10.7	16.0	14.9
Seed yield per plant	40.7	35.1	30.9	38.3	43.2	26.0	35.7
Harvest index	27.6	35.0	31.5	41.0	28.5	38.0	33.6

<sup>a</sup>1, 2, 3, 4, 5, 6 are six F2 populations developed from six independent cross combinations used in this study.

**Table 7.** Coefficient of genetic variability of seven quantitative characters in F2 generation of six soybean crosses, Muneng Experimental Station, dry season of 2014.

Characters	Estimates of genetic variability (%) <sup>a</sup>						Means (%)
	1	2	3	4	5	6	
Days to maturity	40.4	38.7	35.4	32.1	42.4	30.0	36.5
Plant height	51.2	44.6	43.8	50.4	54.0	50.0	49.0
Pod number per plant	48.6	53.1	40.1	37.0	40.0	40.4	43.2
Seed size	35.0	30.1	35.5	29.7	35.2	32.5	33.0
Plant yield	18.7	18.1	17.2	15.3	20.0	24.3	15.6
Seed yield per plant	58.0	55.1	48.7	50.5	54.7	54.0	53.5
Harvest index	35.3	30.8	32.6	33.0	35.9	34.0	33.6

<sup>a</sup>1, 2, 3, 4, 5, 6 are six populations developed from six independent crosses combination used in this study.

high heritability estimates of 49.3%, 47.0%, 45.8% and 45.5% coupled with high expected genetic advances of 41.0%, 38.8%, 33.6% and 29.1% respectively (Tables 5 and 6). The coefficients of genetic variability of these characters were also quite high with the means of 36.5%, 33.0%, 33.6% and 43.2%, respectively (Table 7). This indicates that inheritance for days to maturity, seed size, harvest index and pod number per plant in the next generation (F3) were high, and selection to obtain high yielding soybean genotypes with early maturity and large seed size in F3 progenies would be relatively easy. Therefore, pod number per plant, harvest index, days to maturity and seed size could be suggested as selection criteria to obtain high yielding soybean genotypes with early maturity and large seed size in the F3 generation.

Seed yield per plant had a low heritability estimate. This indicates that inheritance of seed yield per plant in the next generation (F3) was low. Therefore, yield improvement based on this character is relatively difficult. The yield improvement may be enhanced through selection for harvest index.

Results of this study indicated that in a breeding program for improving soybean production, selection of progenies derived from a cross between low yield, late maturity and small seed size varieties such as Muria and Kawi with those having high yielding, early maturity and large seed size such as Grobogan, Burangrang and Panderman should generate several soybean genotypes demonstrating high yield, early maturity and large seed size. Therefore, increasing grain yield of soybean varieties such as Muria and Kawi that currently have early maturity and large seed size through improving pod number per plant, harvest index, days to maturity and seed size should be possible.

## CONCLUSION

Pod number per plant, seed yield per plant, plant yield and harvest index were predominantly controlled by additive gene effects. Similarly seed size was also controlled by additive gene effects with small seed is dominant to that of large seed size. Plant height was predominantly controlled by both additive and nonadditive gene effects. Similarly days to maturity was due mainly to additive and nonadditive gene effects, with earliness is dominant to that of lateness.

Days to maturity, seed size, harvest index and pod number per plant had high heritability estimates coupled with high expected genetic advance. Therefore, pod number per plant, harvest index, days to maturity and seed size could be suggested as selection criteria to obtain high yielding soybean genotypes with early maturity and large seed size in the F3 generation. It should be possible

to increase grain yield of variety Muria and Kawi that currently have early maturity and large seed size by improving pod number per plant, harvest index, days to maturity and seed size.

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