**GENE ACTION AND HERITABILITY ESTIMATES OF QUANTITIVE CHARACTERS AMONG LINES DERIVED FROM VARIETAL CROSSES OF MUNGBEAN (*Vigna radiata (L) Wilczec)***

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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 mungbean. The objective of this study were to determine gene action, genetic variability, heritability and genetic advance of quantitative character that could be realized through selection of segregation progenies. The F1 population and F2 progenies of crosses among five mungbean varieties were evaluated at Kendal Payak experimental station, Malang, East Java during wet season of 2019. The lines were planted in a randomized block design with four replications. The seed of each F1 and F2 progenies and parents were planted in five rows of 3 m long. Plant spacing was 40 cm x 20 cm, one plant per hill. The results showed that day to maturity was predominently controlled by both additive and non aditive gene effects with earliness being dominant to lateness. Plant height was also controlled by additive and non aditive gene effects. Pod number per plant was a significantly controlled by additive gene effects. This indicated that inheritance of pod number per plant was associated with additive gene effects, seed size was also controlled by additive gen effects, with small seed dominant to large seed size. Days to maturity had the highest heritability estimates of 48.4% followed by number of pods per plant 44.1% and seed size 38.7%. Therefore, they could be used in the selection of high yielding mungbean genotype in the F3 generation

Keywords: Gene action, Heritability, Mungbean, Varieted crosses

**Introduction**

In selection program, knowledge of gene action, heritability and genetic variability is useful and permits plant breeder to design efficient selection strategist. Many traits of mungbean are inherited in an agronomic manner. The agronomic characters of mungbean have been extensively studied include the grain yield, 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.

Grain yield of mungbean is an important trait as it measures the economic productivity of the plant. However, inheritance of this character is extremely complex. Studied on combining ability a types of gene action on mungbean by (Imrie *et al*. 2007) indicated that both additive and non additive gene effects contribute to grain yield with parent cultivars difefering in the relative importance of each. Similarly (Murty *et al.* 2009), reported that green yield, harvest index and seed size were predominantly controlled by additive gene effects, while days to maturity was apparently control by both additive and nonadditive gene effects and the dominance effect being more evident in F2 generation.

Research result was reported by (Hakim and Suyamto 2017) that in F2 progenies of six crosses combinations among five soybean varieties, pod number per plant, seed yield, plant height, harvest index and seed size were found to be predominantly controlled by additive gene effects. While plant height and days to maturity were found to be controlled by both additive and non additive gene effects. While (Singh and Singh 2017) reported that non additive gene action is the most important character in the F1 generation of *Phaseolus aureus* with degree of dominance reduced in the F2 and F3. This data ilustrate the complexity of inheritance for seed yield. Knowledge of heritability and genetic advance of mungbean may provide a basis for efficient planning in breeding program for mungbean. The sudies on heritability estimates are helpful in knowing parent performance in hybrids of mungbean (Malhotra *et al.* 2013).

Gravois and Mc. New (1993) stated that increasing grain yield would be most effective if the components involved were highly heritable and genetically independent and positively correlated of physiologically related in positive manner. 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) stated that if the heritability for the character is higher, than selection progress becomes easier and thus response to selection will be greater. Gupta *et al.* (2007) reported that in F2 progenies of two cross combinations among three mungbean varieties, seed yield per plant, plant height and days to maturity had the mean heritability estimates of 36.4%, 56.2%, and 65.1% repectively. Similiar result was found by Abady *et al.* (2013) in F3 progenies of soybean, seed yield per plant, days to maturity and plant height had high heritability estimates of 39.4%, 67.1%, and 63.0% respectively. While Zafar *et al.* (2010) reported in F3 population of soybean that days to flowering, days to maturity and plant height had the highest heritability estimate of 56.0%, 71.1%, and 70.2%. Whereas the heritability estimates for seed weight per plant was low of only 27.4%.

Rahman and Hussain (2008) reported that among seven quantitative characters studied in F2 population of mungbean plant height and pod number per plant had the highest heritability estimates of 73.3% and 78.5% coupled with high genetic advance of 28.0% and 43.4% respectively. Similiar result was found by Aditya *et al.* (2015) in F3 progenies of two cross combinations among three soybean varieties who obtained heritability estimates for plant height of 78.0% and number of pods per plant height of 81.0%. The genetic progress of selection for these characters was predicted 67.4% and 20.9% respectively.

Singh and Singh (1987) reported that pod number per plant and seed size had high mean heritability estimates, than selection for these characters in the next generation (F3) become easier and thus showing a great response to selection. Therefore, selection for high yielding genotypes based on pod number per plant and seed size in the next generation is relatively easy.

The objective 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 segregating progenies. Information obtained from this study would be helpful to specify certain traits as selection indices for identification of potentially high yielding mungbean genotypes.

**Materials and Methods**

**Genetic materials and development of F2 populations**

Genetic materials used and their characteristic are shown in Table 1. Six cross combinations among five mungbean varieties (Sampeong x Vima – 2, Sampeong x Vimil – 1, Sampeong x Local Demak, Camar x Vima – 2, Camar x Vimil – 1, Camar x Local Demak) were conducted in the wet season of 2019 at Kendal Payak Experimental Station, Malang, East Java. The main aims of the crosses were to improve grain yield (> 1,5 t/ha) early maturity (< 60 days), large seed size (65 g/1000 seeds) of variety Sampeong and Camar which at present both varieties have low yield, late maturity and small seed size.

 The F1 seed were planted at Kendal Payak Experimental Station, Malang, East Java during the dry season of 2019. The F1 Plants were harvested through a bulk method. A total of thirty two F2 progenies of each cross were developed from each F1 plant.

**Table 1:** Characteristic of Parental Varieties of Mungbean Used in Crosses Four Developing F2 Progenies

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Code of Parents | Varieties | Days to maturity | Pod Colour at Maturity | Seed Coat Colour | Seed Size (g/1000 seed) | Plant Height (cm) | Yield (t/ha) |
| P1 | Sampeong | 70 | Black | Green Shining | 30 | 80 | 1.0 |
| P2 | Camar | 67 | Black | Green Shining | 39 | 56 | 1.2 |
| P3 | Vima - 2 | 56 | Black | Green Dull | 65 | 60 | 1.8 |
| P4 | Vimil - 1 | 58 | Black | Green Shining | 63 | 60 | 1.7 |
| P5 | Local Demak | 58 | Yellow | Green Dull | 65 | 60 | 1.7 |

Source: Indonesian Center for Food Crops Research and Development (2008)

**Data analysis**

The genetic variation was estimated using a formula suggested by Stuber (1970): additive variance (S2A) = (S2m + S2F), nonadditive variance (S2D) = S2mF, in the F1 generation and S2D = 4S2mF, in the F2 generation whereas, S2m is the variance for male parents, S2F is the variance for female parents, and S2mF is a male x female interaction variance.

 The ratio of additive to nonadditive (dominance) variance was calculated using a formula of S2A / S2D. The heritability (H) was estimated using a formula H = S2A / (S2A + S2D + S2E). Genetic Advance (GA) was estimated using formula GA = K (VF2)½ x H/x̿, based on 10% selection intensity, K = 2.06, VF2 = variance among F2 plants, H = heritability, x̿ = means of F2 population.

The genetic coefficient of variation (VG) was estimated using formula suggested by Empig, et, al (1970) : (VG/x̿) x 100, where VG = VF2- {(VP1)(VP2)}½, VF2 is a variance among F2 plant, VP1 is a variance within female parents, and VP2 is a variance within male parents.

**Field trials of F1 and F2 progenies**

The F2 progenies derived from the six crosses consisted of one hundred eighty progenies each were evaluated together with their parents (Sampeong, Camar, Vima-2, Vimil-1, and Local Demak) at farmer field, Grobogan, Central Java, during the dry season of 2020. In case of expected genetic advance, the F2 populations were selected based on 10% selection intensity.

 The experiment were arranged in a randomized block design with four populations. The seeds of F1 and F2 progenies and their parents were sown in five rows of 3 m long. Plant spacing was 40 cm x 20 cm with one plant per hill. Population of each F1 plants, and F2 progenies and the parents were 75 plants in each plot. Basal fertilizer were applied of the rate of 50 kg urea and 200 kg phonska 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 seventy five 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) harvest index calculated as Sy/(Sy+Py).

**Result and Discussion**

 Estimates of various components based on individual plant in F1 and F2 gene action are presented in Table 2. Days to maturity was predominantly controlled by both additive and nonadditive gene effects. Therefore, inheritance of days to maturity was associated with both additive and nonadditive gene effects, and the dominance effects being more evidance in F2 generation. This observation is comparable with that reported by Murty *et al*. (2009), where days to maturity was mainly controlled by additive and nonadditive gene effects. Singh and Singh (1997) reported that earliness was controlled by additive gene and dominance or partial dominance. In this study the variance analysis indicated that addictive effects were significant in F1, while nonadditive effects were significant in F2 generation, with earliness being dominant to lateness (Table 2).

**Table 2:** Estimates of variance component of seven characters in F1 and F2 mungbean progenies, Kendal Payak Experimental Station, Malang, East Java, Dry season of 2020

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Characters | Gene-ration | Variance components | Male-Femaleinteraction variance (S2mf) | Ratio (S2A/S2D) |
| Male parent(M) | Female parent(F) |
| Days to maturity | F1 | 0.00 | 3.11\* | 3.21 | 3.20 |
| F2 | 0.00 | 2.34 | 7.22\* | 0.18 |
| Plant height (cm) | F1 | 0.01 | 3.21 | 3.01 | 2.08 |
| F2 | 0.04 | 3.06 | 6.53 | 0.21 |
| Pods number/plant | F1 | 0611 | 2.75 | 1303 | 2.05 |
| F2 | 2520 | 3.81 | 190 | 3.08 |
| Seed size (g/100 seed) | F1 | 87.9\*\* | 4.11\* | 1.47 | 2.27 |
| F2 | 45.5\* | 3.27 | 6.23\*\* | 0.18 |
| Plant yield (g) | F1 | 7812\* | 6870 | 0.00 | 1.12 |
| F2 | 3202\*\* | 4218\*\* | 0.00 | 1.39 |
| Seed yield/plant (g) | F1 | 2225\* | 1.18 | 1265 | 1.87 |
| F2 | 1305 | 371 | 163 | 2.57 |
| Harvest index | F1 | 239\*\* | 2337\*\* | 0.00 | 1.18 |
| F2 | 438\* | 1021\* | 1.90 | 2.00 |

\* P < 0.05; \*\* P < 0.01 Male parents = Sampeong and Camar

Female parents = Vima–2, Vimil-1, Local Demak

 Examination of individual crosses for days to maturity revealed underlying simple segregation ratio of 3:1 in progenies of late maturing parent (Sampeong) which matured 70 days, where three parts of the tested plants showed early maturity (< 60 days). However, the progeny of the other late maturing parent (Camar) which matured 67 days, segregated in the ratio 15:1, where fifteen parts of the plants showed early maturity (<60 days) and one part of the plants demonstrated late maturity (>60 days) (Table 3).

**Table 3:** Segregation ratio between earliness and lateness parents in F2 progenies of six mungbean cross combinations, Kendal Payak Experimental Station, Malang, East Java, dry season of 2020

|  |  |
| --- | --- |
| Earlya Parent | Late parentsb |
| P1 | P2 |
| Ratioc | X2d(3 : 1) | Prob | Ratioc | X2d(15 : 1) | Prob |
| P3 | 22 : 3 | 1.811 | P > 0.10 | 15 : 1 | 0.051 | P > 0.90 |
| P4 | 12 : 5 | 0.838 | P > 0.30 | 19 : 1 | 0.023 | P > 0.80 |
| P5 | 25 : 7 | 0.501 | P > 0.50 | 23 : 3 | 1.022 | P > 0.20 |
| Total | 59 : 15 | 1.322 | P > 20 | 57 : 5 | 0.551 | P > 0.70 |

a: Early parents and progenies matured < 60 days,

b: Late parents and progenies matured > 60 days,

c: Ratio of early to late maturity progenies observed from this study,

d: Chi – square test of the tested ratio,

Prob = Probability level

Result 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 Malik *et al*. (2007) who found significant effects of additive and nonadditive genes for tallness in some parents and dwarfness in other parents. Rao *et al*. (2009) reported that dominance effect 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 parent genotypes used in crosses.

 Pod number per plants was significantly controlled by addictive gene effects. This indicated that inheritance of pod number per plant was associated additive gene effects. Similar result 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. Imrie *et al.* (1987) stated that additive effect on pod per plant were larger in F2 generation, while in F1 generation the effects were no significant.

 Seed size were predominantly controlled by additive gene effects. This means that the additional gene effects were significant and played an important role in expression of inheritance on seed size similar result were obtained by Murty *et al.* (2009), reporting that seed size was apparently controlled by additive gene effect in F1 and F2 generation, with small seed size was partially dominant over large with predominantly additive gene.

 Examination of individual cross combinations for seed size in F2 generation revealed underlying segregation ratio of 15 : 1 in early progeny derived from large seed size parents (Vima-2), P4 (Vimil-1) and P5 (Local Demak), which had seed size of 65 g, 63 g, and 65 g per 1000 seeds respectively. Each progeny segregated in the ratio of fifteen progenies demonstrated small seed size (< 39 g/1000 seeds) and one progeny had large seed size (> 39 g/1000 seeds) (Table 4).

**Table 4**:Segregation ratio between large seed and small seed parents in F2 progenies of six mungbean cross combinations, Kendal Payak Experimental Station, Malang, East Java, Dry season of 2020

|  |  |
| --- | --- |
| Largea seed parent | Small seed parentsb |
| P1 | P2 |
| Ratioc | X2d(15 : 1) | Prob | Ratioc | X2d(15 : 1) | Prob |
| P3 | 23 : 1 | 1.510 | P > 30 | 20 : 3 | 1.063 | P > 0.30 |
| P4 | 11 : 5 | 0.517 | P > 20 | 15 : 1 | 0.160 | P > 0.70 |
| P5 | 26 : 6 | 0.503 | P > 30 | 25 : 3 | 1.022 | P > 0.50 |
| Total | 60 : 12 | 1.331 | P > 0.20 | 60 : 7 | 0.791 | P > 0.40 |

a: Large seeds of parents and progenies > 6 g/1000 seeds,

b: Small seeds of parents and progenies < 6 g/1000 seeds,

c: Ratio of small to large seeds size progenies observed from this study,

d: 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 the Table 5. The means of heritability estimates of seven character range from 15.5% to 48.4 %. Days to maturity had the highest heritability estimates of 48.4%, followed by number of pods plant of 44.1% and seed size of 38.7% respectively. This indicates that inheritance of days to maturity, number of pods per plant and seed size in the next generation (F3) are high, and selection to obtain mungbean genotypes with early maturity, high number of pods per plant, and large seed size in the F3 is relatively easy. Similiar results were reported by Murty *et al.* (2009), who obtained heritability estimates of 51.1% for days to maturity, 46.0% for pods number per plant and 50.3% foe seed size. Murty *et al.* (2009) pointed out that days to maturity, pods number per plant and seed size were heritable and days suggested that selection to increase grain yield of mungbean through days to maturity and seed size should consider plant height and pod number per plant.

Plant height showed moderate heritability estimate of 32.6% (Table 5). Tis indicates that inheritance of plant height in the F3 is relatively low. This result is comparable to that observed by Murty *et al.* (2009), reporting the mean heritability estimate for plant height of 35.0% in the F2 and 36.5% in the F3 plants, while Rahman, *et al*. (2003) observed mean heritability for plant height of only 23.1%. Variation of heritability estimate in those study might be mostly due to high differences in environmental condition affecting high variation among the study results.

Pod number per plant also had a high heritability estimate of 44.1%. This result is comparable with that reported by Parida *et al*. (2007). They found that in F3 progenies pod number per plant and seed size had high heritability estimate of 52.2% and 43.6% respectively. While in soybean, Aditya *et al.* (2015) found heritability estimate for number of pod per plant of 53.1% in the F2 segregation population. Abady *et al*. (2013) stated that number of pod number per plant had a high mean heritability estimate (50.3%). Then selection for this character in the next generation (F3) become easier and thus showing a greater response to selection.

In this study, seed yield per plant had a low heritability estimate of only 15.5% (Table 5). This indicate 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. Murty *et al.* (2009) found heritability estimate for seed yield per plant in F2 plant of only 17.0%, with expected genetic advance of 25.3%. 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 al later generation (F6 – F7).

Among six character studied in the F2 progenies, plant yield showed the lowest heritability estimate of only 10.2% (Table 5). This indicates that inheritance of plant yield in the next generation (F3) is small. Singh *et al.* (1987) observed heritability estimate for plant yield in the F3 of only 11.6%. Thus selection based on this character would not be effective. In soybean, Uzun *et al.* (2013) reported that genotypes which had a high plant yield may not always produce high seed yield.

**Table 5:** Estimates of broad sense heritability of six quantitative characters in the F2 generation of six mungbean crosses, Kendal Payak Experimental Station, Malang, East Java, Dry Season of 2020

|  |  |  |
| --- | --- | --- |
| Characters | Broad Sense Heritability Estimates Among Six F2 Populations (%)a | Means (%) |
| 1 | 2 | 3 | 4 | 5 | 6 |
| Days to maturity | 41.0 | 44.2 | 57.3 | 49.6 | 45.1 | 53.1 | 48.4 |
| Plant height | 27.6 | 33.5 | 40.3 | 35.7 | 22.5 | 36.0 | 32.6 |
| Pod number per plant | 35.2 | 39.3 | 45.5 | 49.0 | 40.2 | 55.1 | 44.1 |
| Seed size | 33.2 | 38.4 | 35.2 | 40.5 | 41.2 | 43.7 | 38.7 |
| Plant yield | 9.4 | 11.2 | 10.5 | 9.3 | 4.5 | 11.3 | 10.2 |
| Seed yield per plant | 12.2 | 18.4 | 9.5 | 15.1 | 22.3 | 15.3 | 15.5 |

a: 1, 2, 3, 4, 5, 6 are six F2 population developed from six independent cross combinations

Estimates of genetic advance of six character at 10% selection intensity are shown in Table 6. Genetic advances expected at 10% selection intensity of the six characters observed in this study ranged from 16.7% - 40.8%. Days to maturity, seed size had the highest expected genetic advance of 40.8% and 39.0% respectively (Table 6). The genetic advance of these characters were predicted as a substantial gain for one generation of selection obtaining 40.8% for days maturity and 39.0% for seed size. This result is comparable to that found by Parida *et al.* (2007) who obtained genetic advance of 39.7% for days to maturity and 41.3% for seed size.

Pod number per plant and seed yield per plant also showed high expected genetic advance of 33.0% and 36.9% respectively. The genetic advance of these characters that would be obtained for one generation of selection was estimated to be 33.0% for number of pod per plant and 36.9% for seed yield per plant, A similar result was reported by Murty *et al*. (2009) who found genetic advance of 46.6% for number of pod per plant 45.1% for seed yield per plant. This means that genetic progress for number of pod per plant and seed yield per plant were predicted as a substantial gain for the one generation of selection obtaining 33.0% and 36.9% respectively. Aditya *et al*. (2013) reported that genetic advance for number of pod per plant in F3 generation of soybean was 35.1% and for seed yield per plant was 40.3%, This indicates that genetic progress for number of pod per plant obtained for one generation of selection was estimated to be 35.1%, while for seed yield per plant was 40.3%.

Plant height had moderate expected genetic advance of 26.2% (Table 6). This indicates that genetic progress of plant height was predicted as a substantial gain for one generation of selection obtaining 26.2%. This result was comparable with the genetic advance of plant height that were considered as moderate.

Among the character studied, plant yield show the lowest expected genetic advance of 16.7% (Table 6). This observation was comparable with that reported bt Rahman and Hussain *et al*. (2003) who found genetic progress foe plant yield of only 11.7%. The lowest expected genetic advance for plant yield was due to its low heritability.

**Tabel 6:** Estimates of genetic advance by using 10% selection intensity of six quantitative characters observed in F2 generation of six mungbean crosses, Kendal Payak Experimental Station, Malang, East Java, Dry Season of 2020

|  |  |  |
| --- | --- | --- |
| Characters | Estimates of genetic advance (%)a | Means(%) |
| 1 | 2 | 3 | 4 | 5 | 6 |
| Days to maturity | 40.3 | 45.1 | 44.2 | 39.2 | 36.0 | 40.2 | 40.8 |
| Plant height | 26.1 | 27.4 | 25.7 | 28.3 | 23.5 | 26.3 | 26.2 |
| Pod number per plant | 29.7 | 40.1 | 38.6 | 25.5 | 38.5 | 25.7 | 33.0 |
| Seed size | 35.5 | 42.0 | 37.4 | 39.0 | 36.4 | 44.1 | 39.0 |
| Plant yield | 19.9 | 16.2 | 15.0 | 19.7 | 13.1 | 16.3 | 16.7 |
| Seed yield per plant | 43.3 | 38.8 | 30.8 | 37.5 | 42.2 | 29.0 | 36.9 |

a: 1, 2, 3, 4, 5, 6 are six F2 population developed from six independent cross combinations used in this study

**Genetic variability**

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

Result of this study showed that days to maturity, number of pod per plant and seed size had high heritability estimates of 48.4%, 44.1% and 38.7% coupled with high expected genetic advance of 40.8%, 33.0% and 39.0% respectively (Table 5 and 6). The coefficient of genetic variability of these characters were also guide high with the mean of 36.5%, 43.2% and 33.0% respectively (Table 7).This indicate that inheritance for days to maturity, number of pod per plant and seed size in the next generation (F3) were high, and selection to obtain high yielding mungbean genotypes with early maturity and large seed size in F3 progenies would be relatively easy. Therefore, days to maturity, number of pod per plant and seed size could be suggested as selection criteria to obtain high yielding mungbean genotypes with early maturity and large seed size in the F3 generation

Seed yield per plant and plant yield had low heritability estimate. This indicates that inheritance of seed yield per plant and plant yield in the next generation (F3) was low. Therefore, yield improvement based on these characters is relatively difficult.

**Table 7:** Coefficient of genetic variability of six quantitative characters in F2 generation of six mungbean crosses Kendal Payak Experimental Station, Wet Season, 2019

|  |  |  |
| --- | --- | --- |
| Character | Estimates of Genetic Variability (%) | Means |
| 1 | 2 | 3 | 4 | 5 | 6 | (%) |
| Days to maturity | 40.4 | 38.7 | 35.4 | 32.1 | 42.4 | 30.1 | 36.5 |
| Plant height | 51.2 | 44.6 | 43.8 | 50.4 | 54.0 | 50.0 | 49.0 |
| Number of Pod Per Plant | 48.6 | 53.1 | 40.1 | 37.0 | 40.0 | 40.4 | 41.2 |
| 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 |

\* 1, 2, 3, 4, 5, 6 are six populations developed from six independent crosses combination used in the study

Result of this study indicated that in breeding program for improving mungbean production, selection of progenies derived from a cross between low yield, late maturity and small seed size varieties such as Sampeong and Camar with those having high yielding, early maturity and large seed size such as Vima-2, Vima-1 and local Demak should generate several mungbean genotypes demonstrating high yield, early maturity and large seed size. Therefore, increasing grain yield of mungbean varieties such as Sampeong and Camar that currently have early maturity and large seed size through improving number of pod per plant, days to maturity and seed size should be possible.

**Conclussion**

Days to maturity was predominantly controlled by both additive and nonadditive gene effect, with earliness being dominant to lateness similarly plant height was also controlled by additive and nonadditive gene effect.

Pod number per plant was significantly controlled by additive gene effect. Similarly seed size was also controlled by additive gene effect, with small seed dominant to large seed size.

Days to maturity, number of pod per plant and seed size had high heritability estimate coupled with high expected genetic advance. Therefore, days to maturity, number of pod per plant and seed size could be suggested as selection criteria to obtain high yielding mungbean genotypes with early maturity and large seed size in the F3 generation, It should be possible to increase grain yield of variety Sampeong and Camar that currently have early maturity and large seed size by improving pod number per plant, days to maturity and seed size.

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