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# Genetic Variability, Heritability, and Genotypic Correlation of Soybean Agronomic Characters

*Keragaman Genetik, Heritabilitas, dan Korelasi Genetik Karakter Agronomi Kedelai*

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## ABSTRACT

Genetic parameters are important in genetic improvement and variety development. This study aimed to determine the effective characters that can be applied as selection criterion in soybean breeding using genetic parameters. About 100 soybean genotypes were grown in the Muneng Agricultural Technology Research and Assessment Installation from April to July 2020. The trial was conducted using a randomized complete block design. The results showed that high genetic variability was found on days to maturity, number of branches per plant, number of productive nodes per plant, 100-seed weight, and seed yield. The high heritability was shown by days to maturity, plant height, number of branches per plant, and 100-seed weight. All phenotypic correlations were significant, except for the correlation between seed yield and days to maturity, plant height, number of branches, and number of productive nodes. The seed yield had no genotypic correlation with all agronomic characters observed. The genotypic correlation was only significant for plant height and number of productive nodes, number of branches and number of filled pods, as well as number of productive nodes and 100-seed weight. Therefore, the improvement of seed yield can be conducted through direct selection using the seed yield parameter or indirectly using the 100-seed weight.

Keywords: genetic variability, genotypic correlation, heritability, phenotypic correlation

## ABSTRAK

Parameter genetik sangat penting dalam perbaikan genetik dan perakitan varietas tanaman. Penelitian ini bertujuan untuk menentukan karakter yang efektif digunakan sebagai kriteria seleksi dalam pemuliaan kedelai dengan menggunakan parameter genetik. Seratus genotipe kedelai ditanam di Instalasi Penelitian dan Pengkajian Teknologi Pertanian Muneng pada bulan April hingga Juli 2020 dengan rancangan acak kelompok lengkap. Hasil penelitian menunjukkan bahwa keragaman genetik yang tinggi diperoleh pada umur masak, jumlah cabang per tanaman, jumlah buku subur per tanaman, bobot 100 biji, dan hasil biji. Heritabilitas yang tinggi ditunjukkan oleh umur masak, tinggi tanaman, jumlah cabang per tanaman, dan bobot 100 biji. Korelasi fenotipik nyata diperoleh pada semua karakter agronomi, kecuali korelasi antara hasil biji dengan umur masak, tinggi tanaman, jumlah cabang, dan jumlah buku produktif. Hasil biji tidak memiliki korelasi genotipik dengan semua karakter agronomi yang diamati. Korelasi genotipik nyata diperoleh pada tinggi tanaman dengan jumlah buku subur, jumlah cabang dengan jumlah polong isi, dan jumlah buku subur dengan bobot 100 biji. Oleh karena itu, peningkatan hasil biji dapat dilakukan dengan seleksi langsung menggunakan parameter hasil biji atau secara tidak langsung melalui bobot 100 biji.

Kata kunci: heritabilitas, keragaman genetik, korelasi fenotipik, korelasi genotipik

## INTRODUCTION

Yield is an important character in food crops, including soybean. Most of soybean plant breeding activities focus on improving yield character. The inheritance of low yield character is a challenge in breeding activities. Besides, yield character is strongly influenced by yield component characters such as plant height, number of branches, number of productive nodes, number of filled pods, and seed size (Dabi *et al*. 2016; Kuswantoro *et al*. 2018). The relationship between yield characters and yield component characters can be considered as selection criteria to produce high yielding soybean plants.

Selection criteria are characters that are considered in the selection process. The selection criteria for obtaining high yielding soybeans can be done by studying the relationship between yield characters and yield component characters. The phenotypic and genotypic correlation can describe the degree of association between the characters. Phenotypic correlation is the relationship between plants characters, while genotypic correlation is the relationship among inherited characters or the breeding value of different characters (Muslimin *et al*. 2013; Faot *et al*. 2019). Despite strongly influence phenotypic correlation, environment does not influence genotypic correlation because environmental factors are excluded in calculation. Genotypic correlation is considered to be more stable and expectedly can increase the accuracy in determining the selection criteria.

The correlation between two characters describes a linear relationship.This suggests that an increase in the value of the first character, would follow by the rise in the second character value, and vice versa. Some characters are reported to have a positive phenotypic correlation with soybean yield include days to flowering, plant height, number of branches, number of productive nodes, number of pods, and 100-seed weight (Krisnawati and Adie 2016; Sulistyo *et al*. 2018; Kuswantoro *et al*. 2020). Days to flowering, plant height, and number of pods per plant were also reported to have a positive and significant genotypic correlation with seed yield (Balla and Ibrahim 2017). Faot *et al.* (2019) stated that days to maturity and number of branches had a positive genotypic correlation with seed yield.

The variability of breeding material population is also a determinant for the success of breeding activities. High variability increases the chance to obtain the desired character in selection process (Handayani and Hidayat 2012; Sulistyo and Mejaya 2018; Karyawati *et al*. 2019). The variability observed in breeding material population is phenotypic variability and can be seen from each character mean square in variance test. The significance found in variance test generally indicates that the variability exists (Kuswantoro *et al*. 2018). However, phenotypic variability is derived from the expression of genetic and environmental factors, thus it does not fully represent the genetic characteristics. High genetic variability described by the genetic coefficient of variability (GCV) is considered to have a more critical role as an indicator for successful of plant breeding program.

Genetic variability and heritability are genetic parameters that must be considered in breeding process. The estimated value of both parameters determines the success of breeding activities. Characters with high genetic variability and heritability values are suitable to be used as selection criteria. Heritability describes the effect of genetic factors on phenotypic variability (Akram *et al*. 2016). High heritability means that genetic factors control the character so that it is easily inherited and improved by selection (Karyawati *et al*. 2016; Ali *et al*. 2016). Genetic variability and high heritability are observed on flowering age, plant height, number of productive nodes, number of filled pods, 100-seed weight, and seed yield both per plant and per unit area (Ali *et al*. 2016; Kuswantoro *et al.* 2018; Karyawati *et al*. 2019; Jandong *et al*. 2020). Each population has different genetic parameters from other populations. To increase the effectiveness of selection, the genetic parameters must be found out before the selection is conducted. The objective of the research was to determine effective characters that can be used as selection criterion.

## MATERIAL AND METHOD

The research was conducted from April to July 2020 at Muneng Agricultural Technology Research and Assessment Installation, East Java, Indonesia, with coordinates of -7°48’12 “, 113°9’44" and 10 m asl. The type of soil at the research location is Alfisol. The plant materials consisted of 100 soybean genotypes consisting of local varieties and breeding lines. The genotype was considered as a fixed model. The experimental design was randomized complete block design with two replications.

The soil was cleared from weeds and previous crop residues. Then the soil was tilled to obtain a friable soil, prepared the drainage channels, and followed by planting the seeds. Each soybean genotype was planted in a 3 m × 1.2 m (3.6 m$^2$) plot size, with a plant spacing of 40 cm × 15 cm, two seeds per hill. Inorganic fertilizers of 75 kg ZA + 100 kg SP 36 + 75 kg KCl/ha and organic fertilizer of 5 t/ha manure were applied at planting time. Manual weeding was done at 17 days after planting (DAP). The pest controls were applied at 16, 29, 44, 50, 59 and 68 DAP using supermetrin 50 g/l, deltametrin 25 g/l, fipronil 50 g/l, lambda cyhalothrin 25 g/l, alphamethrin 15 g/l, respectively. Observations were carried out for days to maturity, plant height, number of branches, number of productive nodes, number of filled pods, 100-seed weight, and seed yield at harvesting.

The data were analysed using analysis of variance (Anova). The phenotypic and genotypic variability coefficients and broad-sense heritability were calculated using the expected mean square (Singh and Chaudary 1985). The determination of significant genotypic variability was carried out based on genetic standard deviation. The heritability, phenotypic and genotypic correlations were calculated according to Singh and Chaudary (1985). The descriptive data were performed using Minitab 14. The significance phenotypic and genotypic correlations was determined using t-test based on Falconer (1960) and Dabi *et al.* (2016).

## RESULTS AND DISCUSSION

Genotypes showed significant differences for all agronomic characters observed (Table 1). This suggests that at least one genotype differed to other genotypes. It also indicates that there was variability in genotypes based on those characters.

Days to maturity ranged from 68-78 days, with the mean of maturity was 74.8 days (Fig. 1). Days to maturity was not normally distributed (with P value <0.0005). This was due to the tested genotypes that were previously selected with early maturity as a criterion. The graph skewed to the right, meaning that most of genotypes had days to maturity above the average. All genotypes were early maturity. genotype Tgm/Brg-558 (<80 days) had the shortest days to maturity (68 days). The differences in days to maturity among soybean genotypes is closely related to day length and temperature. Long days generally result in soybean plants with long days to maturity (Liu *et al.* 2017).

Plant height was normally distributed with P value = 0.093. No selection in plant height may lead this normal distribution. The average plant height of soybean genotypes was 58.8 cm. Most of soybean genotypes grew shorter than the average height, so the graph skewed to the left (Fig. 2). Plant height that mostly appeared was 55 cm. Based on the plant height grouping referred to Adie and Krisnawati (2013), the tested soybean genotypes had plant heights from short to very tall. The tallest genotype, namely MLGG 0103, reached 97.8 cm and it was categorized as very tall. Late maturity soybean genotypes generally show high plant height. However, all genotypes in this study belonged to early maturity. It can be caused by environmental factors such as water availability, day length, and temperature. The length of the day is related to the intensity of solar radiation and changes in temperature. High irradiation intensity and increased temperature cause reduction of stem internodes, while the number of productive nodes increased (Allen Jr. *et al.* 2018)

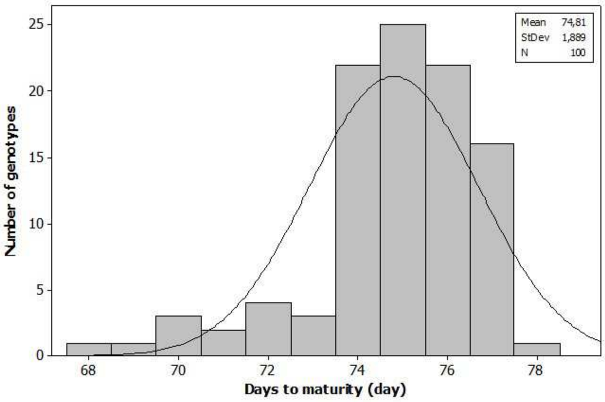

**Figure 1.** Days to maturity of 100 soybean genotypes. Muneng Res Station, April-July panting season

Similar to plant height, there was no selection in number of branches per plant. The number of branches per plant was also normally distributed (P value = 0.100), and it ranged from 1-4 branches. A total of 21 genotypes had four branches, and most of genotypes had three branches or lower. The average number of branches per plant in the population was 2.89 branches (Fig. 3). The number of branches and plant height may associate with seed yield per plant (Akram *et al.* 2011). MLGG 0523 and MLGG 0164 genotypes had four branches per plant and belonged to the tall plant group and with seed yield of 2.01 t and 1.76 t/ha, respectively. The formation of branches in soybean is also influenced by population density per unit area, thus the number of branches per plant is not a stable character. A genotype can have various branches when it was planted at different population densities (Agudamu *et al.* 2016).

The graph of number productive nodes did not follow a normal distribution (P value = 0.006). The tail of the graph appeared to be on the right, or the graph was leaning to the left. It differed from

**Table 1.** Analysis of variance of agronomic characters of 100 soybean genotypes. Muneng Res Station, April-July planting season

| Source | Replication | Genotype | Error |
|---|---|---|---|
| Days to maturity | 27,380** | 6,823** | 1,905 |
| Plant height | 890,420** | 196,241** | 41,209 |
| Number of branches per plant | 1,217 * | 0,813** | 0,261 |
| Number of productive nodes per plant | 23,805** | 5,089** | 1,751 |
| Number of filled pods per plant | 1257,010** | 213,069** | 77,969 |
| 100-seed weight | 0,041 | 25,259** | 2,103 |
| Seed yield | 7,826** | 0,151** | 0,092 |

* Significant at level of 5%, ** Significant at level of 1%

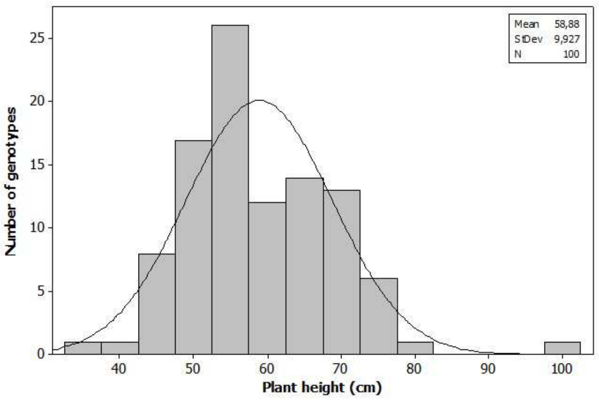

**Figure 2.** Plant height of 100 soybean genotypes. Muneng Res Station, April-July panting season

number of branches per plant but similar to plant height graph. This may be due to the correlation with other characters that were previously set. The average number of productive nodes was 8.88 (Fig. 4), which ranged from six to 13 nodes per plant. The highest number of productive nodes was seen ini MLGG 0714. The productive nodes are the places where pods are set up, so they play an important role in determining seed yield. The yield per unit area is largely determined by population density. Egli (2013) reported that there is a relationship between number of productive nodes and number of pods per unit area at various population densities. The number of pods per acreage is limited by the number of productive nodes in low population, and there is no correlation between number of productive nodes and number of filled pods in high population.

The distribution of number of filled pods per plant was not normal (P=0.009), as the graph skewed to the left. Similar to the number of productive nodes per plant, this character was also not selected due to its correlation with other characters. The genotypes had 28 to 74 filled pods per plant, with the average of 45 per plant (Fig. 5). IAC-100/Kaba-G-67xBurr-358-T-2-261 had the largest number of filled pods, namely 74 pods. The number of productive nodes and number of filled pods generally have a positive linear relationship. The genotypes with many productive nodes had a large number of filled pods (Kuswantoro *et al*. 2020). The number of filled pods is a character that determines seed yield per plant. Kuswantoro *et al*. (2019) reported that number of filled pods associated with seed yield, while Machado *et al.* (2017) stated that the number of seeds per pod directly affected seed yield.

Selection of genotype resulted in abnormal distribution of 100-seed weight (P=0.005). The genotypes tested generally had 14-19 g/100 seeds, and therefore those were categorized as medium to large seed sizes following Krisnawati and Adie (2015). The mean weight of 100-seed in the population was 17.2 g, with a minimum value of 10.2 g and a maximum value of 25.2 g (Fig. 6). The graph peak was in the middle. Less than 50% of the genotypes had medium seed size with 100-seed weight was <14 g, while the rest (>50% of the genotypes) had larger seed sizes (>14 g). The major 100-seed weight values were 20 g, followed by 14 g. IAC-100/Kaba-G-67xBurr-433-T-15-286 had the largest seed size with 100-seed weight was 25.2 g.

The seed yields of population ranged from 0.95-2.1 t/ha, with the average was 2.07 t/ha (Fig. 7). The graph was skewed to the left, meaning that most of genotypes had lower yield than the average yield. The seed yield was normally distributed (P=0.543). This normal distribution may occur randomly. Genotype Glr 76 had the highest yield of 2.1 t/ha. Yield character is controlled by many

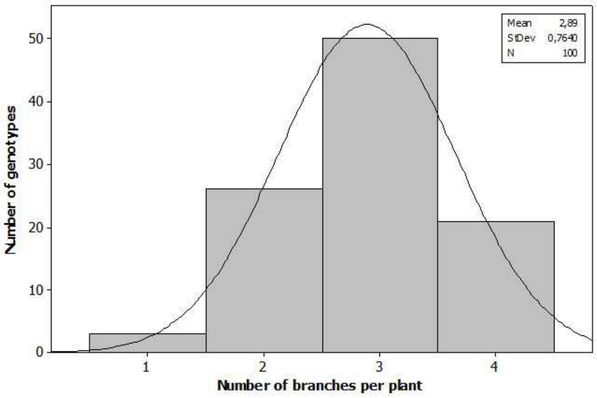

**Figure 3.** Number of branches per plant of 100 soybean genotypes. Muneng Res Station, April-July panting season

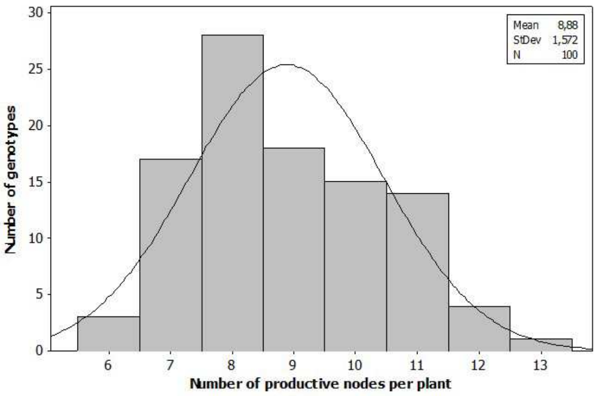

**Figure 4.** Number of productive nodes per plant of 100 soybean genotypes. Muneng Res Station, April-July panting season

**Table 2.** Coefficients of phenotypic and genotypic variability of agronomic characters of 100 soybean genotypes. Muneng Res Station, April-July planting season

| | PCV (%) | GCV (%) | PCV-GCV (%) | GSD | Clasification† |
|---|---|---|---|---|---|
| Days to maturity (days) | 2.80 | 2.10 | 0.70 | 0.52 | Broad |
| Plant height (cm) | 18.53 | 14.97 | 3.56 | 14.40 | Narrow |
| Number of branches per plant | 25.99 | 18.64 | 7.35 | 0.06 | Broad |
| Number of productive nodes per plant | 20.90 | 14.60 | 6.3 | 0.40 | Broad |
| Number of filled pods per plant | 26.80 | 18.26 | 8.54 | 16.88 | Narrow |
| 100-seed weight (g) | 21.50 | 19.79 | 1.71 | 1.79 | Broad |
| Seed yield (t/ha) | 16.69 | 8.34 | 8.35 | 0.01 | Broad |

†The GCV is broad if GCV> 2GSD and narrow if GCVde 2GSD, PCV = phenotypic coefficient variation, GCV = genotypic coefficient variation, GSD = genetic standard deviation

genes and strongly influenced by other characters, such as number of filled pods, 100-seed weight, and seed weight per acreage. Generally, soybean genotypes that have large seed sizes are also have high yields. However, in this study, there was a medium seeded genotype (10.7 g per 100 seeds) with high seed yield (2.01 t/ha), namely MLGG 0523. Meanwhile, IAC-100 / Kaba-G-67xBurr-433-T with the largest seed size (25.2 g per 100 seeds) yielded lower seeds per hectare, 1.6 t/ha. It shows that 100-seed weight does not always linearly associated with seed yield per hectare. This is in accordance with the study conducted by Krisnawati and Adie (2015), Kuswantoro *et al*. (2018), and Soares *et al.* (2013). Plant population also influences seed yield per hectare.

The phenotypic and genotypic coefficients of variability are presented in Table 2. The phenotypic coefficient of variability of all observed characters was greater than the genotypic coefficient of variability. The largest phenotypic coefficient of variability was achieved by number of filled pods per plant, followed by number of branches per plant. The genotypic coefficient of variability does not always follow the magnitude of phenotypic coefficient of variability. The 100-seed weight achieved the highest genotypic coefficient of variability. Small differences between CVP and CVG values showed that the influence of environmental factors is considered to be small, and the appearance of phenotype indicates a genetic value (Reni and Rao, 2013; Malek *et al*. 2014; Ekka and Lal, 2016).

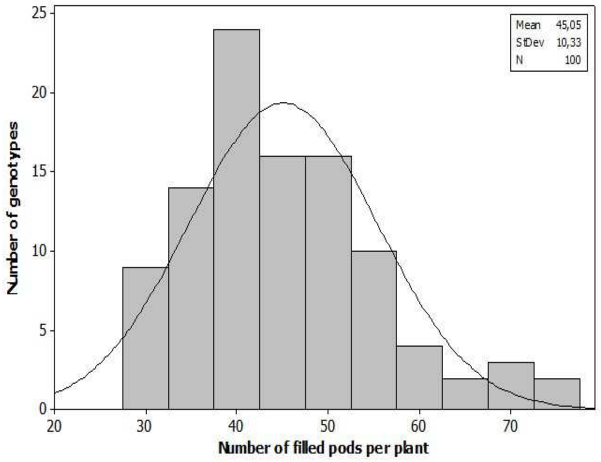

**Figure 5.** Number of filled pods per plant of 100 soybean genotypes. Muneng Res Station, April-July panting season

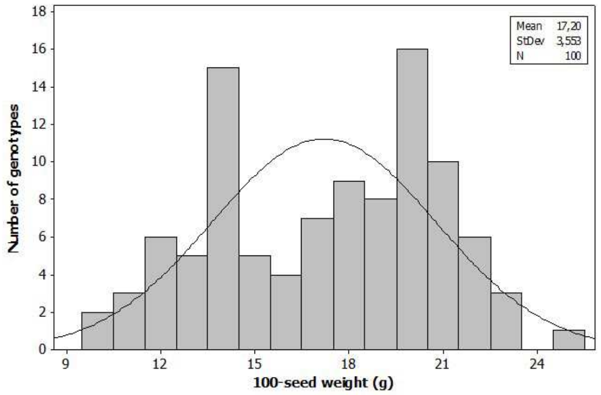

**Figure 6.** The 100-seed weight of 100 soybean genotypes. Muneng Res Station, April-July panting season

The criterion using CVP-CVG is less relevant because if CVP of a character is low, CVP-CVG is also low. For example, CVP of days to maturity was low (2.80%); therefore, CVP-CVG was also low (0.70%). It was different from number of filled pods per plant, which had a relatively high CVP (26.80%); although CVG was also high (18.26%), CVP-CVG was also high (8.54%). Such determination of variability is irrelevant because the character is compared to other characters with different environmental influences. Days to maturity and 100-seed weight that are less influenced by environment will give a lower CVP-CVG than other characters, such as number of filled pods and number of branches per plant, which are more influenced by environment.

In contrast to coefficient of variability, in determining genetic variability using genetic standard

**Table 3.** Phenotypic and genotypic variations and heritability of agronomic characters of soybean genotypes. Muneng Res Station, April-July planting season

| | Vp | Vg | Ve | H bs | Classification[a] |
|---|---|---|---|---|---|
| Days to maturity (days) | 4.37 | 2.46 | 1.91 | 0.56 | |
| Plant height (cm) | 118.73 | 77.52 | 41.21 | 0.65 | High |
| Number of branches per plant | 0.54 | 0.28 | 0.26 | 0.51 | High |
| Number of productive nodes per plant | 3.42 | 1.67 | 1.75 | 0.49 | Medium |
| Number of filled pods per plant | 145.52 | 67.55 | 77.97 | 0.46 | Medium |
| 100-seed weight (g) | 13.68 | 11.58 | 2.10 | 0.85 | High |
| Seed yield (t/ha) | 0.12 | 0.03 | 0.09 | 0.25 | Medium |

[a]Based on Stansfield (1991)

**Table 4.** Phenotypic and genotypic correlations of agronomic characters of soybean genotypes. Muneng Res Station, April-July planting season

| | HIG | BRC | NOD | POD | W100 | YLD |
|---|---|---|---|---|---|---|
| DTM | 0.276** | 0.284** | 0.247* | 0.329** | -0.218* | 0.118 |
| | 0.477 | 0.465 | 0.433 | 0.467 | -0.274 | 0.290 |
| HIG | | 0.416** | 0.774** | 0.430** | -0.585** | 0.012 |
| | | 0.640 | 0.991** | 0.747 | -0.799 | -0.052 |
| BRC | | | 0.440** | 0.444** | -0.530** | 0.049 |
| | | | 0.790 | 0.941* | -0.815 | 0.100 |
| NOD | | | | 0.487** | -0.592** | -0.048 |
| | | | | 0.814 | -0.939** | -0.241 |
| POD | | | | | -0.567** | 0.354** |
| | | | | | -0.840 | 0.771 |
| W100 | | | | | | 0.215* |
| | | | | | | 0.325 |

Upper = phenotypic correlation, Lower = genotypic correlation, **significant at level of 1%, * significant at level of 5%, DTM = days to maturity, HIG = plant height, BRC = number of branches/plant, NOD = number of reproductive nodes/plant, POD = number of filled pods/plant, W100 = 100-seed weight, YLD = seed yield/ha

deviation, determination criteria are measured based on the character itself, thus environmental factors can be completely eliminated. Although the difference in coefficient of variability was small, based on genetic standard deviation of variability in maturity and 100-seed weight in this study, it was broad due to different measurement unit of the characters. The number of filled pods that had the highest difference in coefficient of variability had narrow criteria based on genetic standard deviation. Therefore, it seems that the use of genetic standard deviation is more relevant in determining the genetic variability of a character.

Heritability is a comparison of genetic variance against phenotypic variance (genotypic and environmental variances). Of seven characters observed, four characters (days to maturity, plant height, and number of branches per plant) had high heritability. In comparison, three characters had low heritability (number of productive nodes per plant, number of filled pods per plant, and seed yield). The highest heritability was achieved by 100-seed weight, while the lowest value was achieved by seed yield per plant (Table 3). High heritability shows that genetic factors are more dominant than environmental factors. Kuswantoro (2017) also reported high heritability on days to maturity, seed size, and seed yield. The changes in heritability value could be influenced by plant material as genetic factor and environmental conditions.

The phenotypic and genotypic correlations of the various agronomic characters were tested. In general, the phenotypic correlation was significant, except for the correlation between seed yield and days to maturity, plant height, number of branches, and number of productive nodes per plant (Table 4). The seed yield significantly correlated with number of filled pods and 100-seed weight. Several studies also reported similar results. Machado *et al.* (2017) stated that plant height associated with number of productive nodes, and number of pods per plant correlated with plant height and seed yield. Jiang *et al.* (2018) and (Mahbub *et al.* 2015) also stated that 100-seed weight had a positive phenotypic correlation with seed yield. Seed yield correlated with number of pods was reported by Bekele and Alemahu (2011). Mahbub *et al*. (2015) said that plant height, number branches per plant, number of pods per plant, 100-seed weight significantly had a positive genotypic and phenotypic correlation with seed yield.

In contrast to the phenotypic correlation, genotypic correlation was generally insignificant (Table 4). There were only three significant genotypic correlations, namely correlation between plant height and number of productive nodes, number of branches and number of filled pods, and number of productive nodes and 100-seed weight. Machado *et al.* (2017) also reported significant genotypic correlations of plant height with number of productive nodes and number of pods, and number of pods with seed yield. Similarly, Machikowa and Laosuwan (2011) investigated the correlation between number of pods, number of nodes, and number of seeds per plant. Bekele and Alemahu (2011) stated that a significant genotypic correlation was obtained in seed yield with maturity and number of pods.

Interestingly, phenotypic and genotypic correlations of 100-seed weight in this study were significantly and negatively correlated with all agronomic characters, except for seed yield. It means that soybean genotypes with large seed sizes had early maturity, short plant, fewer branches, fewer productive nodes and pods. Bekele and Alemahu (2011) also reported a negative genotypic correlation between 100-seed weight with number of branches and productive nodes. The trend of negative values on phenotypic and genotypic correlations in 100-seed weight was also observed by Machikowa and Laosuwan (2011). The linear correlation also shows a significant negative correlation between 100-seed weight and other agronomic characters (Krisnawati and Adie 2016; Kuswantoro 2017).

Inspite of genotypic correlation value was greater than phenotypic correlation, genotypic correlation was not always significant, even though phenotypic correlation was very significant. It occurs because the determination of significant genotypic correlation and phenotypic correlation was different. Determining the significance genotypic correlation involved heritability value, while phenotypic correlation was based on linear correlation (Falconer 1960; Debi *et al*. 2016).

## CONCLUSION

Abnormal distribution of a character was caused by the selection of plant materials based on this character or the correlation between the characters with a selected character. Significant genetic diversity was obtained in days to maturity, number of branches per plant, number of productive nodes per plant, 100-seed weight, and seed yield. Not all significant phenotypic correlations were followed by significant genotypic correlations. Significant genotypic correlation was shown by the plant height with number of productive nodes per plant, number of branches per plant with number of filled pods per plant, and number of productive nodes per plant with seed yield. The 100-seed weight could be used as indirect selection criterion for high yield because the phenotypic correlation was significant.

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