

Growth and production of M6 and M7 black soybean mutant genotypes

SYAIFUL ANWAR, FLORENTINA KUSMIYATI*, DWI RETNO LUKIWATI, MUHAMAD GHAZI AGAM SAS, YULIA NUR ARIFAH

Department of Agriculture, Faculty of Animal and Agricultural Sciences, Universitas Diponegoro. Jl. Prof Sudarto SH, Tembalang, Semarang 50275, Central Java, Indonesia. Tel./fax.: +62-24-7474750, *email: fkusmiyati@lecturer.undip.ac.id

Manuscript received: 7 November 2023. Revision accepted: 18 June 2024.

Abstract. Anwar S, Kusmiyati F, Lukiwati DR, Sas MGA, Arifah YN. 2024. Growth and production of M6 and M7 black soybean mutant genotypes. *Biodiversitas* 25: 2541-2546. The seed coat colors of soybeans are yellow, black, green, brown, or bicolor, and in Indonesia, black seed coat color is for used soy sauce. Our black soybean mutation breeding research started with irradiating soybean cultivar Detam 3 with gamma rays at 160, 208, 256, 304, 352, 400, 448, 496, 544, and 592 Gy. Genotypes were selected from M1 (first generation) to M5 (fifth generation) based on saline and/or nonsaline soil productions. This research aims to evaluate the growth and production of sixth-generation (M6) and seven-generation (M7) black soybean mutant genotypes. The research was conducted in Karangharjo Village, Pulokulon Sub-district, Grobogan District, Central Java Province, Indonesia. The plant material was three genotypes of M6 black soybean mutants (BSMG VQ 05-256/1-6-2-28, BSMG VQ 05-400/1-2-2-6 and BSMG VQ 05-256/1-2-9-29), four genotypes of M7 black soybean mutants (BSMG VQ 06-256/1-6-2-28, BSMG VQ 06-400/1-2-2-6 and BSMG VQ 06-256/1-2-9-29 and BSMG VQ 06-256/1-4-2-21) and three cultivar checks (Detam 1, Detam 3/parent variety and Detam 4 variety). The parameters measured consist of plant growth, components, and production. All data collected were subjected to statistical Analysis of Variance (ANOVA); if significantly different, it continued by Duncan Multiple Range Test (DMRT). The results showed that the genotype treatment affected all observed characters except plant height. Selected lines based on the number of leaves, number of pods, number of seeds, weight of 100 seeds, weight of seed, and production were BSMG VQ 05-256/1-2-9-29, BSMG VQ 05-256/1-2-9-29 and BSMG VQ 06-256/1-4-2-21. These selected genotypes provided the prospective source of soy sauce material and needed to examine its stability at different locations (multilocation test).

Keywords: Black soybean, Detam, gamma rays, mutant, production

INTRODUCTION

Soybean (*Glycine max* L. Merr.) is a legume crop that is very popular in Indonesia and many countries. Soybean seed is widely used as food, functional food, feed, and industrial products. Protein from soybean is a high-quality protein comparable to protein from animal sources such as dairy and meat. It contains well-balanced essential amino acids (Qin et al. 2022). The seed coat colors of soybean are yellow, black, green, brown, or bicolor. The difference in seed color is because of evolutionary traits during domestication, from black in wild soybeans to various colors in cultivated soybeans (Li et al. 2013). In Indonesia, soybean's yellow seed coat color is used especially for traditional food ("tempe") and the black seed coat color is for soy sauce. Black soybean has a high content of isoflavones and antioxidants (Choi et al. 2020). Many cultivated varieties of black soybeans in Indonesia, such as "Detam" and "Mallika." Production and weight of 100 seeds of "Detam" variety are 2.5 tons/ha and 14.8 g, respectively. "Detam" variety is also sensitive to saline soil (Kusmiyati et al. 2019; Agam et al. 2020). The improved trait of "Detam" variety can be achieved through plant breeding.

Mutation breeding is one of the plant breeding methods that uses artificial mutagenesis to get new biologically cultivated varieties. Mutagenesis could be done through chemicals or radiation. Chemical agents, such as Ethyl

Methane Sulphonate (EMS), Diethyl Sulfate (DES), and Methyl Methane Sulphonate (MMS), are highly toxic, combustible, and likely carcinogenic chemical compound that cause mostly point mutations in genes. Applications of X-ray and gamma-ray are classified as radiation mutation. Those various rays induce an abundance of genomic mutations, then will speed up mutant trait production through energy deposition indirectly or directly onto DNA (Ma et al. 2021). In plant breeding for agricultural productivity, induced mutation by gamma rays has proven beneficial. Gamma rays have the ability to induce mutation with a high frequency throughout the whole genome. Although mutation breeding is random, the selection and screening carefully of mutated plants allow breeders to propagate and identify the desired characteristics (Ghareeb et al. 2022). For breeders, induced mutation by gamma rays offers a cost-efficient and effective approach for developing new varieties suitable to meet the threat of increasing demand for food and climate change (Mohsen et al. 2023). Recently, 3,402 mutant varieties have been registered in the database of mutant varieties in the IAEA (International Atomic Energy Agency). Most of them, 2,087 mutant varieties, are from Asia (IAEA 2023).

Research on mutation breeding has already been done in many countries. In Bangladesh, a new soybean variety of "Binasoybean-5" that has superior stability in various environmental conditions and steady yield performance has

been released. Breeding of this variety started with the popular cultivar "Bari Soybean-5," subjected to induced mutation with gamma rays (Co60). Selection from the M4 generation resulted in twelve true-breed mutants. The criteria selection is based on plant height, number of branches, and pods, which are considered favorable criteria for improvement of soybean that ensure expected yield. The mutant SBM-18 shows a stable yield performance from those mutants in various environments (Bhuiyan et al. 2022). Induced mutation by gamma rays also improves protein contents and oil of soybeans. Gamma rays at 100 Gy increase protein content, while gamma rays at 200 Gy effectively increase oil content. Four mutant lines have high protein and oil content as potential candidates for multilocation evaluation (Mohsen et al. 2023).

Our research in mutation breeding of black soybean started with irradiation of soybean cultivar Detam 3 with gamma rays at 160, 208, 256, 304, 352, 400, 448, 496, 544, and 592 Gy at the Center for Isotopes and Radiation Application, National Nuclear Energy Agency (BATAN), Indonesia (Agam et al. 2020). Selection of genotypes was done at M1 (first generation) to M5 (fifth generation) based on production in saline soil and or nonsaline soil (Kusmiyati et al. 2019; Agam et al. 2020). This research aims to evaluate the growth and production of sixth-generation (M6) and seventh-generation (M7) black soybean mutant genotypes.

MATERIALS AND METHODS

Materials

The research was conducted in Karangharjo Village, Pulokulon Sub-district, Grobogan District, Central Java Province, Indonesia. The plant material was three genotypes of M6 black soybean mutants (BSMG VQ 05-256/1-6-2-28, BSMG VQ 05-400/1-2-2-6 and BSMG VQ 05-256/1-2-9-29), four genotypes of M7 black soybean mutants (BSMG VQ 06-256/1-6-2-28, BSMG VQ 06-400/1-2-2-6 and BSMG VQ 06-256/1-2-9-29 and BSMG VQ 06-256/1-4-2-21) and three cultivar checks (Detam 1, Detam 3/parent variety and Detam 4 variety), so total were 10 plant material. The seeds were the result of our previous study (Kusmiyati et al. 2019; Agam et al. 2020). Meaning of genotype code, for example: code of genotype BSMG VQ 05-256/1-2-9-29: BSMG VQ: blacksoybean mutant genotype, 05: seeds harvested from fifth generation to get M6 population, 256: the seeds were exposed to 256 Gy for gamma radiation at the M0 generation, 1: first generation (M1) were planted at saline soil, 2: a single plant labeled no. 2 was selected at M1 generation, and then those seeds were planted in a row, and a single plant labeled number 9 was selected at M2 generation, 29: a single plant number 29 was selected at M3 generation. In M4 generation, all plants at each genotype were harvested and all of the seeds were grown as M5 generation. This process was repeated until M6 generation for M7 population.

Methods

The experimental design used was a completely randomized design with three replicates. Each experimental unit was a 2.5 m × 13 m plot size with a 50 cm × 50 cm planting distance. Planting of seed was done by making planting holes in the plot then inserting 2 seeds per planting, then thinning was done after two weeks of planting, so only one plant per hill. Fertilizers of 50 kg urea/ha, 100 kg SP36/ha, and 100 kg KCl/ha were applied. Insects, diseases, and weeds were controlled intensively.

The parameters measured consist of plant growth (plant height and number of leaves), production components (number of pods, number of seeds, weight of 100 seeds), and production (weight of seed per plant and production). Plant growth, production components, and seed weight per plant were taken from the average of 10 randomly sampled plants. Production (ton/ha) was calculated by the weight seed of ten sample plants and converted to ton/ha). All data collected were subjected to statistical Analysis of Variance (ANOVA) (Table 1), if significantly different continued by the Duncan Multiple Range Test (DMRT). The analysis of correlation measured by pairwise-pearson correlation method using OriginPro v.2024

Genetic variability parameters, such as mean, range, genotypic, and phenotypic coefficient of variation, were computed following the methodology proposed by Nilahayati et al. (2018). The assessment of the Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) was categorized into low (0-10%), moderate (10-20%), and high (20% and above) based on the classification suggested by Sivasubramanian and Menon (1973). Broad-sense heritability and genetic advance in the percentage of mean were determined using the approach recommended by Syukur et al. (2015) are categorized as follows: high if $h^2 > 50\%$, moderate if $20\% < h^2 < 50\%$, and low if $h^2 < 20\%$.

The Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) are calculated according to the formula:

$$PCV = (\sqrt{\sigma^2_p} / \text{population mean}) \times 100\%$$

$$GCV = (\sqrt{\sigma^2_g} / \text{population mean}) \times 100\%$$

Where:

σ^2_g : Genotype variance

σ^2_p : Phenotype variance

PCV : Phenotypic Coefficient of Variation

GCV : Genotypic Coefficient of Variation

Table 1. Analysis of variance and genetic parameters

Source of variation	Degree of freedom	Mean square	Expected mean square
Block (r)	(r-1)	M3	$\sigma^2_e + g \sigma^2_r$
Genotypes (g)	(g-1)	M2	$\sigma^2_e + r \sigma^2_g$
Error (e)	(r-1)(g-1)	M1	σ^2_e
Total	rg-1		

RESULTS AND DISCUSSION

Estimating the value of genetic variability parameters

Estimating the value of variation components on soybeans involves analyzing the genetic and environmental factors contributing to the seed yield variation. The estimates of Phenotypic (PCV) and Genotypic (GCV) coefficients of variation (Table 2) indicated that the values of GCV were higher than that of PCV; these indicated that the greater role of genetic components and expression of characters under study was higher influenced due to genetics factors.

Heritability is the ratio of genetic variance to phenotypic variance. The number of pods showed the highest heritability, the number of seeds, and weight of 100 grains, i.e., 52.24, 61.74, and 57.64, respectively. Similar results are reported, in which the number of pods and weight of 100 grains have high heritability (Ojo and Ayuba 2016; Kuswanto 2017). The high value of heritability shows the ability of genotypes to pass on their traits to the next generation. As Ritonga et al. (2018), heritability serves as a genetic parameter employed to gauge the ability of genotypes within a plant population to transmit their traits. Understanding heritability is crucial for estimating the extent to which genetic or environmental factors influence the expression of a trait. The estimated heritability values for quantitative traits, as detailed in Table 2, indicate that high heritability values are observed in traits such as the number of seeds per plant, number of pods per plant, and weight of 100 seeds. Moderate heritability values are identified in traits related to seed weight per plant and seed production. Conversely, low heritability values are associated with traits like plant height and number of leaves. Kuswanto (2017) asserts that a character's estimated heritability value falling into the medium or high categories indicates its susceptibility to genetic influences with minimal impact from environmental factors. Such characters are considered references in the selection process for subsequent plant development.

Plant growth

This study revealed that plant height was not significantly different between mutant genotypes and cultivar checks. Plant height of soybean mutant genotypes was 30.8 to 37.5 cm (Table 3). Genotypes significantly affected the number of leaves. Cultivar check of Detam 1 had the highest number of leaves (27.2 leaves), not significantly different from the mutant genotype of BSMG VQ 05-256/1-6-2-28 (25.9 leaves). The other five soybean mutant genotypes had fewer leaves than the Cultivar check of Detam 1 but were not significantly different from the Cultivar check of Detam 3. Cultivar check of Detam 3 had the lowest number of leaves (20.6).

Soybean mutant genotypes and cultivar check of Detam are determinate plants whose vegetative growth ends in an inflorescence. Gamma-ray radiation did not affect soybean plant height. This result is consistent with the report by Sarker et al. (2014) and Andini et al. (2022). Other reports showed that gamma radiation caused variability in soybean plant height (Nobre et al. 2019). Another research reported

a reduction in plant height because of increasing gamma radiation (Sarker et al. 2014). The different results may be due to different genetic materials and environments. Environment strongly influences quantitative character, such as plant height controlled by multiple genes. Plant height is an important characters of soybean (Xue et al. 2019). The soybean plant height in this research is classified as short and not susceptible to lodging.

Induced mutation by gamma rays affected the number of leaves of M6 and M7 black soybean mutant genotypes. Cultivar check of Detam 1 had the highest number of leaves. The number of leaf Genotypes of BSMG VQ 05-256/1-6-2-28 did not significantly differ with the cultivar check of Detam 1, but the number of leaves of BSMG VQ 05-256/1-6-2-28 is significantly higher than two other cultivar checks (Detam 3 and Detam 4). BSMG VQ 06-256/1-2-9-29 had a number of leaves that did not significantly differ from BSMG VQ 05-256/1-6-2-28. The higher number of leaves will increase the rate of photosynthesis. The response of induced mutation among M6 and M7 black soybeans was different because of the random mutations and the outcomes of changes in plant cells. Based on the number of leaf characters, the selected lines were BSMG VQ 05-256/1-6-2-28 and BSMG VQ 06-256/1-2-9-29.

Production component

The analysis of variance showed that genotypes significantly affected the number of pods, number of seeds, and weight of 100 seeds. The Duncan multiple range test results on the number of seeds, number of pods, and weight of 100 seeds on M6 and M7 black soybean genotypes and their three cultivar checks can be seen in Table 4. Genotype BSMG VQ/05-256/1-2-9-29 had the highest number of pods, number of seeds, and weight of 100 seeds. The number of pod BSMG VQ/05-256/1-2-9-29 was significantly higher than the three cultivar checks, although the number of seeds was not significantly different than the cultivar check of Detam 4. The weight of 100 seeds BSMG VQ/05-256/1-2-9-29 was not significantly different than the cultivar check of Detam 1. Number of pod and number of seed BSMG VQ 05-252/1-6-2-28, BSMG VQ 05-400/1-2-2-6, BSMG VQ/06-256/1-2-9-29 and BSMG VQ 06-256/1-4-2-21 were not significantly difference. Detam 1 had the lowest number of pods.

The number of M6 black soybean mutant pods was 75.5-119.3 pods, which was higher than M7 black soybean mutant (54.4-88.8 pods). The number of seeds and weight of 100 seeds of M6 black soybean mutants were also higher than M7 black soybean mutant. The number of pods, number of seeds, and weight of 100 seeds of M7 was lower than M6 because of the differences in the growing environment at the time of the previous selection. The selection of the fifth generation to get M6 population in Grobogan District, where soil and environmental conditions were suitable for soybean growth. In comparison, the sixth generation was selected to get M7 population in the Semarang district with unfertile soil.

Table 2. Estimated value of genetic variability parameters M7

Parameters	σ^2_e	σ^2_g	σ^2_p	GCV (%)	PCV (%)	Category of PCV	H ² bs (%)	Category of heritability
Plant height	11.25	1.58	12.83	10.33	3.63	L	12.29	L
Number of leaves	7.85	1.04	8.88	12.55	4.29	L	11.67	L
Number of pods	213.14	233.15	446.29	27.40	19.80	M	52.24	H
Number of seeds	906.69	1463.25	2369.94	35.02	27.52	H	61.74	H
Weight of 100 seeds	5.73	7.80	13.53	23.22	17.63	M	57.64	H
Weight of seeds/plant	25.99	9.84	35.83	30.79	16.14	M	27.47	M
Production	4.16	1.57	5.73	30.79	16.14	M	27.47	M

Note: σ^2_e : Environmental variation; σ^2_g : Genotype variation; σ^2_p : Phenotypic variation; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; L: Low; M: Moderate; H: High

Table 3. Plant height and number of leaves of M6 and M7 soybean mutant genotypes

Mutant genotypes	Plant height (cm)	Number of leaves
BSMG VQ 05-256/1-6-2-28	32.5	25.9 ab
BSMG VQ 05-400/1-2-2-6	33.7	23.9 c
BSMG VQ 05-256/1-2-9-29	35.9	22.3 c
BSMG VQ 06-256/1-6-2-28	30.8	22.7 c
BSMG VQ 06-400/1-2-2-6	34.5	22.7 c
BSMG VQ 06-256/1-2-9-29	37.1	25.5 b
BSMG VQ 06-256/1-4-2-21	37.5	25.4 c
Detam 1	36.9	27.2 a
Detam 3	35.5	24.3 c
Detam 4	33.0	20.6 d

Table 4. Number of pods, number of seeds, and weight of 100 seeds of soybean mutant genotype

Mutant genotypes	No. of pods	No. of seeds	Weight of 100 seeds (g)
BSMG VQ 05-256/1-6-2-28	80.7 bcd	131.5 bcd	15.8 ab
BSMG VQ 05-400/1-2-2-6	75.5 cde	136.3 bc	16.0 ab
BSMG VQ/05-256/1-2-9-29	119.3 a	223.5 a	16.6 a
BSMG VQ 06-256/1-6-2-28	54.4 f	104.6 cd	15.9 ab
BSMG VQ 06-400/1-2-2-6	62.5 ef	111.4 bcd	14.2 d
BSMG VQ/06-256/1-2-9-29	80.4 bcd	154.1 b	14.5 cd
BSMG VQ 06-256/1-4-2-21	88.8 bc	154.7 b	16.3 a
Detam 1	53.4 f	85.8 d	16.4 a
Detam 3	67.9 def	149.5 bc	15.3 bc
Detam 4	97.2 b	210.9 a	12.3 e

The number and weight of 100 M6 black soybean mutant seeds in this research were higher than the same genotype planted in Semarang. The number of seeds and weight of 100 M6 black soybean mutant seeds in this research was 131.5-223.5 seeds and 15.8-16.6 g, respectively. In comparison, the number of seeds and weight of 100 seeds of M6 black soybean mutant planted in Semarang district was in the range of 101-137 seeds and 9.22-10.69 g, respectively (Aprianti et al. 2021). The weight of 100 seeds of ten black soybean lines grown in 16 locations ranged from 10.92-13.60 g/100 seeds (Krisnawati et al. 2016). The seed weight of black soybean mutants in this research was higher, and the weight of 100 seeds is also higher than the parent variety description (11.8 g/100 seeds). Increasing seed weight in this research is in line with another research.

Induced mutation by gamma rays at Kipas Putih variety showed that seed size of mutant line increased by 2 g/100 seeds compared to its parents in the M6 generation (Nilahayati et al. 2022). In Indonesia, soybean seed size was divided into three groups: large (>14 g/100 seeds), medium (10-14 g/100 seeds), and small (<10 g/100 seeds) (Krisnawati and Adie 2015). Size was one important trait affecting soybean productivity and performance; all genotypes of black soybean mutants in this research had more than 14 g/100 seeds classified as large.

Genotype BSMG VQ/05-256/1-2-9-29 had the highest number of pods, number of seeds, and weight of 100 seeds. This genotype was M6 genotype that resulted from selection carried out in Grobogan district. The same genotype at M7 (BSMG VQ/06-256/1-2-9-29) had a significantly lower number of pods, number of seeds, and weight of 100 seeds. The number of pods and the number of BSMG VQ/06-256/1-2-9-29 seeds were significantly higher than Detam 1 as a cultivar check. The pod BSMG VQ 06-256/1-4-2-21 number was significantly higher than the two cultivar checks (Detam 1 and Detam 3). The number of seed BSMG VQ 06-256/1-4-2-21 was significantly higher than Detam 1. The 100 seeds' BSMG VQ 06-256/1-4-2-21 weight was significantly higher than Detam 3 and Detam 4 as cultivar checks. Selected lines based on the number of pods, number of seeds, and weight of 100 seeds were BSMG VQ 06-256/1-2-9-29 and BSMG VQ 06-256/1-4-2-21.

Production

The analysis of variance showed that genotypes significantly affected the weight of seed/plant and production of the number of M6 and M7 genotypes and their three cultivar checks. The results of the Duncan multiple test on weight of seed/plant and production can be seen in Table 5. BSMG VQ/05-256/1-2-9-29 had the highest weight of seed and production. The weight of seed and production of BSMG VQ/05-256/1-2-9-29 was not significantly different from Detam 4 as cultivar check and BSMG VQ 06-256/1-4-2-21; cultivar check as parent was Detam 3. The results showed that seed weight and BSMG VQ/05-256/1-2-9-29 production were significantly higher than Detam 3 as the parent. The lowest seed weight/plant and production were found in BSMG VQ 05-262/1-6-2-28 with a seed weight of 13.82 g/plant and production of 0.56 ton/ha, which was not significantly different from BSMG VQ 06-256/1-6-2-28, BSMG VQ 06-400/1-2-2-6 and Detam 3 as parent.

The weight of seed per plant in this study ranged from 13.8-27.4 g/plant, which was higher than the results of Sumardi et al. (2017) with 34 local black soybean genotypes (5.4-14.47 g/plant). This research has a higher weight of seed because of induced mutation by gamma rays for black soybean seed at M0 and selection at each generation (M1-M5) based on production. The local black soybean genotype usually has low production but has a higher tolerance to extreme abiotic and biotic environments. Seed weight per plant in the same genotype (BSMG VQ 05-256/1-6-2-28 and BSMG VQ 05-400/1-2-2-6) was not significantly different between the M6 and M7 generations, except for genotype BSMG VQ/05-256/1-2-9-29. Seed weight per plant of BSMG VQ 05-256/1-6-2-28 and BSMG VQ 05-400/1-2-2-6 is thought to be stable, and BSMG VQ/05-256/1-2-9-29 could not yet be stable. Genotype BSMG VQ 05-256/1-4-2-21 (M6) did not grow very well, so the growth and production of this genotype cannot be observed.

M6 and M7 soybean mutant genotype productions were 0.56-1.1 ton/ha and 0.71-0.96 ton/ha. Production of black soybean mutant in this research was lower than other researchers reported. The average seed production of 17 black soybean genotypes ranged from 0.97 tons/ha to 2.55 tons/ha in 10 locations in the dry and rainy seasons in 2012 (Puspitasari et al. 2019); the seed yield of 10 black soybean lines ranged from 2.46-2.88 ton/ha (Krisnawati et al. 2016). The lower production of black soybean mutants in this research is because of the differences in planting distance. The planting distance in this research was 50 cm x 50 cm (one plant per hill), while the planting distance in other researchers was 15 cm x 40 cm (two plants per hill).

Production of BSMG VQ 05-256/1-6-2-28 (M6) was not significantly different with BSMG VQ 06-256/1-6-2-28 (M7) and Detam 3 as a parent but lower than Detam 1 and

Detam 4 as cultivar check. BSMG VQ 05-400/1-2-2-6 production was similar to BSMG VQ 06-400/1-2-2-6 (M7) and three cultivar checks. The production of BSMG VQ/05-256/1-2-9-29 (M6) is higher than BSMG VQ/06-256/1-2-9-29 (M7) and Detam 3 as parent or Detam 1. BSMG VQ 06-256/1-4-2-21 showed higher production, similar to three cultivar checks (Detam 1, Detam 3, and Detam 4). Selected lines based on the weight of seed and production were BSMG VQ 05-256/1-2-9-29, BSMG VQ 06-256/1-2-9-29 and BSMG VQ 06-256/1-4-2-21.

Correlation analysis

The results of the correlation analysis showed that the characters of weight of seed per plant, number of pod, number of seed, and plant height were positively correlated to the production traits, and also number of leaf are correlated with weight 100 seeds, while the number of leaf is negatively correlated with the number of seed (Figure 1).

Table 5. Weight of seed/plant and production of soybean mutant genotype

Mutant genotypes	Weight of seed/plant (g)	Production (ton/ha)
BSMG VQ 05-256/1-6-2-28	13.82 d	0.56 d
BSMG VQ 05-400/1-2-2-6	21.42 bc	0.86 bc
BSMG VQ/05-256/1-2-9-29	27.39 a	1.10 a
BSMG VQ 06-256/1-6-2-28	17.77 cd	0.71 cd
BSMG VQ 06-400/1-2-2-6	18.45 bcd	0.74 bcd
BSMG VQ/06-256/1-2-9-29	20.92 bc	0.84 bc
BSMG VQ 06-256/1-4-2-21	23.97 ab	0.96 ab
Detam 1	20.15 bc	0.81 bc
Detam 3	19.05 bcd	0.76 bcd
Detam 4	22.39 abc	0.89 abc

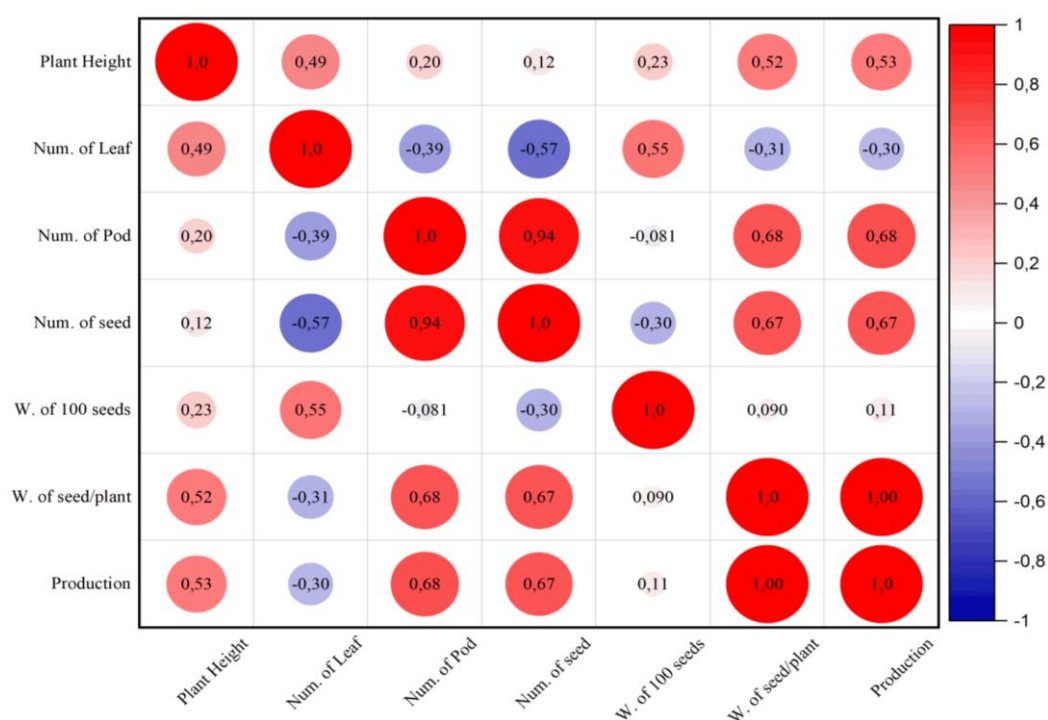


Figure 1. The correlation analysis of agronomic traits

According to Kuswantoro (2017), character correlation plays an important role in plant breeding programs as it can indicate when a character will develop through the interaction with other characters. Faot et al. (2019) stated that the characters that correlate and have an impact on the increase in production are the characters used for the selection of soybean genotypes in the program to increase soybean yield.

In conclusion, the genotype treatment will affect all observed characters except for plant height. The selected lines based on the number of leaves, number of pods, number of seeds and weight of 100 seeds, weight of seed, and production were BSMG VQ 05-256/1-2-9-29, BSMG VQ 06-256/1-2-9-29 and BSMG VQ 06-256/1-4-2-21. These selected genotypes provided the prospective source of soy sauce material and needed to examine its stability at different locations (multilocation test).

ACKNOWLEDGEMENTS

Thanks are conveyed to the Faculty of Animal and Agricultural Sciences, Universitas Diponegoro, Indonesia, following the Research Funding Agreement and Community Service for Fiscal Year 2022.

REFERENCES

- Agam MGSAS, Kusmiyati F, Anwar S, Herwibawa B. 2020. Diversity analysis in soybean (*Glycine max* [L.] Merrill) mutant lines grown in saline soil using agronomic traits and RAPD markers. IOP Conf Ser: Earth Environ Sci 482: 012017. DOI: 10.1088/1755-1315/482/1/012017.
- Andini SN, Sari MF, Septiana S. 2022. Population diversity of black soybean Detam 4 Prida generation M3 mutants. IOP Conf Ser: Earth Environ Sci 1012: 012031. DOI: 10.1088/1755-1315/1012/1/012031.
- Aprianti RD, Kusmiyati F, Karno. 2021. Production characteristic and heritability several mutants of black soybean in M6 generation. Jurnal Agrotech 11: 8-12. DOI: 10.31970/agrotech.v11i1.63. [Indonesian]
- Bhuiyan MSH, Malek MA, Emon RM, Khatun MK, Khandaker MM, Alam MA. 2022. Increased yield performance of mutation induced soybean genotypes at varied agro-ecological conditions. Braz J Biol 84: e255235. DOI: 10.1590/1519-6984.255235.
- Choi Y-M, Yoon H, Lee S, Ko H-C, Shin M-J, Lee MC, Hur OS, Ro NY, Desta KT. 2020. Isoflavones, anthocyanins, phenolic content, and antioxidant activities of black soybeans (*Glycine max* (L.) Merrill) as affected by seed weight. Sci Rep 10: 19960. DOI: 10.1038/s41598-020-76985-4.
- Faot MM, Zubaidah S, Kuswantoro H. 2019. Genetic correlation and path analysis of agronomical traits of soybean (*Glycine max*) lines infected by CpMMV. Biodiversitas 20 (6): 1496-1503. DOI: 10.13057/biodiv/d200602.
- Ghareeb YE, Soliman SS, Ismail TA, Hassan MA, Abdelkader MA, Abdel Latef AAH, Al-Khayri JM, Alshamrani SM, Safhi FA, Awad MF, Abd El-Moneim D, Hassanin AA. 2022. Improvement of German chamomile (*Matricaria recutita* L.) for mechanical harvesting, high flower yield and essential oil content using physical and chemical mutagenesis. Plants 11 (21): 2940. DOI: 10.3390/plants11212940.
- International Atomic Energy Agency. 2023. Mutant variety database. Available online at: <https://nucleus.iaea.org/sites/mvd/SitePages/Home.aspx>. [30 October 2023]
- Krisnawati A, Adie MM. 2015. Selection of soybean genotypes by seed size and its prospects for industrial raw material in Indonesia. Proc Food Sci 3: 355-363. DOI: 10.1016/j.profoo.2015.01.039.
- Krisnawati A, Gatut-Wahyu AS, Adie MM. 2016. Screening of elite black soybean lines for resistance to rust disease, *Phakopsora pachyrhizi*. Biodiversitas 17 (1): 134-139. DOI: 10.13057/biodiv/d170120.
- Kusmiyati F, Sutarno S, Herwibawa B. 2019. Selection in M2 generation of black soybean using RAPD markers associated with salt tolerance. Intl J Adv Sci Res Eng 5 (6): 85-91. DOI: 10.31695/ijasre.2019.33259.
- Kuswantoro H. 2017. Genetic variability and heritability of acid-adaptive soybean promising lines. Biodiversitas 18 (1): 378-382. DOI: 10.13057/biodiv/d180149.
- Li Y-H, Zhao S-C, Ma J-X, Li D, Yan L, et al. 2013. Molecular footprints of domestication and improvement in soybean revealed by whole genome re-sequencing. BMC Genomics 14: 579. DOI: 10.1186/1471-2164-14-579.
- Ma L, Kong F, Sun K, Wang T, Guo T. 2021. From classical radiation to modern radiation: Past, present and future of radiation breeding. Front Public Health 9: 768071. DOI: 10.3389/fpubh.2021.768071.
- Mohsen G, Soliman SS, Mahgoub EI, Ismail TA, Mansour E, Alwutayd KM, Safhi FA, Abd El-Moneim D, Alshamrani R, Atallah OO, Shehata WF, Hassanin AA. 2023. Gamma-rays induced mutations increase soybean oil and protein contents. PeerJ 11: e16395. DOI: 10.7717/peerj.16395.
- Nilahayati N, Nazimah, Handayani RDS, Syahputra J, Rizky M. 2022. Agronomic diversity of several soybean putative mutant lines resulting from gamma-ray irradiation in M6 generation. Nusantara Biosci 14 (1): 34-39. DOI: 10.13057/nusbiosci/n140104.
- Nilahayati N, Rosmayati R, Hanafiah DS, Harahap F. 2018. Genetic variability and heritability on Kipas Putih soybean mutant lines using gamma rays irradiation (M3 generation). IOP Conf Series: Earth Environ Sci 122: 012041. DOI: 10.1088/1755-1315/122/1/012041.
- Nobre DAC, Sediama CS, Macedo WR, Piovesan ND, Arthur V. 2019. Gamma radiation to produce soybean mutants for better plant performance and chemical composition of seeds. Emirates J Food Agric 31 (7): 511-519. DOI: 10.9755/ejfa.2019.v31.i7.1983.
- Ojo GOS, Ayuba SA. 2016. Genetic variation and correlation among seedling and mature plant traits of soybean evaluated in acid sand culture and on acid/neutral soil fields of Nigeria. J Agric Sci 8 (5): 86-94. DOI: 10.5539/jas.v8n5p86.
- Puspitasari W, Tarmizi, Arwin. 2019. Evaluation of yield stability of black soybean mutant lines in ten environments. IOP Conf Ser: Earth Environ Sci 250: 012040. DOI: 10.1088/1755-1315/250/1/012040.
- Qin P, Wang T, Luo Y. 2022. A review on plant-based proteins from soybean: Health benefits and soy product development. J Agric Food Res 7: 100265. DOI: 10.1016/j.jafr.2021.100265.
- Ritonga AW, Chozin MA, Syukur M, Maharijaya A, Sobir S. 2018. Genetic variability, heritability, correlation, and path analysis in tomato (*Solanum lycopersicum*) under shading condition. Biodiversitas 19 (4): 1527-1531. DOI: 10.13057/biodiv/d190445.
- Sarker S, Rahman MS, Islam MR, Hasna S, Islam MS. 2014. Effect of gamma radiation on morpho-physiological characters of soybean. J Environ Sci Nat Resour 7 (2): 25-30. DOI: 10.3329/jesnr.v7i2.22199.
- Sivasubramanian S, Menon PM. 1973. Genotypic and phenotypic variability in rice. Madras Agric J 60: 1093-1096.
- Sumardi D, Pancoro A, Yulia E, Musfiroh I, Prasetyono J, Karuniawan A, Syamsudin TS. 2017. Potential of local black soybean as a source of the isoflavones daidzein and genistein. Intl Food Res J 24 (5): 2140-2145.
- Syukur M, Sujiprihati S, Yuniarti R. 2015. Teknik Pemuliaan Tanaman. Penebar Swadaya, Jakarta. [Indonesian]
- Xue H, Tian X, Zhang K, Li W, Qi Z, Fang Y, Li X, Wang Y, Song J, Li W-X, Ning H. 2019. Mapping developmental QTL for plant height in soybean [*Glycine max* (L.) Merr.] using a four-way recombinant inbred line population. PLoS One 14 (11): e0224897. DOI: 10.1371/journal.pone.0224897.