Genetic Parameters Estimation of Agronomic Traits in Soybean Population Resistant to Whitefly

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Abstract. More knowledge of genetic parameters could assist plant breeders in determining breeding methods and selection criteria. The aim of this study was to estimate the components of variance, heritability, and genetic advance some agronomic traits in F4 generation populations of soybean resistant to whitefly. The research was conducted at greenhouse of Indonesian Legumes and Tuber Crops Research Institute in Malang, Indonesia from April to July 2015. Plant genetic material consists of four soybean populations, each population derived from crosses between soybean genotypes resistant to whitefly with high yielding soybean varieties. All plant genetic material laid out in a randomized complete block design with four replicates. The results showed that all agronomic traits observed had narrow genetic variability. Broad sense heritability varies between 5% and 81%. Days to flowering, intensity of leaf damage, and seed weight per plant had high broad sense heritability (81%, 80%, and 52%, respectively). Selection on the intensity of leaf damage and seed weight per plant will provide the highest genetic advance, respectively by 41.62% and 20.15%. High heritability accompanied by high genetic advance on the intensity of leaf damage and seed weight per plant indicated an effective selection for these traits in this population.

Keywords: genetic advance, genotypic variability, genotype variance, heritability, phenotype variance

1. Introduction

Soybean is one of the food commodities that are used as a source of vegetable protein for the majority of the people of Indonesia. Tempe, tofu, bean sprouts, soy sauce, and soy milk are processed product of soybean and widely consumed by the people throughout the islands of Indonesia. Demand for national soybean consumption continues to increase from year to year with an average increase reached 2.44% per year [1]. But the domestic soybean production of Indonesia can only meet about 33.33% of the domestic demand, and the rest (66.66%) is met through imports [2]. The dependence on imported soybean should be reduces by increased domestic soybean production [3].

One of the strategies that might be done in an effort to increase soybean production is to improve soybean varieties. Until now, the soybean varieties that have been released by the government of Indonesia amounted to 86 varieties [4]. Most of these varieties are obtained through crossbreeding with various objectives of plant breeding. One of the main targets in soybean breeding in Indonesia is to obtained high yielding varieties. In addition, it needs to be assembled soybean varieties resistant to whitefly.
pests and diseases. Among 86 soybean varieties, there is only one variety which was described as soybean varieties with resistance to whitefly, namely Tengger. Thus, increasing the number of soybean varieties that are resistant to whitefly is still needed. Whitefly can causes leaf damage with impaired photosynthesis [5,6] by inducing the growth of sooty mold on the leaves due to the honey dew excreted by the whitefly [7]. Furthermore, whitefly causes the transmission of viral disease [8-10] and eventually leading to yield loss in soybeans up to 80%.

The success of a soybean breeding program for whitefly tolerance is largely determined by the availability of sources of resistance genes and breeding method used. To determine the appropriate breeding method, the breeders need some information about genetic parameters, such as genotypic variance, phenotypic variance, heritability, genetic variability, and genetic advance. The accuracy in estimating genetic parameters can increase the genetic improvement of an agronomic trait [11]. If a character has a high heritability, then the progress of the selection becomes easier, and thus the selection response will be greater [12]. The heritability value reflects the inheritance of genetic factor from parent to offspring [13]. The purpose of this study was to estimate the variance components, heritability, and genetic advances some agronomic traits in F4 generation populations of soybean resistant to whitefly.

2. Materials and methods
This study was conducted at greenhouse of Indonesian Legumes and Tuber Crops Research Institute (ILETRI) in Malang, Indonesia from April to July 2015. Plant genetic material used consisted of four populations of soybean resistant to whitefly. These populations are F4 generations of crosses between soybean genotypes resistant to whitefly with high yielding soybean varieties. All the plant genetic materials were grown following the randomized complete block design (RCBD) with four replicates.

Observation was carried out on days to flowering, number of leaf trichomes, intensity of leaf damage due to attack of whitefly, plant height, number of branches, number of reproductive nodes, number of pods, and seed weight per plant. The observation of number of leaf trichomes per cm2 was performed in laboratory using a light microscope with a magnification of 25 x 25. The fifth leaf from the top of the 8-weeks-old plants are used as leaf sample for observation of trichomes density. The intensity of leaf damage is calculated based on a scale of leaf damage. The scores used are 0 to 4, referring to the scale used by Inayati and Marwoto [14].

The data obtained were analyzed using PKBT-STAT 1.0 software (developed by Center for Tropical Fruits Studies, Bogor Agricultural University) for analysis of variance (ANOVA). The following model was used for ANOVA for all agronomic traits:

\[ Y_{ij} = \mu + r_j + g_i + \varepsilon_{ij} \]

Where: \( Y_{ij} \) = the response of trait Y in the i\(^{th}\) lines and the j\(^{th}\) replication; \( \mu \) = the grand mean of trait Y; \( r_j \) = the effect of the j\(^{th}\) replication; \( g_i \) = the effect of the i\(^{th}\) lines; and \( \varepsilon_{ij} \) = experimental error effect.

Mean square from analysis of variance was used to estimate components of variance follow the equation suggested by Burton and Devane [15]. Estimation of environmental variance (\( \sigma^2_e \)), genotypic variance (\( \sigma^2_g \)), and phenotypic variance (\( \sigma^2_p \)) calculated using the equations contained in Table 1 as follows:

\[
\text{Environmental variance} \ (\sigma^2_e) = \frac{\text{Ms}_{e}}{r}
\]

\[
\text{Genotypic variance} \ (\sigma^2_g) = \frac{(\text{Ms}_{g} - \text{Ms}_{e})}{r}
\]

\[
\text{Phenotypic variance} \ (\sigma^2_p) = \sigma^2_g + \sigma^2_e
\]

Where: \( \text{Ms}_{e} \) = means square of error, \( \text{Ms}_{g} \) = mean square of genotype, and \( r \) = replication
Table 1. Analysis of variance and estimation of variance components from RCBD.

| Source of variation | Df | Mean square | Expected mean square |
|---------------------|----|-------------|---------------------|
| Replication         | r-1| Ms_r        | \(\sigma^2_e + \sigma^2_g + g\) |
| Genotypes           | g-1| Ms_g        | \(\sigma^2_g + r\sigma^2_g\) |
| Error               | (r-1)(g-1)| Ms_e | \(\sigma^2_e\) |

\(\sigma^2_e\) = environmental variance, \(\sigma^2_g\) = genotypic variance, \(r\) = replication, \(g\) = genotypes

Based on the value of genotypic variance (\(\sigma^2_g\)) and the mean of population (X), then genotypic coefficient of variation (GCV) calculated using the equation given by Johnson et al. [16]. The following formula was used to calculated genotypic coefficient of variation (GCV):

\[
\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2_g}}{X} \times 100\%
\]

Where: \(\sigma^2_g\) = genotypic variance, and \(X\) = mean of population

Furthermore, the broad sense heritability (\(h^2\)) was calculated using the equation given by [17] as follows:

\[
\text{Broad sense heritability (} h^2_b \text{)} = \left( \frac{\sigma^2_g}{\sigma^2_p} \right) \times 100\%
\]

Where: \(\sigma^2_g\) = genotypic variance and \(\sigma^2_p\) = phenotypic variance

Broad or narrow of genetic variability of a character is determined by genotypic variance (\(\sigma^2_g\)) and standard deviation of genotypic variance (\(\sigma_{\sigma^2_g}\)). Genetic variability is broad if genotypic variance is greater than two times of standard deviation of genotypic variance (\(\sigma^2_g > 2\sigma_{\sigma^2_g}\)), meanwhile the genetic variability is narrow if genotypic variance is less or equal to two times of standard deviation of genotypic variance (\(\sigma^2_g \leq 2\sigma_{\sigma^2_g}\)) [18]. The following equation suggested by Hallauer and Miranda [19] was used to calculate the standard deviation of genotypic variance:

\[
\text{Standard deviation of genotypic variance} \ (\sigma_{\sigma^2_g}) = \frac{2}{r^2} \left( \frac{\text{Ms}_g}{\text{df}_g} + 2 + \frac{\text{Ms}_e}{\text{df}_e} + 2 \right)
\]

Where: \(r\) = replication, \(\text{Ms}_g\) = mean square of genotype, \(\text{Ms}_e\) = means square of error, \(\text{df}_g\) = degrees of freedom of genotype, and \(\text{df}_e\) = degrees of freedom of error

The estimation value of selection response (R) and expected genetic advance (GA) on the selection intensity of 20% (\(i = 1.40\)) were calculated according to the formula given by Allard [17] as follows:

\[
\text{Selection response (R)} = i \times \sigma_p \times h^2_b
\]

\[
\text{Genetic advance (GA)} = \frac{R}{X} \times 100\%
\]

Where: \(i\) = coefficient of selection intensity, \(\sigma_p\) = standard deviation of phenotype, \(h^2_b\) = broad sense heritability, and \(X\) = mean of population

3. Results and discussion

3.1. Genetic variability

Selection is the basic activity of a plant breeding program in an effort to obtain new superior varieties. Selection will be effective if a breeding population used by breeders have a broad genotypic variation. In other words, variation in genotype plays an important role in determining the success of a selection
activity. A breeding population with a wide variety of genotypes will increase the chances of obtaining individuals with desirable traits.

The genotypic coefficient of variation (GCV) of some agronomic traits in soybean populations tolerant to whitefly is shown in table 2. The number of fertile nodes has the highest GCV (48.73%), followed by the intensity of leaf damage due to attack of whitefly (28.09%). Meanwhile, days to flowering, number of leaf trichomes, plant height, number of branches, number of pods and seed weight per plant have the GCV below 20%. The value of GCV divided into three groups, i.e. low (GCV <10%), medium (10-20%) and high (GCV >20%) [20]. Based on the value of GCV obtained in this study, then number of fertile nodes and leaf damage intensity have high GCV, number of pods and seed weight per plant have medium GCV, and days to flowering, number of leaf trichomes, plant height, and number of branches have low GCV. These results are not in line with other studies that use the same type of generation (F4 population). Hakim and Suyamto [21] found that the seed weight per plant, number of pods and days to maturity are agronomic traits with high GCV. Meanwhile, several agronomic traits with low and medium valued GCV were also reported by other researchers. Chandel et al. [22] and Baraskar et al. [23] found that days to flowering had a low GCV, whereas number of pods, and seed yield per plant had a medium GCV.

Table 2. Genotypic coefficient of variation (GCV) of some agronomic traits in soybean populations tolerant to whitefly.

| Agronomic traits                        | GCV   | $\sigma^2_g$ | $\sigma^2_p$ | $2\sigma^2_g$ | Category  |
|----------------------------------------|-------|--------------|--------------|---------------|-----------|
| Days to flowering                      | 6.64  | 5.71         | 3.82         | 7.64          | Narrow    |
| Number of leaf trichomes              | 4.23  | 24.08        | 37.71        | 75.42         | Narrow    |
| Intensity of leaf damage               | 28.09 | 0.71         | 0.47         | 0.94          | Narrow    |
| Plant height                           | 1.19  | 12.71        | 10.62        | 21.24         | Narrow    |
| Number of branches                     | 0.32  | 0.02         | 0.06         | 0.12          | Narrow    |
| Number of fertile nodes                | 48.73 | 0.95         | 0.85         | 1.70          | Narrow    |
| Number of pods                         | 11.84 | 2.37         | 4.19         | 8.38          | Narrow    |
| Seed weight per plant                  | 18.44 | 0.85         | 0.67         | 1.34          | Narrow    |

GCV = genotypic coefficient of variation, $\sigma^2_g$ = genotypic variance, $\sigma^2_p$ = standard deviation of genotypic variance

Based on table 2, it can be seen that all agronomic traits were observed in this population has a narrow genotype variation. The narrowness of the variation of genotypes in this population is caused by the same genetic background among soybean lines tested. All genetic material used in this study are the progeny of the IAC 100. Genotype IAC 100 is soybean germplasm that used as a source of soybean resistance gene against whitefly. Some researchers found that IAC 100 is one of the soybean genotypes that have a resistance to some major pests on soybean [24,25]. The mechanism of resistance on the genotype IAC 100 is in the form of antibiosis [26,27]. A narrow genotype variation could also mean that the selection of the previous generations has pursued the chosen individual, in terms of this population are individuals soybeans that are tolerant to whitefly. Ribeiro et al. [28] stated that the selection made in the early generation (segregation population) will provide a high probability of success to obtained desirable individuals.

3.2. Heritability

Heritability is one of the important genetic parameters that should be known by breeders. The value of heritability is used to predict the progress of the selection of a character, whether controlled by genetic factors or influenced by environmental factors. Broad sense heritability is the proportion of genotypic variance ($\sigma^2_g$) to phenotypic variance ($\sigma^2_p$) [29]. In this case, genotypic variance was variance total of dominance ($\sigma^2_d$), additive ($\sigma^2_a$), and epistatic ($\sigma^2_e$). Heritability values will range between 0 and 1. The value of heritability will be close to 0 if the variance of phenotype is influenced by environmental factors, and will be close to 1 if the variance of phenotype is controlled by genetic factors.
The estimation value of environmental variance, genotypic variance, phenotypic variance, and broad sense heritability of some agronomic traits in soybean populations tolerant to whitefly are presented in Table 3. The results of the analysis of genetic parameters showed that the heritability estimation value in this population varies between 0.05 and 0.81. The value of heritability classified into three classes, i.e. low (\(h^2 < 0.20\)), medium (0.20 ≤ \(h^2 \leq 0.50\)), and high (\(h^2 > 0.50\)) [30]. Based on these values, then the heritability of this population varies from low (0.05) to high (0.81).

**Table 3.** Components of variance and broad sense heritability of some agronomic traits in soybean populations tolerant to whitefly.

| Agronomic traits        | \(\sigma^2_e\) | \(\sigma^2_g\) | \(\sigma^2_p\) | \(h^2_b\) | Category |
|-------------------------|----------------|---------------|---------------|----------|----------|
| Days to flowering       | 1.33           | 5.71          | 7.04          | 0.81     | High     |
| Number of leaf trichomes| 126.4          | 24.08         | 150.48        | 0.16     | Low      |
| Intensity of leaf damage| 0.18           | 0.71          | 0.89          | 0.80     | High     |
| Plant height            | 15.49          | 12.71         | 28.20         | 0.45     | Medium   |
| Number of branches      | 0.29           | 0.02          | 0.31          | 0.05     | Low      |
| Number of fertile nodes | 1.48           | 0.95          | 2.43          | 0.39     | Medium   |
| Number of pods          | 15.02          | 2.37          | 17.39         | 0.14     | Low      |
| Seed weight per plant   | 0.79           | 0.85          | 1.64          | 0.52     | High     |

\(\sigma^2_e\)= environmental variance, \(\sigma^2_g\)= genotypic variance, \(\sigma^2_p\)= phenotypic variance, \(h^2_b\)= broad sense heritability

In this population, days to flowering, leaf damage intensity, and seed weight per plant has high heritability (0.81, 0.80, and 0.52, respectively). These results are in line with Barmawi et al. [31] who found those days to flowering and seed weight per plant has high heritability (0.83 and 0.96, respectively). Similarly, Osekita and Olorunfemi [32] found the highest heritability value in both characters. The high value of heritability of a character will make it easier for breeders undertake a selection towards that character [33]. This is because there is a close relationship between genotype with phenotype compared with the contribution of environmental influences on the phenotype.

One of the factors that determine the success of a selection in an effort to obtain soybean genotypes resistant to whitefly is accuracy in choosing selection criteria associated with the resistance character. In this study, the number of leaf trichomes and the intensity of leaf damage due to attack of whitefly are characters that have a correlation with resistance to whitefly [14,26,34,35]. In between these two characters, leaf damage intensity has a high heritability. This means that the character of the intensity of leaf damage is inherited. Therefore, these characters might be used as a selection criterion for soybean resistance to whitefly.

### 3.3. Expected genetic advance

Table 4 shows the expected genetic advance of the selection of agronomic traits in soybean populations tolerant to whitefly. In the selection intensity of 20%, it is seen that the value of expected genetic advance varies from 2.05% to 41.62%. The intensity of leaf damage has the highest expectations value of genetic advance that is equal to 41.62%. This illustrates that progress which will be obtained within one generation of selection for these characters is estimated at 41.62%. Other agronomic trait that has a genetic advance with rather high expectations value is the weight of seeds per plant. In this population, it has expectation genetic advance with a value of 20.15%. These results are consistent with Hakim et al. [36] who found that genetic advance on the character of seed yield per plant amounted to 35.5%.

Among the agronomic traits were observed, leaf damage intensity and seed weight per plant are two characters that had highest heritability and highest genetic advance. This indicates the effectiveness of the selection made on the intensity of leaf damage and seed weight per plant. Abady et al. [37] and Baraskar et al. [23] stated that the selection based on phenotype expression can be effective if a character has a high value both in heritability and genetic advance. Rohman et al. [38]
explain that the high heritability and genetic advance of a character indicate the role of additive genes in controlling the character.

Table 4. Selection response and expected genetic advance of some agronomic traits in soybean populations tolerant to whitefly.

| Agronomic traits       | X   | σp  | h²b | R    | GA   | Category |
|------------------------|-----|-----|-----|------|------|----------|
| Days to flowering      | 36.42 | 2.32 | 0.81 | 2.63 | 7.23 | Medium   |
| Number of leaf trichomes | 116.06 | 13.03 | 0.16 | 2.92 | 2.52 | Low      |
| Intensity of leaf damage | 2.61 | 0.98 | 0.80 | 1.09 | 41.62 | High     |
| Plant height           | 44.46 | 5.02 | 0.45 | 3.17 | 7.12 | Medium   |
| Number of branches     | 2.20 | 0.66 | 0.05 | 0.05 | 2.05 | Low      |
| Number of fertile nodes | 13.02 | 1.97 | 0.39 | 1.08 | 8.29 | Medium   |
| Number of pods         | 25.98 | 5.32 | 0.14 | 1.01 | 3.90 | Low      |
| Seed weight per plant  | 4.64 | 1.29 | 0.52 | 0.93 | 20.15 | High     |

X = mean of population, σp = standard deviation of phenotype, h²b = broad sense heritability, R = selection response, GA = genetic advance

4. Conclusion

Based on the results obtained in this study, it can be concluded that the genetic variability of agronomic traits observed in F4 populations of soybean tolerant to whitefly was narrow. The heritability and genetic advance of these traits varies from low to high. The intensity of leaf damage due to attack of whiteflies and seed weight per plant had high heritability with high genetic advance, thus the selection to obtain soybean lines that are resistant to whitefly and high yields in the next generation is relatively easy to do.

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