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## GENETIC DIVERSITY, HERITABILITY, AND GENETIC GAIN IN BLACK SOYBEAN (*GLYCINE SOJA L. MERRILL*) IN WEST JAVA, INDONESIA

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### SUMMARY

Genetic diversity and genetic gain are valuable parameters in plant breeding for assembling new cultivars. The presented study sought to identify the genetic diversity of the black soybean (*Glycine soja* L. Merrill) populations from crossbreeding and identify the broad sense heritability and genetic gain in yield-related traits. The set experiments proceeded in a randomized complete block design with three replications at two different environments/locations—Indramayu and Majalengka, Indonesia. The genetic material comprises 19 black soybean genotypes. The results showed that the genetic diversity in black soybean genotypes for grain yield and its attributes were broad, based on the principal component analysis, with a cumulative value of 80.55%. The environment greatly influenced heritability and genetic gains. High heritability and genetic gain were notable for seed length in the Majalengka location. In the Indramayu location, the demonstration of high heritability and genetic gains appeared for the number of fertile nodes and seed length. This information can serve as a basis for plant breeders to develop black soybean high-yielding cultivars in the future.

**Keywords:** Black soybean (*Glycine soja* L. Merrill), heritability, genetic gain, principal component analysis, yield related traits

**Key findings:** Information on genetic diversity, heritability, and genetic gain in yield-related traits is necessary to develop cultivars in crop plants. In black soybean populations, the genetic diversity for planting at two locations based on the principal component analysis was 80.55%. Heritability and genetic gain values among the populations for traits in two locations showed moderate to high values. This information can be beneficial in further selection to develop black soybean high-yielding cultivars.

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## INTRODUCTION

Black soybean is one of the potential agricultural commodities and is highly strategic for further development in Indonesia. In addition to food ingredients, black soybeans can serve as ingredients in pharmacy and functional foods. In contrast to other legumes, black soybean contains a higher content of saponins, anthocyanins, and isoflavones (Sumardi *et al.*, 2017; Lee *et al.*, 2023) and protein (He and Chen, 2013; Chatterjee *et al.*, 2018). Based on the contents, black soybeans are beneficial for people's health.

Genetic diversity is a vital genetic parameter in plant breeding programs. Genetic diversity may occur in individuals, populations, and species (Mukhopadhyay and Bhattacharjee, 2016). For the development and maintenance of genetic diversity, the black soybean collection and evaluation can proceed through a systematic plant breeding program. The information about genetic diversity, heritability, genetic gain, and genotype by environment interactions (GEIs) (Ruswandi *et al.*, 2016; Amien *et al.*, 2021) play an essential role in improving black soybeans (Wijaya *et al.*, 2022; Susanto *et al.*, 2023). Genetic diversity informs plant breeders how much diversity of plant-breeding lines can serve as germplasm in the next breeding program (Maulana *et al.*, 2023). The diversity that occurs can result from influences by the genetic makeup of genotypes, environments, and their interactions. These three factors require analysis through a quantitative genetic approach (Amien *et al.*, 2021). Genetic parameters estimation aims to provide basic information to improve the expected traits through selection (Insan *et al.*, 2016).

Selection for promising genotypes with desirable traits is one of the crucial stages in plant breeding programs. Soybeans are sensitive to environmental variations; therefore, the selection process must continue carefully. The reason is soybeans are vastly delicate to changes in the growing environment, and each character has a very close correlation relationship; thus, the selection process becomes more complex (Maranna *et al.*, 2021). Leite *et al.* (2018)

reported that yield components and environmental factors intensely influenced soybean grain yield. In addition, grain yield also bore effects from GEI (Wijaya *et al.*, 2022; Susanto *et al.*, 2023). Several researchers have also succeeded in making selection based on yield and other traits, including wheat (Nuraeni *et al.*, 2021), sweet potatoes (Karuniawan *et al.*, 2021; Maulana *et al.*, 2022), maize (Ruswandi *et al.*, 2016; Wicaksana *et al.*, 2022; Maulana *et al.*, 2023), Stevia (Amien *et al.*, 2021, 2022), butterfly pea (Filio *et al.*, 2023), and turmeric (Aulia *et al.*, 2022). Selection based on multi-traits allows the researchers and farming community to use superior genotypes for several traits.

Genetic parameters, diversity, heritability, and genetic gain are valuable tools for developing superior cultivars. A high heritability value for a character indicates the dominance of additive genes (Annicchiarico *et al.*, 2010). Conversely, if the heritability and genetic gain are low, then environmental influences will be higher than the additive gene effects in various crop plants (Atnaf *et al.*, 2017; Diniz and de-Oliveira, 2019; Amien *et al.*, 2021; Maulana *et al.*, 2023). The results on genetic parameters in soybeans have many reports. So far, genetic diversity, heritability, and genetic gain have undergone extensive analysis across generations.

Segregating populations (F3, F4, and F5 generations) used through bulk methods, can enhance the genetic gain in soybean seed yields (Charnai *et al.*, 2014; Silva *et al.*, 2018). Azevedo *et al.* (2021) reported that high genetic diversity among the tested populations indicates high heritability. However, the assessment of genetic parameters can also transpire through GEIs (Amien *et al.*, 2021; Maulana *et al.*, 2023). It allows breeders to assess genetic diversity, heritability, and genetic gain under diverse environments. The presented study sought to determine the genetic diversity, heritability, and genetic gain of black soybean lines planted in two different environments (locations). The results will help estimate the genetic parameters for economic traits and serve as information to develop high-yielding black soybean cultivars.

## MATERIALS AND METHODS

### Plant genetic material and study Location

Soybean field trials commenced at two locations, namely, Majalengka and Indramayu Regencies, West Java, Indonesia (180 and 54 meters above sea level, respectively). The experiments ran from March to October 2021. Soil acidity at both criteria locations is slightly acidic. At the Majalengka location, the total N content is low, P is medium, and K is low, while at the Indramayu location, the total N is moderate, P is low, and K is very high. Climatic conditions at the Majalengka location comprised rainfall of 70-250 mm/month, an average temperature of 27 °C, and humidity of 78% to 82%. In Indramayu, rainfall is 100 to 380 mm/month, average temperature is 26 °C to 28 °C, and humidity is 78% to 86%.

The study used genetic materials comprising 19 black soybean genotypes, including 17 lines and two check cultivars (Table 1). The 19 black soybean genotypes used in this research were from a selection from previous research. Selection progressed on the characteristics of seed weight per plot and weight of 100 grains. The 19 genotypes are sixth-generation black soybean genotypes.

### Field design

The field experiments at both locations continued in a randomized complete block design (RCBD) with three replications. Seventeen black soybean lines (resulting from crosses) and two check cultivars served as treatments. The size of the experimental subplot was 4 m × 5 m. The distance among subplots is 50 cm, spacing is 40 cm × 15 cm, and the total plant population of each genotype in a subplot was 330 plants.

Among all black soybean genotypes, the recorded data were on various characteristics, i.e., plant height (cm), number of branches, fertile nodes, pod contents, empty pods, and seeds, seed weight per plant (g), 100-seed weight (g), seed diameter (mm), seed length (mm), and grain yield per plot (kg).

### Data analysis

Analysis of field observation data continued for homogeneity. Data homogeneity test using Quantile-Quantile Plot (QQ plot) followed the Kolmogorov-Smirnov statistical test (Kolmogorov, 1934; Smirnov, 1991):

$$Z \text{ score} = \frac{x - \bar{x}}{\sigma} \quad (1)$$

Where:  $\bar{x}$  = Population mean,  $\sigma$  = standard deviation

$$\sigma = \sqrt{\frac{\sum(x_i - \bar{x})^2}{n-1}} \quad (2)$$

Where:  $x_i$  = data -  $i$ ;  $\bar{x}$  = means;  $n$  = number of data

If the homogeneity analysis results show the homogeneous values, then the analysis progresses using combined ANOVA. The combined ANOVA analysis follows according to the method of Bianchi *et al.* (2020):

$$y_{ijkl} = \mu + p_i + r_{j(l)} + b_{k(jl)} + a_l + (ta)_{il} + e_{ijkl} \quad (3)$$

Where:

$y_{ijkl}$  = observation concerning progeny  $i$  in replicate  $j$  in block  $k$  in environment  $l$ ;

$\mu$  = general constant associated with all observations;

$p_i$  = random effect of progeny  $i$ ;

$r_{j(l)}$  = random effect of the replicate  $j$  within the environment  $l$ ;

$b_{k(jl)}$  = random effect of block  $k$  within the replicate  $j$  in the environment  $l$ ;

$a_l$  = fixed effect of the environment  $l$ ;

$(ta)_{il}$  = random effect of interaction progenies  $\times$  environments;

$e_{ijkl}$  = random experimental error associated with observation  $y_{ijkl}$

**Table 1.** The black soybean lines and check cultivars used in field trials.

No.	Genotypes	Pedigree	S.No.	Genotypes	Pedigree
1.	BS 66	122 x 106 E10 (3)	11.	BS 102	122 x 106 G8 (12)
2.	BS 64	122 x 106 E10 (1)	12.	BS 111	122 x 106 G8 (F4)(5)
3.	BS 69	122 x 106 E10 (6)	13.	BS 114	122 x 106 G8 (F4)(8)
4.	BS 72	122 x 106 B16 (1)	14.	BS 123	122 x 106 E10 (1)(1)
5.	BS 77	122 x 106 B16 (6)	15.	BS 140	106 x 122 A33 (5)
6.	BS 79	122 x 106 B16 (8)	16.	BS 141	106 x 122 A33 (6)
7.	BS 84	106 x 122 E17 (2)(1)	17.	BS 144	122 x 106 G8 (1)
8.	BS 87	106 x 122 E17 (2)(4)	18.	Detam 1	BALITKABI
9.	BS 99	122 x 106 G8 (9)	19.	Mutiara 3	BALITKABI
10.	BS 100	122 x 106 G8 (10)			

Genetic diversity estimation used the Principal Component Analysis (PCA) based on Mooi *et al.* (2018). PCA analysis proceeded using the Excelstat software, with ANOVA analysis performed using the SPSS version 25. Heritability and genetic gain analyses followed the formula of Fehr (1991) below:

$$\sigma_f^2 = \sigma_g^2 + \sigma_e^2 \quad (4)$$

Where:

$\sigma_f^2$  = phenotypic variance;

$\sigma_g^2$  = genotypic variance;

$\sigma_e^2$  = environmental variance;

$$h = \frac{\sigma_g^2}{\sigma_f^2} \quad (5)$$

For the heritability criteria, the findings of Acquaah (2012) were the basis, i.e.,  $h < 0.20$  = low heritability,  $0.20 \leq h \leq 0.50$  = moderate heritability, and  $h > 0.50$  = high heritability.

Genetic gain analysis followed the formula:

$$R = I \times h \quad (6)$$

Where:

R = Response to selection;

i = selection intensity;

h = value heritability.

$$G = \frac{R}{\bar{x}} \times 100 \quad (7)$$

Where:

G = genetic gain and

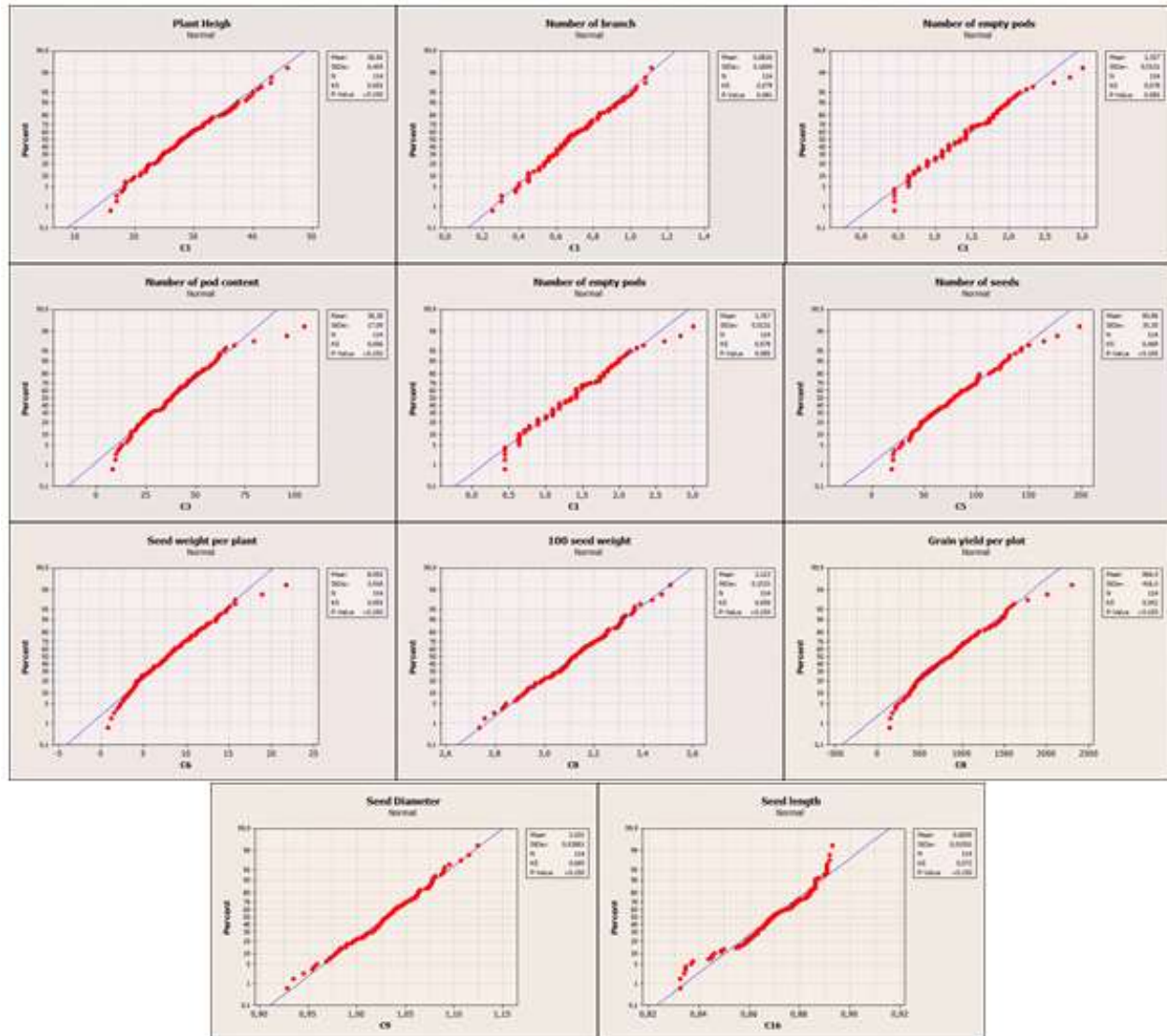
$\bar{x}$  = population mean.

For genetic gain criteria, the study employed the classification of Acquaah (2012), i.e.,  $G > 14\%$  = high,  $7\% \leq G \leq 14\%$  = moderate, and  $G < 7\%$  = low.

Heritability and genetic gains assessment engaged the help of the PBstat online software.

## RESULTS AND DISCUSSION

The homogeneity test is a critical step in statistical analysis to ensure that the data used meets the assumptions of normal distribution. One method to test population normality is the Quantile-Quantile Plot (QQ Plot). QQ Plot is a visual method for testing normality data by comparing data distribution with the expected normal distribution. The test results showed that all the tested traits had a normal distribution, as implied by the  $P$ -value  $> 0.05$  for each trait tested (Figure 1). The QQ Plot graph shows the extent of the data following a diagonal line representing a normal distribution. The QQ plot graph maps the cumulative probability of a variable against that of a specific distribution (Ghasemi and Zahediasl, 2012). Thus, the data used in this research is suitable for testing the analysis of variance (ANOVA).



**Figure 1.** QQ plot for all traits tested.

Genetic  $\times$  environmental interaction analysis progressed to determine its influence on the appearance of a plant genotype. The genetic-environment interaction phenomenon will cause differences in plant appearance if planted in different environments. Table 2 shows the results of combined ANOVA analysis to determine genetic-environment interactions. Based on table 2 shows that the genetic  $\times$  location interaction non-significantly affected all the characters observed. It shows that genetic influence or location influence is more dominant than genetic  $\times$  location interactions

in determining the genetic appearance of black soybean plants. Location remarkably influenced the characteristics of plant height, number of filled pods, number of empty pods, number of seeds, seed weight per plant, weight per plot, seed diameter, and seed length. It implies that these attributes will attain vast influences from the planting location.

Table 6 on environmental data shows that the soil fertility level and other environmental factors, such as temperature, humidity, and rainfall, significantly differed between Majalengka and Indramayu. The

**Table 2.** Combined ANOVA of characters for 19 genotypes in two locations.

Source of Variation	d.f.	Plant height	Number of branches	Number of fertile nodes	Number of pod content	Number of empty pods	Number of seeds	Seed weight per plant	100 seed weight	Grain yield per plot	Seed diameter	Seed length
Location	1	1318.86*	4.89	2.03	8981.23*	97.13*	32742.99*	347.74*	1.37	3666003.74*	13.29*	0.30*
Replication (in Location)	2	6.74	1.31	0.09	226.59	0.85	440.33	10.96	0.52	214427.57	1.01	0.08
Genotype	18	72.43*	4.8	3.78	292.5	2.03	1223.16	15.84	0.88	206566.19	0.5	0.52*
Genotype x Location	18	23.46	10.3	1.8	154.26	1.58	769.21	8.850	1.7	101292.09	0.34	0.14
Error	74	22.38	4.43	2.67	209.58	1.54	963.82	12.46	1.26	134086.84	0.34	0.08
Total	114											

\*: significant at 0.05.; d.f: Degree freedom

**Table 3.** The Eigenvalue and cumulative percentage of all the characters studied.

PCs	Initial Eigenvalues		
	Total	% of Variances	Cumulative %
1	5.80	52,69	52,69
2	2.06	18,69	71,38
3	1.01	9,17	80,55
4	0.76	6,93	87,48
5	0.53	4,81	92,29
6	0.46	4,19	96,48
7	0.19	1,76	98,24
8	0.14	1,32	99,56
9	0.03	0,26	99,82
10	0.01	0,13	99,95
11	0.01	0,05	100,00

PCs = Principal components

reason may be because the heights of the two experimental locations are highly different. The most visible differences are in the parameters of rainfall and altitude. High rainfall will cause soybean plants to suffer due to too much soil water content and disturbed nutrient balance. This condition will cause an abnormal soybean plant appearance, lowering the yield. Yoseph *et al.* (2022) reported similar research results on the seed characteristics of *Vigna radiata*, incurring immense influences from location and genetic interaction between locations. Valencia-Ramírez *et al.* (2022) also reported vast effects of planting location and genetic × location interactions on agronomic traits in soybean plants. The low impact of genetic × location interactions in the appearance of a plant means that selection can continue at one of the test locations with the most profitable value.

### Genetic diversity

In the pertinent study, the genetic diversity estimation of black soybean cross populations and check cultivars used the principal component analysis (PCA). PCA helped to determine the traits that affect the genetic diversity of black soybean genotypes. The PCA method served to identify significantly different variables in the data to facilitate the selection process (Bhartiya *et al.*, 2012; Placide *et al.*, 2015; Barus *et al.*, 2023). According to Jolliffe and Cadima (2016), PCA can simplify complex data by converting several huge variables into small variables called principal components (PCs). Principal components (PCs) have eigenvalues that can explain cumulative factors and variances greater than and or equal to unity. Therefore, determining the number of PCs used progressed by an eigenvalue greater than or equal to unity. The measurement results showed that only three PCs have an eigenvalue higher than the unity, namely, PC1, PC2, and PC3 (Table 3). Therefore, only the initial three PCs can better define the characters affecting diversity.

The PCA values for the 19 black soybean genotypes tested based on grain yield and its component traits were three axes with eigenvalues between 5.80–1.01 and a

cumulative value of 80.55% (Table 3). The first component (PC1) showed a variation of 52.69%, with influential characteristics being plant height, the number of fertile nodes, pods, and seeds, seed weight per plant, 100-seed weight, grain yield per plot, and seed length (Table 4). In the second component (PC2), the variation contribution (18.69%) had influential traits, i.e., the number of branches, empty pods, and seed diameter. The variation contribution in the third component (PC3) was 9.17%, with affective traits including 100-seed weight and seed length. Based on the obtained results, all the tested attributes significantly contributed to genetic variation. These traits became the difference between the tested black soybean genotypes. The character values that affect the genetic diversity of the 19 soybean genotypes are available in Table 4.

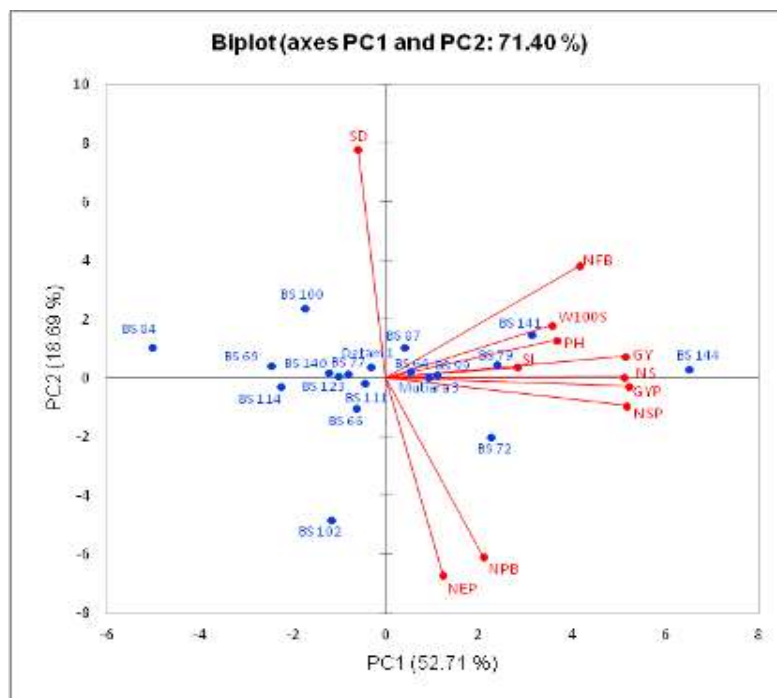
Based on the results, several traits revealed positive and negative contributions (Table 4). Positively contributing characters indicated that these traits added to maximum diversity, while unfavorable contributing variables indicated these parameters supplied minimum genetic diversity (Maulana *et al.*, 2023). In addition, a negative contribution also indicates the trait separates the genotype from the other groups and vice versa (Jolliffe, 2002). Therefore, in PC1, the traits of plant height, number of fertile nodes, number of pod content, number of seeds, seed weight per plant, and seed length provided the maximum contribution to genetic diversity and gathered the black soybean genotypes in the same group. In PC2, the trait seed diameter showed an optimal contribution. In contrast, the qualities of the number of branches and empty pods showed a suboptimal contribution, thus separating the black soybean genotypes into different groups. In PC3, the characteristic that contributed the most was seed length, while 100-seed weight shows even less than optimal contribution.

Visualization of the black soybean genotypes distribution and the traits tested through the PCA graph appear in Figure 2. The results showed the widespread black soybean genotypes evaluated over several groups. Closely related lines have high similarity, while the separate lines showed the highest

**Table 4.** PC values for grain yield and its attributes in black soybean genotypes.

Traits	PC1	PC2	PC3
Plant height (PH) (cm)	0.69	0.14	0.05
Number of branches (NPB)	0.39	-0.68	0.03
Number of fertile nodes (NFB)	0.78	0.43	0.18
Number of pod contents (NSP)	0.97	-0.11	-0.01
Number of empty pods (NEP)	0.23	-0.75	0.21
Number of seeds (NS)	0.96	0.00	-0.20
Seed weight per plant (GYP) (g)	0.98	-0.03	-0.16
100-seed weight (100-SW) (g)	0.67	0.20	-0.51
Grain yield per plot (GY) (kg)	0.97	0.08	0.10
Seed diameter (SD) (mm)	-0.11	0.87	0.18
Seed length (SL) (mm)	0.53	0.04	0.75

Numbers in bold print have a real influence on genetic diversity; PC = principal component.



**Figure 2.** Distribution of black soybean genotypes and traits tested based on PCA. (For the genotype codes, see Table 1, and for the trait codes, see Table 3).

dissimilarity to other genotypes (Maulana *et al.*, 2023). Black soybean genotypes, viz., BS84, BS102, and BS144, occurred far away from the genotypes in other groups. It indicates that these genotypes have high dissimilarity with other lines. In addition, the distribution between the traits tested also showed a relationship among each other, where traits that have an acute angle (<90°) have a strong correlation (Maxiselly *et al.*,

2023). Figure 2 also showed that seed diameter negatively correlates with all other traits. Grain yield has a significant positive correlation with plant height, 100-seed weight, the number of fertile nodes, seed length, the number of seeds, seed weight per plant, and the number of pods. Other traits providing positive correlations were the number of branches and empty pods.



In Figure 2, the black soybean line BS84 has the lowest value for all traits because it has an opposite position versus all the evaluated traits. In contrast, genotype BS144 has the highest value because it was in the same direction as all traits and exceeded all other trait vectors. Moreover, the soybean genotype BS72 has the best value for the trait of the number of branches, BS 141 has the best value for the number of fertile nodes, genotype BS64 has the best value for the 100-seed weight, BS79 has the best value for plant height, BS99 has the best value for seed length and grain yield per plot, and the genotype Mutiara-3 has the best value for the number of seeds. According to previous studies, the genotype closest to the trait vector has the best value for that trait (Aziza *et al.*, 2021; Maulana *et al.*, 2023).

#### **Heritability and genetic gains in each location**

Results combined with ANOVA analysis showed no interaction between genetic and environmental influences on tested black soybeans' appearance. Ecological factors and genotype influenced the variation appearance more (Table 2). Analysis of heritability and genetic gains ensued for each location. Based on the results, the heritability and genetic gain values on each location showed that heritability and genetic gain on tested characteristics in the Majalengka location revealed the criteria ranging from low to high (Table 5). The traits, tall plants, the number of branches, empty pods, the number of seeds, weight of seeds per plant, weight per plot, and seed diameter showed low heritability. Attributes with medium heritability emerged for the number of fertile nodes, pod contents, and 100-seed weight. However, the seed length characteristic gave high heritability in the Majalengka location.

Genetic gains on-site Majalengka's criteria are low until high. The characteristics with low genetic gains included plant height, the number of branches, fertile nodes, pod contents, empty pods, seeds, seed weight per plant, 100-seed weight, grain yield per plot, and seed diameter. Meanwhile, the trait with

progressive genetics is tall, or the seed length. On the Majalengka location, part of the massive character shows low genetics gain criteria.

One of the factors that cause heritability and genetic gain is an environmental factor. Environmental factors show significant effects (Table 2). According to Xu *et al.* (2020), ecological factor regulation can influence the expression process of genetically modified plants; hence, controlling the environment's condition is a must. Xu *et al.* (2017) reported that genetic gain could be better with methods that increase the potency of genetics by using modern breeding techniques and the practice of good agronomy. Apart from these factors, Gielen *et al.* (2008) reported that a factor required in analyzing heritability and genetics gains is taking the exact number of samples and complexity-tested characteristics. Environmental data during the test is visible in Table 6.

Results analysis and heritability across locations revealed the Indramayu location with currently high criteria; however, on genetic gains, the tested characteristics enter into low criteria and then high. Traits with moderately marked heritability included the number of fertile internodes, the number of pod contents, the number of empty pods, weighty seeds per plant, the weight of 100 grains, weight per plot, and seed diameter. Attributes marked with high heritability comprised the height of plants, number of branches, number of seeds, and long seeds. Results from a study by Amoros *et al.* (2020) indicated that heritability is high when additive genes control the character, with further manipulations through repetitive selection.

Genetic gains on-site Indramayu shows criteria low until tall. The character shows genetic gains are low and include tall plants, the number of pod contents, total seeds, weight of 100 grains, and weight per plot. The trait showed progress. Moderate genetic criteria are the amount of book fertile, the weight of seeds per plant, and seed diameter. The character also progresses. Genetic criteria were highest for the attributes of the number of branches, number of empty pods, and long seeds.

**Table 5.** The minimum, maximum, and average values, heritability, and genetic gain of black soybean genotypes for various traits in each environments.

Traits	Majalengka							Indramayu						
	Min	Mean	Max	$\sigma^2_g$	$\sigma^2_f$	$h^2$	Genetic gains (%)	Min	Mean	Max	$\sigma^2_g$	$\sigma^2_f$	$h^2$	Genetic gains (%)
PH	20.43	25.26	32.73	0.5686	100.84	0.06	0.39	21.85	32.06	41.38	163.59	218.84	0.75	4.10
NPB	4.00	5.46	10.33	0.3615	19.56	0.18	5.95	2.5	5.05	9.73	16.81	30.76	0.55	19.05
NFB	8.38	9.60	11.80	0.348	10.16	0.34	6.28	6.87	9.59	12.75	0.75	17.28	0.44	7.99
NSP	39.57	50.70	70.13	149.053	756.230	0.20	0.68	12.67	29.50	46.27	367.26	743.67	0.49	2.95
NEP	1.60	3.01	4.83	0.05	0.89	0.06	3.24	0	1.17	2.27	0.13	0.32	0.40	59.95
NS	82.28	105.49	139.33	205.602	310.96	0.07	0.11	28.5	63.93	98.2	1854.58	3604.04	0.51	1.42
GYP	8.37	10.72	14.77	0.34	40.91	0.08	1.38	2.3	6.31	8.96	23.49	48.25	0.49	13.57
100 SW	8.37	9.96	11.46	0.14	0.43	0.33	5.79	8.5	9.61	11.2	0.16	0.54	0.30	5.41
GY	761.07	876.97	1584.00	1,206.97	49,385.03	0.02	0.00	194.67	659.11	1200	26,665.17	57,926.53	0.46	0.12
SD	3.77	4.32	5.07	0.02	0.10	0.17	6.98	4.02	5.00	5.49	0.04	0.18	0.22	7.87
SL	4.87	6.38	6.78	0.13	0.16	0.81	22.33	5.83	6.49	6.83	0.04	0.06	0.67	18.11

Plant height (PH) (cm), number of branches (NPB), number of fertile nodes (NFB), number of pod contents (NSP), number of empty pods (NEP), number of seeds (NS), seed weight per plant (GYP) (g), 100-seed weight (100 SW) (g), grain yield per plot (GY) (kg), seed diameter (SD) (mm), and seed length (SL) (mm);  $\sigma^2_p$  = variance phenotype;  $\sigma^2_g$  = variance genotype;  $h^2$  = heritability.

**Table 6.** Environmental conditions in both locations.

Parameters	Locations	
	Majalengka	Indramayu
pH	6,11 (slightly acidic)	5,61 (slightly acidic)
C-organic	2,79 (medium)	1,77 (poor)
N-total	0,24 (medium)	0,16 (poor)
P <sub>2</sub> O <sub>5</sub>	5,35 (poor)	9,33 (medium)
K <sub>2</sub> O	75,94 (very high)	10,36 (poor)
Altitude	120	57
Temperature (°C)	26	30
Relative Humidity (%)	86	83
Rainfall (mm)	400	250

The genetic parameters of heritability and genetic gain determine the selection progress in a population. The greater the heritability and genetic gain values, the greater the possibility of improving the selection progress (Amien *et al.*, 2021). The characters tested must have high diversity and heritability to obtain targets for selection progress (Narasimhamurthy *et al.*, 2018). Therefore, the high genetic diversity and heritability are complementary for high genetic gain. High heritability values also authenticate that selection can proceed in the early segregating generations (Fehr, 1991).

The selection of characters with high heritability values can begin in the early generations because these variables are easily inherited (Maulana *et al.*, 2023). The selection of populations with high heritability proved more effective than populations with low heritability. Therefore, high heritability is desirable in plant selection programs. Information on the heritability and genetic gain of black soybean genotypes is available in Table 5.

High heritability values indicated that genetic factors controlled the traits rather than environmental factors (Lai *et al.*, 2017). In the black soybean lines, the heritability values were high for almost all the traits except for the number of branches, empty pods, and seed length. A higher heritability value among the populations for target traits is vital in sustaining plant breeding programs (Maulana *et al.*, 2023). According to Narasimhamurthy *et al.* (2018), heritability values depend on populations, generations, and estimation methods. The high heritability values of the observed characteristics indicate that the selection can be efficient. Conversely, if a character's heritability value is low, the selection process becomes inefficient (Amien *et al.*, 2021). Based on these results, the selection process for the tested black soybean populations will be faster for characters with high heritability values, high genetic gain criteria, and a high correlation between them.

All the traits tested showed high genetic gain except for plant height, the number of empty pods, and seed length, which showed moderate values. The high values of

genetic gain for all the characters tested indicate that genetic factors were more dominant than the environment, and the progress in character selection will be more efficient (Narasimhamurthy *et al.*, 2018; Amien *et al.*, 2021). Selection in the tested population will be better because it provides high genetic gain. Ritonga *et al.* (2017) stated that a high heritability value for a character in a population would increase the effectiveness of selection, with the hope that selection activities will achieve high genetic gain. The research results of Meriaty *et al.* (2021) on genetic gain signified that the selection method used influenced a character. The research results of Badu-Apraku *et al.* (2021) reported that accelerating the acquisition of genetic gain from the selection process must proceed under various environmental conditions. Thus, selecting tested black soybean populations with high genetic gain will be efficient and valuable in future soybean breeding programs.

## CONCLUSIONS

The genetic diversity of the black soybean population depended on the principal component analysis (PCA) with a cumulative value of 80.55%. All the characters tested significantly contributed to genetic variation, indicating these traits became the difference between the evaluated soybean genotypes. The heritability and genetic progress in the attributes tested acquired environmental influences. The grain yield, the number of branches, fertile nodes, pod content, the number of seeds, seed weight per plant, 100-seed weight, and seed diameter showed the highest genetic gain values. In contrast, plant height, the number of empty pods, and seed length showed medium values. This information can serve the plant breeders as a basis for assessing and developing high-yielding black soybean cultivars.

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