



# Genetic Parameters Estimation of High Yielding and Large Seed Size of Soybean [*Glycine max* (L.) Merrill] Genotypes

Gatut Wahyu Anggoro Susanto<sup>1</sup>, Didik Harnowo<sup>1</sup>, Rudy Soehendi<sup>1</sup>, Yusmani Prayogo<sup>1</sup>, Purwantoro<sup>1</sup>, Made Jana Mejaya<sup>1</sup>, Anna Satyana Karyawati<sup>2</sup>

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## ABSTRACT

**Background:** Seed yield and seed size are agronomic traits needed by farmers and consumers. The objective of the study was to assess the potential yield and seed size of soybean promising lines.

**Methods:** The field trials were conducted in two locations (Malang and Ngawi), East Java, Indonesia during dry season of 2018. Thirty soybean lines and two check cultivars (Anjasmore and Dega 1) were set in a randomized completely block design, replicated three times.

**Result:** The study showed that there were differences in genotypic variance of soybean between Ngawi and Malang locations on plant height, filled pods number/plant, maturity days and seed weight/plant. Maturity days and 100 seeds weight showed similar heritability values in both locations. In Malang, the value of expected genetic advance was less than that in Ngawi, suggested that Ngawi is better location for soybean selection for high yield potential and large seed size (100- seed weight). The soybean lines G 5 (Anjasmore × MD6)-11 and G 21 (Grob × Argopuro) × (Pangrango)-41-10 have the highest seed yield of 3.03 and 3.07 t/ha, respectively, which is significantly higher than the check variety Anjasmore (2.30 t/ha). G 21 also has larger 100-seed weight than the check variety Anjasmore.

**Key words:** Genetic parameters, Genotype, High yield, Seed size, Soybean.

## INTRODUCTION

In Indonesia, the soybean [*Glycine max* (L.) Merrill] seed yield and seed size are two important agronomic traits needed by farmers. Therefore, genetic improvement through breeding activity to derive the intended lines or cultivars is necessary. Plant breeders need to identify the genetic diversity in soybean to select genotypes with high productivity supported by desirable yield components. The availability of desirable source genes and breeding method used highly determine the success of a soybean variety development for high productivity. To broaden the genetic base of soybean cultivars, it is necessary to exploit the availability of germplasm lines based on the mean performance having excellent source of genetic variability (Kumar *et al.* 2020).

The success of a variety development is influenced by the genetic parameters of certain trait of the genotype. The genetic parameters include genotypic and phenotypic variances, heritability and genetic advance. Heritability is one of the important genetic parameters that is used to predict the progress of the selection in the breeding activity of a certain character. Based on the value of the heritability, a certain character could be controlled by genetic factors or influenced by environmental factors. Broad sense heritability is the proportion of genotypic variance ( $\sigma_g^2$ ) to phenotypic variance ( $\sigma_p^2$ ). The genotypic variance is a variance total of dominance ( $\sigma_D^2$ ), additive ( $\sigma_A^2$ ) and epistatic ( $\sigma_I^2$ ). The combination of the high heritability and high genetic advance provides the degree of selection progress

<sup>1</sup>Research Center for Food Crops, Research Organization for Agriculture and Food, National Research and Innovation Agency (BRIN), Jalan Raya Jakarta-Bogor KM. 46, Bogor, West Java, Indonesia, 16911.

<sup>2</sup>Agriculture Faculty, Brawijaya University, Malang, East Java, Indonesia.

**Corresponding Author:** Made Jana Mejaya, Research Center for Food Crops, Research Organization for Agriculture and Food, National Research and Innovation Agency (BRIN), Jalan Raya Jakarta-Bogor KM. 46, Bogor, West Java, Indonesia, 16911. Email: mmejaya@yahoo.com

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for crop improvement programme (Jain *et al.* 2018; Sulisty and Mejaya, 2018).

The improvement of seed size of existing varieties together with other superior varieties having large seed size is necessary. Some genetic criteria were estimated for agronomic traits that enable to obtain the effective improvement of the soybean genotypes. The objective of this study was to estimate the genetic advance of soybean genotypes to obtain the new large-seeded and high yielding varieties.

## MATERIALS AND METHODS

### Experimental site

The trials were conducted in two locations in East Java Province, Indonesia, *i.e.* at Jambegede, Malang (-8°10'22" S; 112°33'40"E; 305 m asl) and Ngale, Ngawi (-7°24'56" S; 111°22'11"; 56 m asl) Experimental Farms during the 1<sup>st</sup> dry season (1<sup>st</sup> DS) 2018.

Thirty soybean homozygous lines and two national check cultivars (Anjasmoro and Dega 1 which were released in 2001 and 2016, respectively) were arranged in a randomized completely block design, with three replication (Table 1). Each genotype was planted in a plot of 5.6 m<sup>2</sup>.

The soybean in two locations was planted after rice, manual planting with spacing of 40 cm inter-row and 15 cm within row, two plants/hill. Fertilizer at the rate of 100 kg ha<sup>-1</sup> SP36 (36% P2O5), 250 kg/ha of Phonska (15-15-15) and 1.5 t/ha manure were applied to each trial. The fertilizers were applied at planting time in a line of 5 cm from the planting rows and the manure was used as planting hole cover.

### Measurements on agronomic characteristics

Measurements on 10 random sample plants were taken on plant height, main branches number, fertile nodes number, filled pod number, seed weight/plot. Seed weight/plot, flowering and maturity days and 100 seed weight were observed on plot basis. The seed weight/plot (5.6 m<sup>2</sup>) was converted to t/ha using formula (1) and then converted to seed yield at 12% moisture content using formula (2). Potential yield was calculated based on seed weight of 10 plants which was converted to t/ha on the assumption full plant stand.

$$Y = (10/A) \times X \quad \text{.....(1)}$$

Where

Y= Seed yield (t ha<sup>-1</sup>).

A= Plot area (m<sup>2</sup>).

X= Seed yield in harvested plot (kg).

$$Y_{12} = [(100 - W_i) / 88] \times Y \quad \text{.....(2)}$$

Where

Y<sub>12</sub>= Seed yield at 12% moisture content (t ha<sup>-1</sup>).

W<sub>i</sub>= Initial seed moisture content (%).

Y= Seed yield calculated using formula (1).

### Analysis of variance

Estimation of variance components (genotypic variance, phenotypic variance and environmental variance) were calculated from the analysis of variance as described by Hallauer and Miranda (2010). Genotypic and phenotypic variance was calculated based on the following equation:

$$\sigma^2_g = (MS_g - MSe) / r$$

$$\sigma^2_p = (\sigma^2_g + MSe)$$

Broad sense heritability values (h<sup>2</sup>) are classified as low criteria if the h<sup>2</sup> value is < 0.2, moderate criteria if 0.2 ≤

h<sup>2</sup> ≤ 0.5 and high criteria if h<sup>2</sup> > 0.5. Determination of heritability values using the following equation:

$$h^2 = \sigma^2_g / \sigma^2_p$$

The determination of the value of the expected genetic advance was calculated using the following equation:

$$KGH = i \times h^2 \times \sigma_p$$

## RESULTS AND DISCUSSION

Combined variance analyses over the two locations showed the significant interaction on flowering days, maturity days, number of filled pods and 100 seed weights (Table 2). The existence of G × E interaction results in the response of the genotypes to environments (Morsy *et al.*, 2016).

### Heritability

There were differences in genotypic variance of soybean between Ngawi and Malang locations, especially in plant height, filled pods number /plant, maturity time and seed weight/ plant (Table 3). The genotypic variance for plant height in Ngawi (83.61) is higher than that in Malang (6.95). The same case occur on filled pods number /plant, maturity time and seed weight/ plant. The phenotypic variance for plant height in Ngawi (103.79) is higher than that in Malang (26.61). The same case occur on filled pods number /plant, maturity time and seed weight/ plant.

The phenotypic variances was found higher than the genotypic variances for all characters in both locations indicate the significant effect or important role of environment in the expression of the characters. In Ngawi, the phenotypic variance for plant height (103.79) is higher than the genotypic variance (83.61). In Malang, the phenotypic variance for plant height (26.61) is higher than the genotypic variance (6.95) (Table 3).

The heritability estimation values in Ngawi ranged from 0.31 (seed weight/ plant) to 0.81 (plant height) (Table 3). In Malang, the heritability ranged from 0.09 (seed weight/ plant) to 0.61 (100-seeds weight). Two traits (maturity days and 100 seeds weight) consistently showed similar heritability values in both locations.

The closer differences between estimates values of phenotypic variances and genotypic variances, for certain traits (100-seeds weight) indicate that expression of this characters under study was less influenced by environmental factors. The high values of phenotypic variances and genotypic variances indicate the presence of sufficient genetic variability for selection of the traits (Baraskar *et al.* 2014). Narrow differences between phenotypic variances and genotypic variances of the characters revealed that less environmental influence on the expression of the characters (Malek *et al.* 2014).

The phenotypic variances was found higher than genotypic variances which indicates the significant effect or important role of environment in the expression of the characters (Kuswantoro *et al.* 2018). The high genotypic and phenotypic variances were exhibited by the seed

weight and plant height (Jain *et al.*, 2015; Jandong *et al.*, 2020). High heritability with high genetic advance for seed yield/plant, number of pods/plant and 100-seed weight was observed by Kumar *et al.* (2020) which indicated the predominance of additive gene action in controlling these traits.

#### Expected genetic advance

Table 4 shows that soybean genotypes evaluated in Ngawi produced higher seed yield (2.59 t/ha) compared to that in Malang (1.98 t/ha). This was supported by a higher filled pod number/plant and larger 100-seed weight and seed weight/plant compared to the same traits measured in Ngawi. The difference in elevation and daytime temperature between the two sites could be responsible to the difference in maturity days. Elevation in Malang site is higher than in Ngawi site and temperature in Malang site during the daytime is 1-3°C lower than that in Ngawi.

In selection intensity of 20%, the value of expected genetic advance in Ngawi varies from 0.78% (filled pod number/plant) to 27.22% (branches number/plant) (Table 4). In Malang, the value of expected genetic advance varies from 0.70% (filled pod number/plant) to 15.34% (plant height). In Ngawi, other agronomic traits that have a genetic advance above 10% are maturity days, fertile node number/plant, 100 seed weight/plant and seed yield. In Malang, there was no other agronomic trait that have a genetic advance above 10%.

The highest genetic advance value of branches number/plant and plant height could be used as soybean selection criteria in Ngawi and Malang locations, respectively. The 100 seed weight had high both heritability and fertile node number/plant with genetic advance values in Ngawi suggested that this trait could be used as soybean selection criteria in Ngawi condition. The varied responses on

**Table 1:** Pedigree of 30 soybean genotypes having high yield potential and large seed size (>14 g/100 biji).

Genotypes	Pedigree
AMMD 1	(Anjasmoro × MD6)-19
UB2AM 1	(UB 2 × Anjasmoro 500)-16
AMMD 2	(Anjasmoro × MD6)-21
AMMD 3	(Anjasmoro × MD6)-23
AMMD 4	(Anjasmoro × MD6)-11
UB2AM 2	(UB 2 × Anjasmoro 1000)-10
UB4AM 1	(UB 4 × Anjasmoro 1000)-4
IACB 1	(IAC-100 × Kaba-G-67) × (Burr)-282
IACBKAP 1	(IAC-100 × Burangrang) × (Kaba × Argopuro) -25
IACBKA 2	(IAC-100 × Burangrang) × (Kaba × Argopuro)-27
GIAC 1	(Grobogan) × (IAC-100 × Tanggamus)-5
IACKGIACBK 1	(IAC-100 × Kaba-G-67) × (Gro × IAC-100 × Burr × Kaba) -1-76
GLJS 1	((Grobogan × LJ) × Sinabung)-13
APG 1	(Argopuro × Gcp)-1
IACKGIACBK 2	(IAC-100 × Kaba-G-67) × (Grobogan × IAC-100 × Burr × Kaba)-1-91
IACBKAP 3	(IAC100 × Burangrang × Kaba) × (Grobogan)-220-14
SLJ 1	(Sibayak × Lokal Jateng)-5-61-5-127
LJSA 1	(LJ × Sinabung)-13 × (Anjasmoro)
IACKGIACBK 2	(IAC-100 × Kaba-G-47) × (Gro × IAC-100 × Burr × Kaba)-13-247
GIAC 2	(Grobogan × IAC-100) × (Tanggamus)-7
GAP 1	(Grobogan × Argopuro) × (Pangrango)-41-10
IACKGIACBK 3	(IAC-100 × Kaba-G-67) × (Grobogan × IAC-100 × Burr × Kaba) -1-30
GAP 2	(Grobogan × Argopuro) × (Pangrango)-41-11
IACBGIACBK 1	(IAC-100 × Burr-P-94) × (Grobogan × IAC-100 × Burr × Kaba)-13-841
IACBGIACBK 2	(IAC-100 × Kaba-G-47) × (Grobogan × IAC-100 × Burr × Kaba)-13-859
GP 1	(Grobogan × Panderman)-35
IACBGIACBK 3	(IAC-100 × Kaba-G-47) × (Grobogan × IAC-100 × Burr × Kaba)-13-241
GS 1	(Grobogan × Sinabung)-1036-114
BA 1	(Brawijaya × Argomulyo)-7
BAP 1	(Brawijaya × Argopuro)-8
Dega 1*	Grobogan × Malabar
Anjasmoro*	Mansuria-395-49-4

\*check varieties.

vegetative and generative periods determine the seed yield which are attributed to pod number, seed number per pod and seed size (Hu and Wiatrak, 2012).

High heritability and genetic advance of a character indicates additive genes in controlling the character by inheriting the genetic factor from parent to offspring. Combination of genetic variability, high heritability and genetic advance could be effective on selection based on phenotype traits (Singh *et al.* 2020; Baraskar *et al.* 2014; Osekita and Olorunfemi 2014). The number of filled pods, plant height and 100 seed weight were also considered an effective trait as a direct selection criteria to obtain high seed yield and large seed size in soybean breeding (Ghodrati

2013; Malek *et al.* 2014; Sulistyo *et al.*, 2021; Mejaya *et al.*, 2022; Putri *et al.*, 2022;).

#### The selected lines

The seed weight/plant can be used as an indicator of yield potential of a certain genotype. Potential seed yield of 32 soybean genotypes tested ranged from 1.73 to 3.48 t/ha in Ngawi and 4.82 t/ha and from 1.25 to 2.93 t/ha in Malang with average of two locations ranged from 1.96 to 3.06 t/ha (Table 5).

Average of two locations, 12 out of 30 soybean lines showed higher seed yield than the check variety Anjasmoro, by which 6 lines showed higher 100-seed weight than the

**Table 2:** Variance analysis of seed yield and other agronomic traits of 30 soybean genotypes in two locations.

Characters	P-value of variance analysis			Coefficient of variation (%)
	Genotype (G)	Location (L)	G × L	
Flowering days 50% (days)	<.0001	<.0001	0.0086	2.95
Maturity days 95% (days)	<.0001	<.0001	<.0001	2.90
Plant height (cm)	<.0001	<.0001	0.9500	18.38
Number of branches per plant	0.0193	<.0001	0.2375	28.00
Number of fertile nodes per plant	0.8201	<.0001	0.8151	20.49
Number of filled pods per plant	0.0006	0.0213	0.0390	20.40
100 seed weight (g)	<.0001	<.0001	<.0001	9.58
Seed weight per plant (g)	0.0069	<.0001	0.0377	22.48
Seed yield (t/ha)	0.0024	<.0001	<.0001	19.04

**Table 3:** Genotypic and phenotypic variances of nine agronomic traits of 30 soybean genotypes in two locations.

Agronomic traits	$\sigma^2g^*$		$\sigma^2p^*$		Heritability*	
	Ngawi	Malang	Ngawi	Malang	Ngawi	Malang
Flowering time (days)	1.81	0.98	2.88	1.95	0.63	0.50
Maturity time (days)	8.69	1.44	17.40	3.06	0.50	0.47
100-seed weight (g)	3.83	4.25	6.10	6.92	0.63	0.61
Plant height (cm)	83.61	6.95	103.79	26.61	0.81	0.42
Branches number/plant	0.29	0.07	0.80	0.84	0.36	0.08
Fertile node number/plant	0.60	1.42	1.17	8.00	0.51	0.18
Filled pod number /plant	31.19	1.65	79.02	43.25	0.39	0.51
Seed weight/ plant (g)	3.24	0.35	10.40	4.01	0.31	0.09
Seed yield (t/ha)	0.11	0.08	0.26	0.31	0.42	0.26

**Table 4:** Mean, selection response and genetic advance of agronomic traits of 30 soybean genotypes in two locations.

Agronomic traits	Mean in location		Selection response		Genetic advance (%)	
	Ngawi	Malang	Ngawi	Malang	Ngawi	Malang
Flowering time (days)	34.71	33.92	1.49	0.98	4.30	2.89
Maturity time (days)	79.75	77.20	0.31	0.19	12.16	9.72
100-seed weight (g)	18.05	14.75	2.92	1.15	3.66	1.49
Plant height (cm)	42.21	48.79	2.17	2.26	12.01	15.34
Branches number/plant	3.31	2.71	11.49	0.87	27.22	1.77
Fertile node number/plant	8.50	13.31	0.45	0.11	13.70	3.93
Filled pod number/plant	34.52	32.23	0.51	0.18	0.78	0.70
Seed weight/ plant (g)	12.54	8.81	4.91	0.35	14.23	1.09
Seed yield (t/ha)	2.59	1.98	1.41	0.25	11.24	2.79

**Table 5:** The minimum, maximum and mean values of 30 soybean genotypes in two locations.

Agronomic traits	Ngawi		Malang		Average	
	Mini-mum	Maxi-mum	Mini-mum	Maxi-mum	Mini-mum	Maxi-mum
Flowering time (days)	31.0	36.0	32.0	36.0	32.0	36.0
Maturity time (days)	76.0	85.0	74.0	79.0	76.0	85.0
100 seed weight (g)	13.9	21.8	10.6	18.8	12.9	20.5
Plant height (cm)	22.7	56.3	33.7	80.7	28.2	65.7
Branches number/plant	2.0	5.0	2.0	4.0	2.0	4.0
Fertile node number/ plant	7.0	10.0	11.0	17.0	10.0	13.0
Filled pod number /plant	22.0	46.0	25.0	41.0	25.0	39.5
Seed weight/plant (g)	5.8	17.5	6.8	11.2	8.0	13.6
Seed yield (t/ha)	1.73	3.48	1.25	2.93	1.96	3.07

**Table 6:** The selected soybean genotypes based on seed yield (t/ha) and 100-seed weight (g) average of two locations.

Genotypes code	Pedigree	100-seed weight (g) <sup>a</sup>	Seed yield (t/ha) <sup>a</sup>
G 1	(Anjasmoro × MD6)-19	15.48 ns	2.31 ns
G 5	(Anjasmoro × MD6)-11	14.72 ns	3.07*
G 6	(UB 2 × Anjas 1000)-10	15.35 ns	2.55 ns
G 10	(IAC-100 × Burangrang) × (Kaba × Argopuro)-27	18.35*	2.46 ns
G 13	(Grob × LJ) × Sinabung)-13	19.22*	2.51 ns
G 16	(IAC100 × Burangrang × Kaba) × (Grobogan)-220-14	18.88*	2.32 ns
G 19	(IAC-100 × Kaba-G-47) × (Gro × IAC-100 × Burr × Kaba)-13-247	16.73 ns	2.45 ns
G 21	(Grob × Argopuro) × (Pangrango)-41-10	17.48*	3.03*
G 27	(IAC-100 × Kaba-G-47) × (Gro × IAC-100 × Burr × Kaba)-13-241	14.68 ns	2.31 ns
G 28	(Grobogan × Sinabung)-1036-114	16.73 ns	2.44 ns
G 29	(Brawijaya × Argomulyo)-7	14.27 ns	2.50 ns
G 31	Dega 1 (check variety)	16.15	2.25
G 32	Anjasmoro (check variety)	15.62	2.30
LSD (5%)		1.79	0.49

<sup>a</sup>ns= Non-significant; \* = Significant (at 0.05) compared to the Anjasmoro check variety.

check variety Dega 1. The soybean lines G 5 (Anjasmoro × MD6)-11 and G 21 (Grob × Argopuro) × (Pangrango)-41-10 showed the highest seed yield of 3.03 and 3.07 t/ha, respectively, which are significantly higher than the Anjasmoro (2.30 t/ha) (Table 6).

## CONCLUSION

The maturity time and 100 seeds weight traits have similar heritability values in both Ngawi and Malang locations. In Malang, the value of expected genetic advance was less than that in Ngawi, suggested that Ngawi is better location for soybean selection for high yield potensial and large seed size (100-seed weight). The soybean lines G 5 (Anjasmoro × MD6)-11 and G 21 (Grob × Argopuro) × (Pangrango)-41-10 have the highest seed yield of 3.03 and 3.07 t/ha, respectively, which is significantly higher than the check variety Anjasmoro (2.30 t/ha). G 21 also has larger 100-seed weight than the check variety Anjasmoro.

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