

# Genetic variability and heritability of acid-adaptive soybean promising lines

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**Abstract.** Kuswanto H. 2017. *Genetic variability and heritability of acid-adaptive soybean promising lines. Biodiversitas 18: 378-382.* Genetic variability and heritability are very important in a variety improvement. The high genetic diversity can increase the probability on obtaining a new superior variety, while heritability can accelerate the selection process. In acidic dry land, genetic variability is also needed in order to increase such probability. The objective of this study was to estimate the genetic variability of acid-adaptive soybean promising lines. Ten advanced soybean-promising-lines derived from Tanggamus × Anjasmoro varieties crossing were used as the materials. Results showed that the characters of days to flowering, the number of branches plant<sup>-1</sup>, the number of reproductive nodes plant<sup>-1</sup>, 100 grains weight and grain yield had broad genetic variability, while days to maturity, plant height and the number of filled pods plant<sup>-1</sup> had narrow genetic variability. Characters of days to flowering, days to maturity, the number of filled pods plant<sup>-1</sup> and 100-grain weight showed high broad sense heritability; characters of a number of branches plant<sup>-1</sup>, and the number of reproductive nodes plant<sup>-1</sup> had moderate broad sense heritability; and plant height and grain yield had low broad sense heritability. Characters with broad genetic variability and high heritability can be used as sources in soybean variety improvement. The positive correlation between number of branches plant<sup>-1</sup> with number of reproductive nodes plant<sup>-1</sup> and number of filled pods plant<sup>-1</sup> were significant. Significant positive correlations were also found between number of reproductive nodes plant<sup>-1</sup> with number of filled pods plant<sup>-1</sup>. Negative correlations were found between weight of 100 grains with number of reproductive nodes plant<sup>-1</sup> and number of filled pods plant<sup>-1</sup>. Similarly, negative correlations were also found between days to flowering with grain yield. Negative correlation between days to flowering and grain yield suggests to develop variety with early days to flowering.

**Keywords:** Acid soil, genetic variability, heritability, soybean

## INTRODUCTION

Soybean is one of the important crops after rice and corn in Indonesia. The demand of soybean has not been fulfilled from domestic production. Most of the demand is for food ingredient likes tempeh, tofu, and soy sauce. Indonesian government urges to grown soybean in various agroecology such as in paddy field after rice, dry land, acid soil and tidal swamp land. Acid soil occupies about 69% of total dry land in Indonesia (Mulyani 2006). Developing acid-adaptive soybean variety in this area will increase domestic soybean production. Therefore, many efforts have been being conducted in developing acid-adaptive soybean variety through various agricultural practices including germplasm screening, artificial crossing and mutation, selection of segregated population, potential yield trial, and genetic × environment interaction.

In plant breeding program, genetic variability is the primary factor in developing a superior variety. Broad genetic variability allows superior variety can be developed faster. Plant breeders attempt to make their genetic material broader through many programs such as landraces exploration, artificial mutation, and germplasm introduction from other countries. Landraces exploration is very useful to find out genetic material for specific

purposes, especially for adaptation in a specific agroecology. Artificial mutation can be served as a technique to broaden genetic variability by damaging plant DNA. The damaged DNA will constitute new DNA sequence that can express the different performance of a character or whole characters in a plant. Germplasm introduction from other countries can broaden genetic variability. There is a geographical correlation that can be detected in a population (Wang and Li 2012). Usually, germplasm introduction express different response to the new environment. Therefore, pretreatment such as acclimation should be performed to find out the genetic value of the introduced germplasm before they are used as new genetic material in a breeding program.

Similar to genetic variability, heritability is also the main factor in plant breeding program. Heritability has main role in estimating inheritance ability (Omoigui et al. 2006), by expressing phenotypic value as breeding value. The magnitude of heritability determines the similarity of the parents to the offspring. A trait with high heritability is not relatively affected by the environment, where its performance is most influenced by the genes constitution. Therefore, heritability can also indicate the easiness of a trait to be improved through selection (Bekele et al. 2012).

## MATERIALS AND METHODS

### Research site and design

The experiment was conducted in the acid soil of South Lampung in Rainy Season II, from February to May 2011. Ten soybean lines were grown at Natar Research Station, South Lampung, Indonesia. The coordinate of this site is 5°18'52.2"S 105°10'36.2"E. The altitude was 135 m above sea level. The soil type was Ultisols. The design was randomized completely block with four replications. The plant materials were ten soybean promising lines derived from "Tanggamus" and "Anjasmoro" crossing.

### Soil preparation and cultural practice

Before planting, soil preparation was carried out by plowing the soil. Leveling the soil was done by using a rake. Every soybean line was grown in a plot with the size of 2.4 m × 4.5 m. The planting space was 0.4 m × 0.15 m. In one hill there were two plants. Fertilizer was applied at the sowing time by using Urea, SP36 and KCl with the doses of 50, 75 and 75 kg ha<sup>-1</sup> respectively. Weed control was conducted manually at two and four weeks after planting. Pests and diseases controls were intensively applied by monitoring.

### Data collection

Observations were conducted for days to flowering, days to maturity, plant height, the number of branches plant<sup>-1</sup>, the number of reproductive nodes plant<sup>-1</sup>, the number of filled pods plant<sup>-1</sup>, grain size and grain yield. Days to maturity was carried out after the crop was physiologically matured. It was designated by yellowing or browning pods and falling leaves. Grain size was measured by weighing 100 grains.

### Data analysis

Analysis of variance was performed by using PKBT STAT 1.0. Genetic variance was calculated based on the expected mean squares. The criteria of genetic variability were classified based on the deviation of genetic variance. If the coefficient of genetic variance is higher or equal to two times of the genotypic standard deviation ( $GCV \geq 2$ ), the genetic variability is broad. If the coefficient of genetic variance is lower than the genotypic standard deviation ( $GCV < 2$ ), the genetic variability is narrow.

## RESULTS AND DISCUSSION

The results showed that all the characters were observed significantly different or very noticeable, except for plant height and grain yield plant<sup>-1</sup> (Table 1). The significant difference among the genotypes based on the analysis of variance indicates the sufficient amount of variability the tested genotypes (Raulji et al. 2014). This indicates that at least one variety has a different character among the 10 varieties. Similar results were obtained in ILETRI germplasm collection (Kuswanto 2012), and the germplasm collection from Korea (Kuswanto 2013). However, in both studies, plant height and grain yield were

significantly different. Calculation of the variance (Table 1), still involved environmental variance, where the difference was assessed as individual difference based on the phenotypic performance, not genotypic performance

Days to flowering ranged from 35.5-43.5 days with the average of 38.6 days (Table 2). Based on the phenotypic performance, the value of this range is narrow when compared to the studies that use soybean germplasm originated from various regions in Indonesia and some introduced varieties with a range of 20-61 days and average 46 days (Kuswanto 2012). However, this study is similar to Kuswanto (2013) that uses introduced varieties from Korea with 25-32 days and average of 28 days. Allegedly, the narrow variability of the phenotypic performance of days to flowering is due to the genetic material are derived from the same crossing (Tanggamus × Anjasmoro). Similar to the days to flowering, days to maturity also had a narrow range of 81.8-86.0 days (Table 2) when compared to the ILETRI's germplasm collection ranging from 72.5 to 95 days (Kuswanto 2012) although the average days to maturity is slightly similar (84.4 days) (Table 2).

Plant height ranged from 51.4-68.6 cm with an average of 63 cm. Despite growing in the acid dry land, soybean can still show plant height as high as when grown in an optimal land. Kuswanto et al. (2014a) reported higher plant height in the acid dry land than in the optimal land. Similarly, the number of filled pods plant<sup>-1</sup> and reproductive nodes in this study are also equivalent to the soybeans grown in an optimal land (Kuswanto et al. 2014b). This similarity may be due to the sufficiency of water supply for soybean growth and development. In acid soil, water supply is more important than the acidity itself (Kuswanto and Zen, 2013). Even though the pH of the soil in this study was quite low, the plants still able to grow and develop properly. It is also caused by the lines that are selected from a series of activities of plant breeding for tolerance to acid dry land.

As shown by the analysis of variance of quantitative characters in Table 1, the performance differences among the genotypes in this study were significant unless plant height and grain yield. It indicates that at least one genotype differed to the other genotypes. Basically, the variance calculation measures individual differences based on the phenotypic performance. Therefore, it is necessary to measure the genetic coefficient of variance (GCV) in

**Table 1.** Analysis of variance of some soybean quantitative characters

Character	MS <sub>g</sub>	MS <sub>e</sub>
Days to flowering (day)	23.96**	1.53
Days to maturity (day)	8.07**	0.81
Plant height (cm)	127.44	75.03
Number of branches plant <sup>-1</sup>	2.58*	0.83
Number of reproductive nodes plant <sup>-1</sup>	57.17**	17.07
Number of filled pods plant <sup>-1</sup>	533.23**	44.72
Weight of 100 grains (g)	11.93**	1.46
Grain yield (t/ha)	0.08	0.05

Note: \*\*significant at level of 1%, \* significant at level of 5%, MS<sub>g</sub> = genetic mean square, MS<sub>e</sub> = error mean square

determination the involvement of genetic factors and environmental factors in phenotypic performance. Broad or narrow the genetic variability criteria based on the genetic standard deviation showed that the character of days to maturity, plant height, and number of filled pods were

narrow; whereas characters of days to flowering, the number of branches and the number of reproductive nodes plant<sup>-1</sup>, the weight of 100 grains and grain yield were broad. This classification applies specifically to 10 promising lines in this study.

**Table 2.** Range, average and standard deviation of some soybean agronomical characters

Character	Range	Average	Standard deviation
Days to flowering (day)	35.5-43.5	38.6	2.45
Days to maturity (day)	81.8-86.0	84.4	1.42
Plant height (cm)	51.4-68.6	63.0	5.64
Number of branches plant <sup>-1</sup>	1.6-4.2	2.8	0.80
Number of reproductive nodes plant <sup>-1</sup>	13.2-24.5	17.3	3.78
Number of filled pods plant <sup>-1</sup>	25.0-68.4	47.6	11.55
Weight of 100 grains (g)	10.16-16.00	12.05	1.73
Grain yield (t/ha)	1.36-1.83	1.57	0.14

**Table 3.** Phenotypic and genotypic coefficient of variance and variability criteria of some soybean agronomical characters

Character	PCV	GCV	$\sigma_{\sigma_g^2}$	Criteria
Days to flowering (day)	6.92	6.13	2.57	Broad
Days to maturity (day)	1.92	1.60	0.87	Narrow
Plant height (cm)	14.91	5.75	19.46	Narrow
Number of branches plant <sup>-1</sup>	40.79	23.97	0.32	Broad
Number of reproductive nodes plant <sup>-1</sup>	30.12	18.32	6.87	Broad
Number of filled pods plant <sup>-1</sup>	27.16	23.24	57.45	Narrow
Weight of 100 grains (g)	16.75	13.42	1.30	Broad
Grain yield (t/ha)	15.25	5.51	0.01	Broad

Note: PCV = phenotypic coefficients of variation, GCV = genotypic coefficients of variation

**Table 4.** Phenotypic and genetic variance, and heritability of some soybean agronomical characters

Character	$\sigma_g^2$	$\sigma_p^2$	$\sigma_e^2$	H <sub>bs</sub>
Days to flowering (day)	5.608	7.138	1.53	0.786
Days to maturity (day)	1.815	2.625	0.81	0.691
Plant height (cm)	13.103	88.133	75.03	0.149
Number of branches plant <sup>-1</sup>	0.438	1.268	0.83	0.345
Number of reproductive nodes plant <sup>-1</sup>	10.025	27.095	17.07	0.370
Number of filled pods plant <sup>-1</sup>	122.128	166.848	44.72	0.732
Weight of 100 grains (g)	2.618	4.078	1.46	0.642
Grain yield (t/ha)	0.0075	0.058	0.05	0.130

Note:  $\sigma_g^2$  = genetic variance,  $\sigma_p^2$  = phenotypic variance,  $\sigma_e^2$  = environmental variance, H<sub>bs</sub> = broad sense heritability

**Table 5.** Correlation among some soybean agronomical characters

	DTM	HIG	BRC	NOD	POD	W100	YLD
DTF	0.225	0.035	-0.048	0.148	-0.198	0.140	-0.550*
DTM		0.147	-0.176	0.283	0.239	-0.361	-0.392
HIG			0.076	0.140	0.217	-0.281	0.089
BRC				0.832**	0.716**	-0.338	0.426
NOD					0.659*	-0.556*	0.146
POD						-0.595*	0.538
W100							-0.333

Note: \*\*significant at level of 1%, \* significant at level of 5%, DTF = days to flowering, DTM = days to maturity, HIG = plant height, BRC = number of branches plant<sup>-1</sup>, POD = number of filled pods plant<sup>-1</sup>, NOD = number of reproductive nodes plant<sup>-1</sup>, YLD = grain yield t ha<sup>-1</sup>

The values of phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) (Table 3). Some authors also reported similar results (Baraskar et al. 2014; Dilnesaw et al., 2013; Eka and Lal 2016; Sudhanshu et al. 2015; Yadav et al. 2015). There were four characters that had farther values between these two estimates, i.e. plant height, the number of branches plant<sup>-1</sup>, the number of reproductive nodes plant<sup>-1</sup> and grain yield. Closer values between PCV and GCV were shown by characters of days to flowering and days to maturity, the number of filled pods plant<sup>-1</sup>, and weight of 100 grains. The slight differences suggest that these characters were relatively less influenced by the environment and per se (Dilnesaw et al. 2013). The slight differences indicating the presence of wider adaptability for these traits suggest the less influence of environment in characters expression (Reni and Rao 2013) and the greater role in these traits expression (Eka and Lal 2016; Nidhi et al 2015).

Heritability is the ratio of genetic variance to phenotypic variance. The highest heritability was shown by days to flowering, the number of filled pods, days to maturity and weight of 100 grains, i.e. 0.786, 0.732, 0.691 and 0.642 respectively. Similar results are reported by Kuswanto et al. (2006), Kuswanto (2012) and Ojo and Ayuba (2016), in which the number of filled pods and days to maturity have high heritability. However, the heritability of weight of 100 grains varied from low (Alt et al. 2002), moderate (Kuswanto et al. 2006) and high (Aidya et al. 2011; Ekka and Lal 2016; Kuswanto 2012; 2013; Reni and Rao 2013) depending on the difference in the genotype, environments and measurement methods. Moderate heritability was shown by the number of branches plant<sup>-1</sup> and number of reproductive nodes plant<sup>-1</sup> (Table 4). Reni and Rao (2013) reported high heritability on the character of the number of branches plant<sup>-1</sup>. Heritability of plant height in this study was low, while some authors reported as high (Malek et al. 2014; Reni and Rao 2013; Yadav et al. 2015). Grain yield is a character supported by other characters, especially number of pods and weight of 100 grains. In this study, low heritability was shown by grain yield, although the primary components of the number of pods and weight of 100 grains had high heritability (Table 4). This may be due to the different number of grains plant<sup>-1</sup>. In this study, the number of seed plant<sup>-1</sup> reflecting the number of grains per pod was not observed.

Heritability determines the progress of the selection and selection methods that will be used in the developing of variety. In this study high heritability values was shown by days to flowering, days to maturity, plant height, and weight of 100 grains. These four characters will have high selection response. On the other hand, the number of branches plant<sup>-1</sup> and the number of reproductive nodes plant<sup>-1</sup> will lead moderate selection response due to the moderate heritability. Similarly, the number of branches plant<sup>-1</sup> and seed yield plant<sup>-1</sup> that had low heritability will lead low selection response.

Correlation among characters is important in plant breeding program because it can predict the improvement a

character through other characters. The number of branches plant<sup>-1</sup> (BRC) had a significant correlation with the number of reproductive nodes plant<sup>-1</sup> (NOD) and the number of filled pods plant<sup>-1</sup> (POD) (Table 5). Kuswanto et al (2014b) reported a significant correlation between these two characters with the number of branches plant<sup>-1</sup> in acid soil and optimal condition. It reflects that higher number of branches plant<sup>-1</sup> lead higher number of reproductive nodes plant<sup>-1</sup> and number of filled pods plant<sup>-1</sup>. Soybean nodes are located on primary stem and branches. In this study, reproductive nodes on the primary stem were included in the calculation. Therefore, the correlation confirms that the most reproductive nodes were located on the branches.

Reproductive node is a node in soybean plant that have one or more pods. Reproductive node can be found both in primary stem and branches. The number of reproductive nodes plant<sup>-1</sup> had positive correlation with the number of filled pods plant<sup>-1</sup> (Table 5). It meant that many reproductive nodes plant<sup>-1</sup> increased number of filled pods plant<sup>-1</sup>. Kuswanto et al. (2014b) revealed that the correlation is consistent in acid soil and optimal land condition.

Significant correlation between the number of branches plant<sup>-1</sup> and number of filled pods plant<sup>-1</sup> may be due to the pods were located on the branches. Iqbal et al. (2010) also reported similar result in the optimal land condition. The branches that can develop optimally lead increasing number of filled pods plant<sup>-1</sup>. Besides, this relationship may also be due to the indirect effect from the branches through reproductive nodes producing the number of filled pods.

The weight of 100 grains reflects grain size. The relationship between the weight of 100 grains (W100) with the number of nodes plant<sup>-1</sup> and number of filled pods plant<sup>-1</sup> showed negative value (Table 5). This relationship suggests that larger grain size would cause lower number of nodes plant<sup>-1</sup> and number of filled pods plant<sup>-1</sup>; and vice versa. This phenomenon may be due to the low availability of nutrients in the soil with low pH (Kuswanto 2014) causing small materials availability to be processed as assimilates. Essential nutrients are also suppressed when entering the plant (Bose et al. 2011). A Higher number of filled pods plant<sup>-1</sup> leads smaller grain size because the limited materials availability has to be shared to many pods. Therefore, the pod is not filled by grains completely causing small grain size. However, Iqbal et al (2010) reported no relationship between the weight of 100 grains with the number of filled pods plant<sup>-1</sup>.

Yield, the complex character, is supported by other agronomical characters (Athoni and Basavaraja 2012; Egli 2013; El-Badawy and Mehasen 2012; Koladiya et al. 2012; Malik et al. 2011). However, among the observed characters in this study, there was only one character that had a significant negative correlation to grain yield (YLD), i.e. days to flowering (DTF) (Table 5). Negative correlation between these two characters is also reported by Kuswanto and Zen (2013). The negative value of this correlation indicates that longer days to flowering causes lower grain yield. Days to flowering is a phase from seedling establishment to flowering. In a plant with late

flowering or longer days to flowering, the duration of days to maturity is shorter. It means that the increasing vegetative phase is shortening reproductive phase. The metabolic processes in reproductive phase are directed to produce grains. The short duration in producing grain leads little grain size or a small number of grains. Finally, grain yield is low due to the short reproductive that is limited by the longer days to flowering phase.

To summarize, crossing of Tanggamus  $\times$  Anjasmoro produced selected offspring with broad genetic variability on characters of days to flowering, the number of branches plant<sup>-1</sup>, the number of reproductive nodes plant<sup>-1</sup>, the weight of grains and grain yield per hectare. On the other hand, narrow genetic variability was found on characters of days to maturity, plant height and the number of filled pods plant<sup>-1</sup>. High broad sense heritability were found on the characters of days to flowering, days to maturity, the number of filled pods plant<sup>-1</sup> and the weight of 100 grains, middle broad sense heritability were found on the character number of branches and the number of reproductive nodes plant<sup>-1</sup> is classified, whereas low broad sense heritability were found on characters of plant height and grain yield per hectare. Significant correlation among some agronomical characters can be used to improve a targeted character. Development new superior variety should consider early days to flowering due to the negative value of the correlation between days to flowering and grain yield.

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