INNSPUB

International Journal of Biosciences | IJB |
ISSN: 2220-6655 (Print), 2222-5234 (Online)
http://www.innspub.net
Vol. 6, No. 6, p. 29-36, 2015

RESEARCH PAPER

OPEN ACCESS

Heritability estimation in resistant soybean towards cowpea mild mottle virus (CPMMV)

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Key words: Heritability, Soybean, Disease of Cowpea Mild Mottle Virus.

http://dx.doi.org/10.12692/ijb/6.6.29-36

Abstract

Objective of the research was to obtain information on the heritability estimation in resistant soybean toward CPMMV to determine the method of selection on seeds quality. The research was conducted at Mlilir Village in Madiun from August to December 2012 at the altitude of 115 m asl. This study used Complete Randomized Design by three replications. Population of female parents is Argopuro and Gumitir as the susceptible parents, MLG 0278 and MLG 0120 as the resistant parents. Whereas, population F1, population BC.1.1 and BC1.2 comprises of 30 plants and population F2 comprises of 300 plants. CPMMV inoculation was mechanically conducted at the age of 10 days after planting. Observed parameters include: plant height, number of branch, age of flowering, number of filled pod, number of empty pod, number of fertile node, age of harvesting, seed's weight per plant, and intensity of disease infection. Parameter of CPMMV infection intensity was assessed at the age of 35 days after inoculation (45 days after planting). Results of the research showed that parameter of the infection intensity has high value of broad sense heritability and low value of narrow sense heritability for all crossbred series, thus we suggested for further research to apply bulk selection method.

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Introduction

One of the main diseases which frequently reduce the soybean production is *Cowpea mild mottle virus* (CPMMV) (Buchen-Osmond, 2002). However, CPMMV has spread over the soybean production centre and obstruct in the increasing of the soybean production. The existence of CPMMV was reported at the first time on soybean in Java in 1984 (Iizuka *et al.*, 1984b), after that CPMMV has infected almost the entire soybean plants in Indonesia that has reached 100% (Iizuka *et al.,* 1984a; Kuswantoro *et al.,* 2006). The infectious CPMMV could stand great loss for about 11.9–81.5% (Saleh *et al.,* 2004). *Cowpea mild mottle virus* belongs to carla-virus, which is mechanically infected by *Bemisia tabaci* as the non-persistent vector (Iwaki *et al.*, 1982; Muniyappa and Reddy, 1983).

In general, CPMMV virus is frequently controlled by the application of pesticide. So far, the appropriate pesticide has not been found to control the virus, while the insecticide can only be applied to control the vector of *B. tabaci.* Therefore, the control has relied on the application of insecticide, such as acetamiprid (Zabel *et al.,* 2001), buprofezin and diafenthiuron (Gerling and Naranjo, 1998), as well as Carbosulfan (Manzano *et al.,* 2003). However, controlling by the application of insecticides, such as imidacloprid, thiamethoxam, pyriproxyfen, buprofezin, pyridaben, and pymetrozine have not been able to control *B. tabaci.* As reported by Palumbo *et al.* (2001), the application of insecticide could create resistance to *B. tabaci.* In fact, controlling the vector of *B. tabaci* was also ineffective. Therefore, the only way to control it is by providing CPMMV resistant variety of soybean, which is not only economic beneficially, but also hospitable to environment.

In assembling the soybean variety that resistant to CPMMV, it requires some information about resistance hereditary pattern, particularly estimation of the heritability values. Heritability can be used as a basis in determining the selection program. Selection is done when the initial generation produces high heritability values. Otherwise, if it is lower, then the selection of the next generation will succeed because the chances of increasing diversity in the population. Based on the description above, a research has been conducted in relation with estimation on the heritability value of resistance to CPMMV in soybean. The study aimed to obtain information on the heritability estimation in resistant soybean toward CPMMV to determine the method of selection on seeds quality.

Material and method

Research model

This research on CPMMV resistant hereditary conducted in the greenhouse at Mlilir Village, Madiun, at the altitude of 115 m above sea level from August to December 2012. Materials of the research includes all populations of F1 as a result of crossbred between the susceptible varieties (Argopuro and Gumitir) and CPMMV resistant genotype (MLG 0278), as well as both parents, which were used to establish F1, F2, BC1.1 and BC1.2 (Figure 1). Review on CPMMV resistant hereditary used a Randomized Complete Design by three replications. Each population comprise of 30 plants, except for population F2 comprises of 300 plants. CPMMV inoculation has mechanically conducted in the previous research.

The planting of 3 parent populations, 2 populations of F1, 2 populations of F2, 2 populations of BC.1.1, and 2 populations of BC1.2 were done in Madiun. The soybean seeds were planted in 40 x 20 cm. Maintenances includes weeding, irrigation, as well as pest and disease control. Weeding conducted once in two weeks to improve the plant growth, while irrigation conducted twice in a week to maintain the available of water for optimal growth of the plant.

Observation

We observe the plant height, number of branch, age of flowering, number of filled pod, number of empty pod, number of fertile node, age of harvesting, seed weight per plant, and intensity of CPMMV infection.

Intensity of CPMMV Infection

Intensity of CPMMV infection observed visually per plant at 35 dai (days after infection). Scores for the observed infection referred to Zubaidah *et al.* (2006), based on visible symptoms on leaves of each plant (Table 1). Thus, we can classify the resistance category based on the intensity of infection (Table 2). Intensity of CPMMV infection is calculated as follows:

$$I = \frac{\sum(n \times v)}{N \times Z} \times 100\%$$

Description:

I = Intensity of infection per plant (%)
n = Number of the infected leaves in certain category
v = Score of category in certain infected leaf
N = Number of observed leaf per plant
Z = Value of the highest category

Broad Sense Heritability

Heritability was analyzed to assess the proportion of genetic variance toward the phenotypic variance (Falconer, 1989). The heritability value in broad sense of a character is calculated using the equation below:

$$h^2{}_{b.s.} = \frac{\sigma^2 - \left(\frac{1}{3}\right) \times (\sigma^2{}_{F1} + \sigma^2{}_{P1} + \sigma^2{}_{P2})}{\sigma^2{}_{F2}}$$

Description:

$h^2_{b.s.}$= heritability in broad sense
σ^2_{F2} = variance of F_2 population
σ^2_{F1} = variance of F_1 population
σ^2_{P1}= variance of parent P_1 population
σ^2_{P2}= variance of parent P_2 population

Narrow Sense Heritability

Whereas, heritability in narrow sense was calculated using the equation below.

$$h^2{}_{n.s} = \frac{2\sigma^2{}_{F2} - \sigma^2{}_{B1} - \sigma^2{}_{B2}}{\sigma^2{}_{F2}}$$

Description:

$h^2_{n.s.}$ = heritability in narrow sense
$\sigma^2_{B1.}$ = variance of population on reversed crossbred with P_1
$\sigma^2_{B2.}$ = variance of population on reversed crossbred with P_2

Heritability Values

The heritability values were classified based on Bianchi-Hall *et al.* (1998) as follow:

< 0.25 = low
0.25 – 0.50 = rather low
0.51 – 0.75 = rather high
> 0.75 = high

Result and discussion

Heritability in Broad and Narrow Sense

Heritability is a genetic parameter, which is used to measure the ability of genotype in plant population to bequeath its character. It is also an estimation to measure the extent of appearance variability of a genotype in population, particularly due to the role of genetic factor. Heritability value implied the influence of genetic factor or environment towards a character or trait. There are two types of heritability, such as heritability in broad sense and heritability in narrow sense. Heritability in broad sense is a ratio between genetic variance and phenotypic variance.

Table 1. Score of CPMMV infection on the soybean leaves.

Symptom of the infection	Score
Healthy plant without any infectious symptom	0
Plant looks health with a little mottle (yellow spot), but obscure	1
Distinct yellow spots, unwrinkled	2
Distinct yellow spots, little wrinkled, slightly mozaic	3
Distinct yellow spots, wrinkled, distinct mosaic, no necrosis	4
Distinct yellow spots, wrinkled, distinct mosaic, necrosis on veins of leaf surface at the bottom part, malformation, dwarf leaf, curved downward or upward	5

Source: Zubaidah *et al.* (2006).

The heritability value of a character is not constant. This is due to some factors, such as: character of population, sample of the evaluated genotype, estimation method, linkage gene, extensive genotype evaluation, and the experiment implementation (Fehr, 1987). Thus, the same characters may have different values even in two identical populations. Even though the estimation methods are similar, heritability of a character is not always identical, and vice versa. Moreover, Zen (1995) described that selection which was based on heritability value, genetic correlation and phenotype, could assist the accuracy of selection.

Table 2. Classification of resistance based on intensity of infection

Intensity of infection (%)	Category
0 – 25	Resistant
26 – 50	Less Resistant
51 – 75	Less Susceptible
76 – 100	Susceptible

Source: Zubaidah *et al.* (2006).

The heritability values in broad sense of both pairs of crossbred on high resistant character were 0.76 and 0.83. The higher the heritability value leads to the stronger effect of genetic factor, and vice versa. Conversely, the lower heritability value leads to the higher effect of environmental factor. For character that has slightly high to higher value of heritability, the progeny's traits are mostly identical with the parents. There is a dominant effect of genetic factor on those traits. Similarity traits between the progeny and the parents are mostly affected by additive variances, which determine the value of heritability in narrow sense.

The character which has low value of heritability in narrow sense tends to have character that slightly different from the parents due to mostly affected by the environment factor. Moreover, as described by Ullah *et al.* (2011), climate change (planting season) or soil (location) will cause trait changes that have low heritability values. It means that most of the traits have not been inherited from the parents to the progeny.

Table 3. Heritability values of broad and narrow sense on some characters in F_2 of two crossbred series of soybean.

Pair of crossbred	plant height		branch		fertile node		flowering age		filled pod		empty pod		harvesting age		seed weight per plant	
	h^2b	h^2n	h^2b	h^2n	h^2b	h^2n	h^2b	h^2n	h^2b	h^2n	h^2b	h^2n	h^2b	h^2n	h^2b	h^2n
Argopuro and MLG 0278	0.63	0.44	0.14	0.10	0.43	0.27	0.76	0.27	0.68	0.42	0.25	0.43	0.81	0.74	0.33	0.16
Gumitir and MLG 0278	0.62	0.39	0.44	0.31	0.34	0.11	0.88	0.65	0.70	0.63	0.73	0.64	0.80	0.30	0.06	0.03

Notes: h^2b = heritability of broad sense, h^2n = heritability of narrow sense.

The heritability values in broad sense (h^2b) for both series of crossbred on intensity of the observed diseases categorized as high. The heritability values on pairs of Argopuro X MLG 0278 and Gumitir X MLG 0278 were 0.83 and 0.76, respectively. Whereas the heritability values in narrow sense (h^2n) were 0.32 and 0.02, respectively (Figure2). Heritability in narrow sense is the ratio between additive variance and phenotypic variance. Low value of heritability in narrow sense describes that the character is controlled by non-additive gene (dominant and epitasis) in high level. As described by Pandiangan (2008), heritability would be meaningful if the genetic variances are dominated by additive variances due to the additive effect of each allele that will be inherited to the progeny.

High heritability in broad sense for intensity of infection on both series of crossbred showed that the genetic factor is crucial for phenotypic appearance, and environment played less important roles in appearance. Figure 2 shows high heritability values in broad sense, whereas narrow sense shows low value on intensity of infection in series of crossbred.

Characters that have low values of heritability in broad and narrow senses are easily directed to the selection method, which is occur on further generation, i.e. the bulk selection method.

Both series of crossbred have high value for heritability in broad sense and lower value for heritability in narrow sense. It indicates that the effect of genotypic variance of resistant F2 population is higher than the environmental variance, but the additive gene plays less important role, thus direct selection on the traits is less beneficial because it may create low selection progress. However, the selection would be more effective if it applied on further generation using Bulk method. It is expected that such method would be able to establish more families because each individual of plant F2 will formed a family following 4-5 times of pollination, thus variances among families of homozygote will be formed.

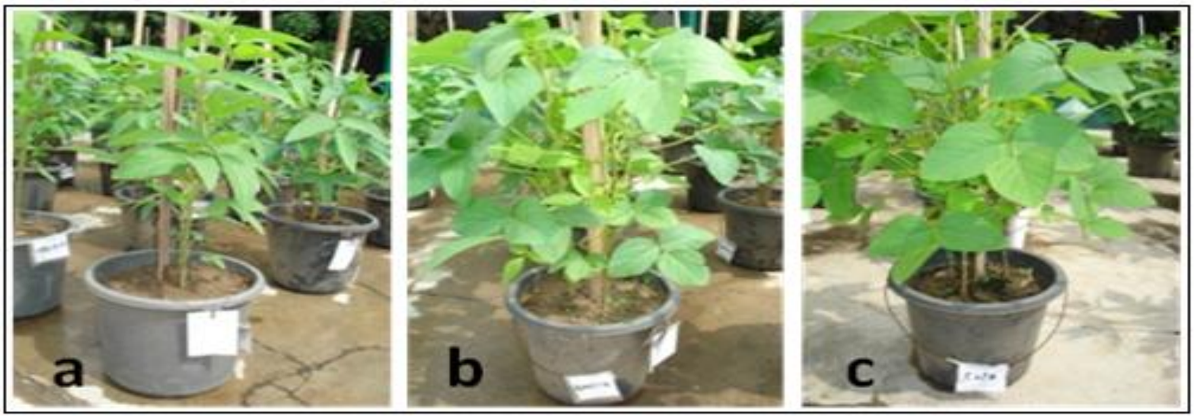

Fig. 1. Genotype of soybean: Argopuro (a) and Gumitir (b) as female parents which are susceptible to CPMMV, and MLG 0278 (c) as resistant male parent.

High heritability character implied that the genotypic variance plays more important roles than environmental variance. If the genotypic variance plays more important role, thus selection on the trait will bring about highly significant genetic progress. Low heritability value describes that the character is mostly affected by the environmental factor, so that the hereditary would be difficult and choosing the selection method would be effective for further generation. If the genetic variance is narrow, it means that individuals in the population are relatively uniform. Therefore, selection for trait improvement would be less effective (Wilson, 1981). On the contrary, the broader the genetic variance is, the greater opportunity will be had for success selection in increasing frequency of gene as desired. In other word, it provides greater opportunity to gain more favorable genotype through selection (Allard, 1960; Poespodarsono, 1988).

Heritability can be used as base in determining the selection program. Selection on early generation was done if the heritability value was high. On the contrary, if the value was low, selection for the next generation would be succeeding because it creates an opportunity to increase variant in population. Jain (1982) described that heritability would be significant if the genetic variance is dominated by additive variance due to additive effect of each allele that inherited from parents to their progeny.

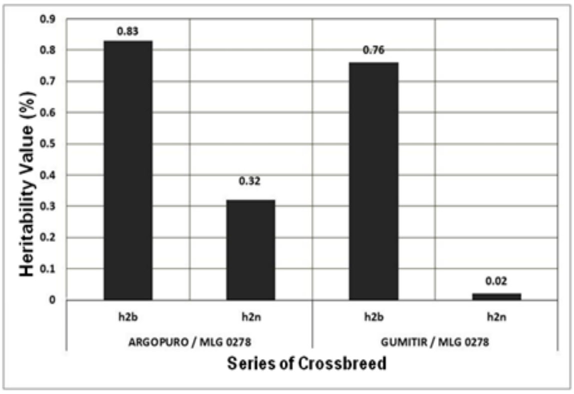

Fig. 2. Heritability values in broad sense (h^2b) and narrow sense (h^2n) intensity of CPMMV resistant on two series of crossbred in soybean.

Heritability values of broad and narrow senses for characters of plant range from low to high category (Table 3). The highest heritability values are for characters of flowering and harvesting age on both crossbreds' series. It shows that varied flowering ages and harvesting on such condition are due to genetic factors. If required, selection on character of flowering age will produce a significant genetic progress.

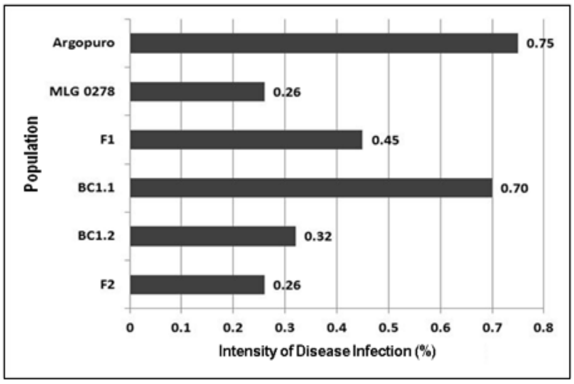

Fig. 3. Intensity of CPMMV infection in crossbred of Argopuro and MLG 0278.

Infection Intensity

Values of CPMMV infection intensity on the pairs of crossbred Argopuro and MLG 0278 presented in Figure 3. The results shows that intensity of the disease infection on F2 population is lower than Argopuro as the female parent, and it indicates that segregation has occurred on the character of resistant to CPMMV. This infection intensity is higher compared to the population of Gumitir and MLG 0278 (Figure 4). Such difference is caused by higher infection intensity of Argopuro parent (0.75) in comparison with the Gumitir parent (0.55).

Values of CPMMV infection intensity on the pairs of crossbred Gumitir and MLG 0278 are presented in Figure 4. It shows that intensity of the disease infection on population F2 is lower than both parents, and it indicates that segregation has occurred on trait of resistant to CPMMV. If it is compared with population of Argopuro x MLG 0278, such infection intensity is lower, and it is caused by lower infection intensity of Gumitirparent (0.55) in comparison with the Argopuro parent (0.75). Lower value of such infection intensity will be more resistant in the next generation. By planting in bulk, the F2 population may experience natural selection on resistance character and by other environmental factors. However, when the infection intensity value is low, it has greater possibility to obtain more resistant lines.

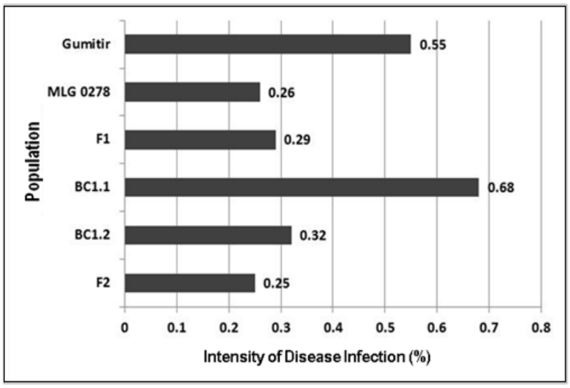

Fig. 4. Intensity of CPMMV infection in crossbred of Gumitir and MLG 0278.

We can conclude that the crossbred series of Argopuro – MLG 0278 and Gumitir – MLG 0278, have high values for broad sense heritability and low value for narrow sense heritability. Characters for ages of flowering and harvest can be considered as criteria of selection and could accelerate the selection time. We recommend bulk method for selection on the further research.

Acknowledgement

The author would like to express his gratitude to Directorate General of Higher Education (DIKTI) for the doctoral scholarship and the Head of BALITKABI Malang for the assistance in providing the seedling, as well as all parties who have offered assistances, both directly and indirectly.

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