Genetic analysis and selection of short harvest period in F2 population of mungbean

S Marwiyah¹, SH Sutjahjo²*, Trikoesoemaningtyas², DW Wirnas², WB Suwarno²

¹Program of Plant Breeding dan Biotechnology, Graduate School, Bogor Agricultural University (IPB University), Jl Raya Dramaga, Kampus IPB Darmaga, Bogor, Indonesia 16680
²Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural University, (IPB University), Jl Meranti, Kampus IPB Darmaga, Bogor, Indonesia 16680

*Email: surjonoagh@apps.ipb.ac.id

Abstract. The short harvest period is one of the major focuses of mungbean breeding programs. Improvement of harvesting period can be reached by recombination among the best parents. The objectives of this research were to study performance, genetic inheritances, identified and to select of transgression segregants for short harvest period in F2 (Lombok x No.129) population. This research was conducted in Leuwikopo-IPB Farm, Bogor, Indonesia, from March to July 2019. The genetic materials were F2 (538 plants), Lombok/P1 (40 plants), No.129/P2 (40 plants) and F1 (40 plants). The results showed that the mean values of the F2 population were early than parents for plant age traits, respectively days to first pods maturity, days to 90% pods maturity, and harvesting period. Seed weight and the number of pods characters increased from parent mean values. Harvesting period was dominated by genetic ($h^2_{bs}>55\%$) with wide genetic diversity, and controlled by additive-duplicate epistatic gene action with many genes (polygenic) involved. Transgressive segregation for harvest period divided into 84 plants as short that harvested less than 14 days, 258 plants as medium (14-28 days), and 196 plants as long (>28 days). Short harvest period selection gives out high genetic advance (20.739%).

1. Introduction
Mungbean (Vigna radiata L. Wilczek) is one of the most important pulse crops in South and Southeast Asia, including Indonesia, grouped as an indigenous vegetable legume [1,2,3,4]. Today, it is as a popular food legumes consumed worldwide[5]. Mungbean is a source of dietary protein that cheap and easy to get[3]. It is a simple solution to improve the quality of human nutrition. The other primary nutrients in mungbean include vitamin A, iron, calcium, zinc, and folate. Vitamin C is an excellent antioxidant that produced mungbean sprouts[3,5]. Mungbean consumed in several food products such as fried snacks, dessert, and bean sprouts[1].

The Flower of mungbean blooms gradually and causes harvesttime to become long [4,6]. Commonly, it is found in local mungbean cultivars. Harvestin a long period is not advantageous for yield and competition with other commodities that have higher economic value in terms of land use. Therefore, genetic modification needs to be done to change the long harvest period to be shorter. Several advantages of the short harvest period in mungbean are reducing production input and yield
loss, also increasing land productivity. The short harvest period on mungbean is also beneficial for them because of keeping them from stress exposure. The short harvest period of mungbean varieties as the same as the synchronous of maturity will be suitable for cultivation systems on productive land, like a paddy field. Indonesia has released several national varieties that claimed as synchronous varieties. The number of mungbean varieties in Indonesia is still limited compared to soybeans and peanuts varieties. causes the limitations of mung bean seeds and their cultivation efforts[7,8]. The latest varieties that have been released by Balitkabi (Indonesia) are Vima 1, Vima 2, and Vima 3.

Improvement of harvesting traits in local cultivation can be done through hybridization by utilizing the phenomenon of gene recombination and gene segregation. Hybridization developed the F2 population as a segregated population that provides wide genetic diversity. The availability of wide genetic diversity and genetic information is important in plant breeding programs[9], belonging short harvest period on mungbean. In the F2 population can be identified the putative transgressive segregants as homozygous candidates lines[10]. Days to first flowering, days to first pod maturity, and days to 90% pod maturity traits have the high narrow and broad-sense heritability with additive gene action[11,12]. The objectives of this research were to study genetic inheritances and selection for a short harvest period trait in the F2 (Lombok x No.129) population.

2. Methodology
The study was carried out at KP Leuwikopo IPB from March to July 2019. A total of 538 F2 plants derived Lombok x 129, parent 1, parent 2, and F1 were involved to estimated values of mean, variance component, broad-sense heritability, and genetic variation of coefficient, by the following formula:

\[
\sigma^2_e = 1/3(\sigma^2_{p1} + \sigma^2_{p2} + \sigma^2_{e1}) \quad \text{Notes:} \quad \sigma^2_{p2} = \sigma^2_p = \text{F2 generation variance = phenotypic variance} \\
\sigma^2_g = \sigma^2_p - \sigma^2_e ; \sigma^2_p = \sigma^2_{e2} \quad \sigma^2_g = \text{environment variance} \\
\sigma^2_h = \frac{\sigma^2_g}{\sigma^2_p} \times 100\% \quad h^2 = \text{genetic variance} \\
GVC = \frac{\sigma^2_g}{\bar{x}} \quad GVC = \text{broad-sense heritability} \\
GVC = \text{genetic variation of coefficient}
\]

Criteria of heritability [13]: low (h^2 < 20%), medium (20-50%), high (> 50%).
Genetic variability grouped into narrow (GVC <10%), moderate (GVC 10-20%), and wide (>20%) [14].

Gene action and the number of genes in agronomic characters and harvest periods inheritances estimated from segregations of the first-generation offspring (F2). Harvest period in Classification of harvest periods was formed based on the range value to identify transgressive segregants of short harvest periods [15, 16]: \( \Delta P = \frac{1}{n} (b - a) \), \( \Delta P = \) changes of harvest period, \( a = \) minimum values of harvest period, \( b = \) maximum value of harvest period, \( n = \) number of harvest period number of harvest period classification. There were three classification of harvest period: (1) short, if \( x < \Delta P \), (2) medium, if \( \Delta P + a < x < (\Delta P + a) + \Delta P \), and (3) long harvest periods, if \( x > (\Delta P + a) + \Delta P \); \( x = \) observation value of individual harvest period.

Skewness and Kurtosis values used to estimate gene action and number of genes that controlled characters[13,16]. Skewness is visual number of genes that controlled a character based on data distribution. The character was controlled by aditif gene, if skewness = 0; duplicate epistatic, if skewness < 0; and complementary epistatic, if skewness > 0. Kurtosis is indicative of the number of genes controlling the trait, such as platycurtic, if kurtosis = negative (polygenic), and leptocurtic, if kurtosis = positive (few genes/oligogenic)[16]. Selection to F2 individu (short harvest period) will be done about 20% (=1.40) and expected genetic advance/GA[17] is:
\[ GA = \frac{R}{\bar{x}} \times 100\% \], with \( R = \text{i}.H.\sigma_P \), \( R \) = selection response, \( \bar{x} \) = mean of F2 population, \( i \) = selection index, \( H \) = broad-sense heritability, \( \sigma_P \) = standard deviation of F2 population. Criteria for genetic advance grouped into low (GA < 7%), medium (GA 7-14%), and high (GA > 14%). Descriptive data analysis was performed using software SPSS version 22 and Microsoft Excel.

3. Result and Discussion

3.1. Agronomic character performances among populations

Table 1 shows the mean values of characters in each population. The parent range value is not displayed. The mean values of harvesting days characters of F2 population lower than one or both of the parents, namely days of the first maturity, days of 90% maturity, and harvesting period. This indicates that there are reduce harvesting days in the F2 population with shorter harvest periods than a parent. The mean value of days of flowering is higher than parents, but range value for this character shows that there are some individual F2 that have early flowering time. The determination of the harvesting period shows the same tendency. So, we can select them too. When the mean value of the characters shows a wider value than the parent, it indicates the presence of transgressive segregants[18]. All characters showed a wider range value in the F2 population with minimum values were lower than one parent and maximum values were higher with others. The other research reported the same data distribution and selected the best individual in the F2 population on mungbean[19], pepper[20,21], and sorghum[16].

Selection for flowering and harvesting days on mungbean is a negative selection, while yield is a positive selection. Similar ways on selection have been reported in the evaluation of the F2 population on mungbean for the days of flowering, days of 90% maturity and yield components[18,19]. The mean value for seed weight and the number of pods in the F2 population was higher than parents and range value was wider from them (Table 1). The results of this study indicated the probability to select of transgressive segregants for a short harvest period based on the harvesting period trait.

| Characters                                  | P1       | P2       | F1       | F2       | Range value of F2 |
|---------------------------------------------|----------|----------|----------|----------|-------------------|
| Days to flowering                           | 39.344   | 36.800   | 38.810   | 39.434   | 34.000 - 57.000   |
| Days to first maturity                       | 58.414   | 54.200   | 62.190   | 57.041   | 51.000 - 93.000   |
| Days to 90% maturity                         | 80.690   | 83.200   | 82.000   | 79.868   | 58.000 - 93.000   |
| Harvesting period                           | 22.821   | 29.000   | 19.810   | 22.743   | 0.000 - 42.000    |
| Determination of harvesting period           | 27.327   | 34.619   | 23.986   | 27.612   | 0.000 - 44.090    |
| Seed weight                                 | 9.250    | 9.373    | 15.709   | 10.818   | 0.320 - 35.780    |
| Number of pods                              | 20.724   | 18.250   | 29.667   | 21.125   | 2.000 - 61.000    |

3.2. Genetic variability and Gene Control

Estimation of broad-sense heritability and genetic diversity coefficient shows in Table 2. Both of them are important in selection on plant breeding program[16]. Selections can be done in the early generation if influenced by a high genetic factor. Furthermore, the presence of wide genetic diversity will increase of easy and success of selection. This study shows that all characters observed controlled by genetic factor, so that selection can be done in the early generation of inbreeding (F2 generation). But, only harvesting period, determination of harvestperiod, seed weight, and number of pods characters have wide genetic diversity. Based on means value and range value of F2 on Table 1, presence of genetic control also wide genetic diversity (Table 2), the harvesting period in this study can be selected in F2 generation. Selection by high heritability and wide genetic diversity has been reported in rice (Oryza sativa)[22], eggplant (Solanum melongena)[23], sorghum (Sorghum bicolor)[24], long beans (Vigna sinensis)[25], and peanuts (Arachis hypogea)[26].
Table 2. Estimation of broad sense heritability and genetic variability coefficient of agronomic characters in F2 population of mungbean

| Characters                  | $\sigma^2_P$ | $\sigma^2_E$ | $\sigma^2_G$ | $h^2_G$ | Criteria | GVC       | Criteria |
|-----------------------------|--------------|--------------|--------------|---------|----------|-----------|----------|
| Days to flowering           | 10.769       | 2.181        | 8.588        | 79.747  | High     | 7.432     | Narrow   |
| Days to first maturity      | 17.378       | 9.640        | 7.738        | 55.473  | High     | 5.443     | Narrow   |
| Days to 90% maturity        | 70.055       | 46.093       | 46.597       | 65.795  | High     | 8.501     | Narrow   |
| Harvest Period              | 89.737       | 64.597       | 71.985       | 79.747  | High     | 35.339    | Wide     |
| Determination of harvesting period | 101.151 | 73.697       | 51.146       | 44.392  | Medium   | 34.956    | Wide     |
| Seed weight                 | 64.068       | 14.300       | 14.300       | 42.998  | Medium   | 33.854    | Wide     |

Note: $\sigma^2_P$ = phenotypic variability, $\sigma^2_E$ = environment variability, $\sigma^2_G$ = genetic variability, $h^2_G$ = broad-sense heritability, GVC = genetic variability coefficient.

The standard of a normal distribution for bidirectional testing has a value of 1.96 for $Z_{0.05/2}$ and 2.57 for $Z_{0.01/2}$ [15]. The z-skewness test values were significantly different for all characters (Table 3). Additive gene action controlled all characters with the effect of complementary epistatic on days to flowering, days to first maturity, seed weight, and the number of pods. Duplicate epistatic is contributing to controlling days to 90% maturity, harvesting period, and determination of harvesting period. The yield component of mungbean for seed weight per plant was reported to be additive with the involvement of many genes [11, 27] and some self-pollinated plants, such as rice [10] and sorghum [28]. The number of genes controlled in days to 90% maturity and harvesting period of mungbean are polygenic (Table 3). Whereas, many genes with several major genes were detected in all other characters (oligogenic). The result showed that the characters with polygenic or many genes controlling refer means as a quantitative trait [13].

Table 3. Gene action and number of gen controlled agronomic characters of F2 population

| Characters                  | S    | Zs-test | Gene action | K    | Zk-test | NG |
|-----------------------------|------|---------|-------------|------|---------|----|
| Days to flowering           | 1.992| 18.201**| A-CE        | 6.891| 31.546**| OG |
| Days to first maturity      | 2.745| 26.016**| A-CE        | 14.370| 68.227**| OG |
| Days to 90% maturity        | -0.436| -4.135**| A-DE       | -0.159| -0.757tn| PG |
| Harvest Period              | -0.687| -6.527**| A-DE       | -0.088| -0.419tn| PG |
| Determination of harvesting period | -1.164 | -11.053**| A-DE     | 0.791| 3.764**| OG |
| Seed weight                 | 0.693| 6.582**| A-CE       | 0.458| 2.176* | OG |
| Number of pods              | 0.616| 5.846**| A-CE       | 0.028| 0.133tn| OG |

Note: S = skewness, K = kurtosis, NG = number of gene, A-CE = additive-complementary epistatic, A-DE = additive-duplicate epistatic, OG = oligogenic, PG = polygenic.

3.3. Transgressive segregation of harvest period trait in F2 population and genetic advance

Distribution of harvest period values in population F2 (Lombok x 129) in Figure 1 shows a continuous line with extreme values on the left and right sides of P1, P2, and F1 range values. The extreme values on both sides show transgressive segregation which indicates the existence of putative transgressive segregants [16,18,20,28,29], respectively short harvest period on left sides and long harvest period on other sides of the curve. Selection of transgressive segregants in F2 population has been reported for yield of mungbean [19], the thick nature of fruit flesh on F2 Capsicum annuum derived from Jalapeno x Tricolor Variegata (TCV) [20], rice yield components [10], rice to iron stress [18], seeds weight per sorghum panicle [16]. Another study confirmed that the putative transgressive segregation found in F2 not always showed the stability of phenotype values and variability in F3 as homogeneous families, as reported in F3 of peanut and C. annuum [26]. So that, need to crosscheck in the next generations for stability character after self-pollinated (segregation).
Figure 1. Distribution of harvesting period data in F2 population of mungbean

Data distribution for harvest period trait of the F2 population grouped into three classes (n = 3) [15,30] based on harvest period character. The classes of harvest period were short (x < 14 days), medium (14 – 28 days), and long (> 28 days), and it was followed by the number of individuals, respectively 84, 258, and 196 plants (Table 4). The one of the major targets for mungbean improvement is about 15 days for the harvesting period with synchronous maturity for easy in harvesting[31]. About 84 individual F2 have less than 14 days for harvesting period. The results of other studies about mungbean suggested that 13 days as a standard for short harvesting period on mungbean[32].

Table 4. Classification and number of individual F2 for harvest period trait of mungbean

| Classes  | Harvest period (days) | Number of individual F2 (plants) |
|----------|-----------------------|----------------------------------|
| Short    | < 14                  | 84                               |
| Medium   | 14 – 28               | 258                              |
| Long     | > 28                  | 196                              |

The Harvesting period trait is controlled by genetic (Tabel 2), so it will be inherited to the next generation[13]. Measurement of genetic advance for harvesting period can predict the new generation with a shorter harvest period on mungbean. Including amount of 108 F2 individual with 0-14 days harvesting period in selection [31] or about 20% selected from population (i = 1.40)[17]. There is an improvement for the harvest period of mungbean becomes shorter about 8.661 days from base population 22.743 days (Table 5). Expected genetic advance for short harvest period is about more than 20% . The expression of genetic advance to mean population F2 shows > 91% (high). There was an opportunity to develops mungbean varieties that shorter harvest periods. The same way in selection for yield (as a selection target) on mungbean and gives high probability in the success of yield selection, when genetic advance expressed were high, as a percent of mean showed more than 15% for seed yield per plant)[33].
Table 5. Selection response and expected genetic advance for harvest periode on mungbean

| Parameters                          | Values       |
|-------------------------------------|--------------|
| $\bar{x}S_0$ (days)                | 22.743       |
| $\bar{x}S_1$ (days)                | 8.661        |
| Selection response                  | 472.142      |
| Genetic advance                     | 20.759       |
| Genetic advance expressed as percent of mean | 91.280       |

Notes: $\bar{x}$ = mean value, $S_0$ = base population before being selected, $S_1$ = population after selection

4. Conclusion

F2 population has early times for days to first maturity, days to 90% maturity, and harvesting period traits with produced seed weight and the number of pods higher than parents. Broad-sense heritability was high for all characters observed, except seed weight and the number of pods. The genetic variability of coefficient for harvesting period is wide. The harvest period controlled by polygenic with additive- duplicate epistatic genes. Other agronomic traits were influenced by complementary epistatic with moderate to high genetic influences. The segregation of the F2 population for the harvest period trait grouped into short (< 14 days; 84 plants), medium (14-28 days; 258 plants), and long (> 28 days, 196 plants). Short harvest period selection gives out high genetic advance (20.759%).

Acknowledgement

We acknowledged the Directorate General of Higher Education, Ministry of Research, Technology and Higher Education of the Republic of Indonesia for supporting this research through the BUDI-DN 2016 Scholarship to Siti Marwiyyah and Penelitian Hibah Doktor 2019 Scheme to Prof. Surjono Hadi Sutjahjo and team.

References

[1] Chadda MI 2010 Short Duration Mungbean: A New Success in South Asia (India, AVRDC)
[2] Katiyar M and Kumar A 2015 IJIRD 4 119-121
[3] Nair RM et al 2012 Sabrao J. Breed. Genet. 44 177-190
[4] Shanmugasundaram S 2011 Mungbean Varietal Improvement (Taiwan: AVRDC)
[5] Xue Z et al 2016 Czech J. Food Sci. 34 68-78
[6] Huyghe C 1998 Agroinomic 18 383-411
[7] Trustinah et al 2014 Prosiding Seminar Hasil Penelitian Tanaman Aneka Kacang dan Umbi 2014. (Indonesia: Balitkabi-Malang). p 729-740
[8] Balai Penelitian Tanaman Kacang-kacangan dan Umbi-umbian 2014 Deskripsi Varietas Unggul Kacang Hijau 1945-2014 (Indonesia: Balitkabi-Malang)
[9] Khattak GSS et al 2001 Kasesart J. (Nat.Sci.) 35 1-7
[10] Khattak GSS et al 2002 Hereditas 137 52-56
[11] Kumar S and Kumar R 2014 IJTA 32 683-687
[12] Knight R 1979 Practical in Statistic and Quantitative Genetic (Brisbane: Australian Vice-Chancellors Committee)
[13] Reddyyamini B et al 2019 Int. J. Curr. Microbiol. App. Sci. 8 2450-2455
[14] Roy D 2000 Plant Breeding: Analysis and Exploitation of Variation (New Delhi: Narosa Pub.)
[15] Wallpole RE 1982 Pengantar Statistik Edisi 3 (Indonesia: Gramedia)
[16] Maryono MY et al 2019 J. Agron. Indonesia 47 163-170
[17] Kristamtini et al 2016
[18] Rini FM et al 2018 Bul. Agrohorti 6 326-335
[19] Salunke MD et al 2016 Int.J.Curr.Res. 8(12): 4340-43433.
[20] Widiatmiko GW 2016 Vegetalika 5 26-37
[21] Yunandra 2016 Pewarisan Karakter Komponen Hasil dan Pemanfaatan Segregan Transgresif Persilangan Cabai Besar dan Keriting dalam Rangka Perbaikan Hasil (Indonesia: Pascasarjana Institut Pertanian Bogor)

[22] Anshori MF et al 2019 Sabrao J. Breed. Genet 51 161-174

[23] Putri FD et al 2017 J. Agron. Indonesia 45 182-187

[24] Saniaty A et al 2016 J. Agron. Indonesia 44 271-278

[25] Sa’diyah N et al 2009 J. Agrotropika 14 37-41

[26] Nurhidayah S et al 2017 J. Agron. Indonesia 45 162-168

[27] Khattak et al 2004 Pak. J. Bot 36 589-594

[28] Sulistiyowati Y et al 2016 J. Biologi Indonesia 12 175-184

[29] Jambormias E 2014 Analisis Genetik dan Segregan Transgresif Berbasis Informasi Kekerabatan Untuk Potensi Hasil dan Panen Serempak Kacang Hijau (Indonesia: Pascasarjana Institut Pertanian Bogor)

[30] Sastrosumardjo S et al 2004 Prosiding Simposium Perhimpunan Ilmu Pemuliaan Tanaman, Bogor (Indonesia: Perhimpunan Ilmu Pemuliaan Indonesia) p 260-264

[31] Chauhan YS and Williams R 2018 Preprint doi:10.20944/preprints201805.0182.v1

[32] Putri ID et al 2014 Bul.Agrohorti 2 11-21

[33] Yusufzai et al 2017 Int. J. Pure. App. Biosci 5 532-535