Agronomic performance of soybean mutant lines based on preliminary and advance yield at dryland area

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Abstract. Since 2013, researchers at ICABIOGRAD have established a development program for soybean varieties with bigger seeds, medium maturity and high productivity through cross-pollination combined with mutation by γ irradiation. In 2016, about 36 homozygous M_6 lines with high productivity and excellent agronomic characteristics were selected for subsequent preliminary and advanced yield test. The research aimed to study the agronomic performance of mutant lines (M_6 and M_7) and to select the best lines that will be used for adaptation testing at different locations and environments. The study was conducted at the Village of Gunung Menyan, Pamijahan Sub-district, Bogor during the first and second planting season of 2017. The experiment was arranged in a randomized block design with three replications. During the first planting season of 2017, a preliminary yield testing was conducted on 36 M_6 lines along with 4 check varieties. For the second season, 20 lines were selected along with 4 check varieties to be tested for advanced yield testing at the same location and method. Advanced yield trial showed that nine mutant soybean lines produced higher yields with excellent agronomic performance, which were 15−26% higher than Panderman's check varieties and 27−31% higher than the Anjasmoro check variety. The nine selected soybean line were SSD-C-M7-342-10, SSD-C-M7-350-18, SSD-D-M7-372-14, SSD-E-M7-387-1, Bulk-C-M7-458, Bulk-C-M7-493-1, Bulk-C-M7-493-20, Bulk-C-M7-499 and SSD-E-M7-404-18. These selected lines will be further assayed for adaptation at different locations and environments in the following year.

Keywords: soybean, mutant lines, yield test, high productivity.

1. Introduction

Soybean is the main food commodity after rice which needs more attention [1]. National production of soybean in Indonesia during 2015 was around 2.33 million tons, which was still far below national consumption, so that import of 1.37 million tons of soybean is still needed. To reduce soybean import, the Indonesian government has made various efforts to increase production, such as expanding the area of soybean plants and increasing productivity and quality in accordance with consumer preferences.

Imported soybeans generally have the large seed (>15 g/100 seeds). Therefore, they are prevalent in tofu and "tempe" industry. However, until now the number of soybean varieties with large seeds that have been released in Indonesia is still limited. Since 2013, ICABIOGRAD has been developing large-

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seeded soybean varieties by increasing genetic diversity through cross-pollination combined with mutation by γ ray irradiation [2].

The development of superior soybean varieties is a dynamic and continuous activity, depending on consumer preferences. The breeding procedures typically start with increasing the genetic diversity through various methods such as crossing, mutation by physical or chemical induction, and genetic transformation, followed by selection using various methods (such as bulk, pedigree and SSD method), preliminary and advanced yield test and multilocation yield test [3–7].

The use of irradiation techniques in plant breeding is well-established and does not need a long time to produce results. Gamma irradiation can penetrate seeds and alter the structure and number of chromosome pairs in plant seeds, which in turn causes changes the characteristics of the plants and their offspring. This phenomenon has been used to improve qualitative and quantitative plant traits, such as pest resistance, drought resistance, and early maturity [8–11] Increasing genetic diversity of soybean genetic resources by crossing potential parents (with early maturity and high yielding potential for example) has also been carried out in ICABIOGRAD.

The combination of cross-pollination and irradiation mutations provided more opportunity for success. Since 2009, ICABIOGRAD has been creating improved soybean varieties through mutations [12]. Currently, M_6 mutant lines with early maturity of <75−80 days, higher yield (15−33 g/plant or 15−59% higher than check varieties, and 25−93 pods/plant or 23−59% more than check varieties) have been obtained. These genetic materials need to be evaluated further in preliminary and advanced yield trial.

Preliminary and advanced yield trials are the stages to select the best promising lines before adaptation test at different locations (multilocation test). The best lines that are selected at the multilocation trial will have the opportunities to be released as newly improved varieties.

2. Materials and methods

2.1. Preliminary yield trial

The yield test was conducted during the first season of 2017, at the Village of Gunung Menyan, Pamijahan Sub-district, Bogor. The genetic material used here were 36 M_6 soybean selected lines that originated from irradiated homozygote lines (F10:G.10428 × Panderman) along with 4 check varieties (Mo:F10 G.10428 × Panderman, G.10428, Panderman and Anjasmoro). The experiment was designed in a randomized block design with three replications. Soil tillage was conducted optimally, and a total of 500 g limes (dolomite) with 1 t/ha of manure were applied a week before planting. The genotypes were planted in a plot of 2.4 m × 3 m, with 2 plants/hole. Fertilizers used were 50 kg of urea, 250 kg SP36 and 100 kg/ha KCl were applied 10 days after planted. Pest, diseases and weeds control were carried out as needed. Data were collected for uniformity of plant in the same lines, days to harvesting, seed yield and other agronomic characters.

2.2. Advanced yield trial

The experiment was conducted during the second planting season of 2017 at Pamijahan, Bogor District. The genetic materials used here were 20 M_7-selected lines from preliminary yield testing along with 4 check varieties. The experiment was designed in randomized block design with three replications. Soil tillage was conducted optimally, and a total of 500 g limes (dolomite) with 1 t/ha of manure were applied a week before planting. The genotypes were planted in a plot of 3 m × 4 m, with 2 plants/hole. Fertilizers used were 50 kg of urea, 250 kg SP36 and 100 kg/ha KCl were applied 10 days after planted. Pest, diseases and weeds control were carried out as needed. Data were collected for the flowering date, maturity date, seed yield per plant and seed yield per ha.

3. Results and discussion

3.1. Preliminary yield trial

The yield and other agronomic characters of the genotypes in the preliminary trial at Pamijahan during the first planting season of 2017 are shown in Table 1. There were two lines (SSD-C-M6-338-6 and

SSD-C-M6-342-10) that produced higher yield and better agronomic characters, such as pods number, compared to the four check varieties. Nine mutant lines produced higher yields (36−61% higher than Panderman, or 3−21% higher than Anjasmoro), these lines were: SSD-C-M6-338-6, SSD-C-M6- 342-10, SSD-C-M7-352-20, SSD-D-M6-372-14, SSD-E-M6-387-1, Bulk-C-M6-467, Bulk-C-M6-493, Bulk-D-M6-507 and Bulk-E-M6-567. These lines, along with several other lines, would be included in adaptation tests at various locations and seasons in the following year. The higher yield of SSD-C-M6-342-10 and SSD-C-M6-342-10 lines are mainly contributed by the higher number of pods/plant. Based on previous observation of Asadi et al. [4], the number of pods/plant has a direct effect on seed yield, and more pods will contribute to higher yield.

3.2. Advanced yield trial

The results of the advanced yield trial in Pamijahan during the second planting season of 2017 was shown in Table 3. There were nine soybean lines that produced yield 15−26% higher than Panderman and 20−31% higher than Anjasmoro (Table 3 and 4). These lines mature at 88−91 days, with the height of 41−50 cm, and their seed size ranged from 24−26 g/100 seeds. The seed size of the selected lines was much larger than the two check varieties (Panderman and Anjasmoro) (Table 3). The nine soybean selected lines were SSD-C-M7-342-10, SSD-C-M7-350-18, SSD-D-M7-372-14, SSD-E-M7-387-1, Bulk-C-M7-458, Bulk-C-M7-493-1, Bulk-C-M7-493-20, Bulk-C-M7-499 and SSD-E-M7-404-18. Among the nine selected lines, SSD-C-M7-350-18 and Bulk-M7-E-557 lines produced seed yield above 2.5 t/ha, which were 26% higher than Panderman, and 31% higher than Anjasmoro. The nine selected lines need to be tested in multilocations and seasons, and 1−3 of the best lines (with the highest potential and yield) will have the opportunity to be released as newly improved varieties.

Total seed yield is influenced by other agronomic characters, such as maturity date, plant height, number of branches, number of pods and the number of fertile nodes, as well as the size of seeds (100-seed weight). Correlation analysis between agronomic characters (Table 4) in advanced yield trial detected a significant positive correlation between seed weight (100-seed weight) and maturity date. On the other hand, seed weight had significant negative correlation with the number of pods. Seed yield was negatively correlated with the number of pods/plant, but had a significant positive correlation with seed weight (100-seed weight). The strong correlation means that 100-seed weight can be used as one of the determining characters in soybean selection for high productivity trait. However, to find out the direct or indirect effects between agronomic characters on seed yield, it is necessary to do path analysis between the agronomic characters [4,13,14].

Table 1. Yield and agronomic characters of M_6 soybean lines under preliminary yield trial at Pamijahan, Bogor (2017).

Mutant lines	DF	DM	PH	NB	NP	Yield (t/ha)
SSD-C-M6-338-6	**38**	**95**	**53.1**	**2**	**26**	**2.586**
SSD-C-M6 -342-10	**37**	**93**	**57.4**	**2**	**25**	**2.636**
SSD-C-M6 -350-18	37	93	49.5	1	22	2.072
SSD-C-M6-351-19	37	93	47.9	2	20	1.934
SSD-C-M6-352-20	**38**	**93**	**53.3**	**1**	**23**	**2.277**
SSD-C-M6-353-21	37	93	51.1	2	24	2.212
SSD-C-M6 -358-26	37	93	44.3	2	28	1.935
SSD-D-M6-360-2	37	93	50.2	2	22	2.152
SSD-D-M6-362-4	38	91	50.2	2	21	2.026
SSD-D-M6-372-14	**38**	**92**	**49.0**	**2**	**26**	**2.262**
SSD-D-M6-373-15	38	94	39.5	2	27	1.681
SSD-D-M6-377-19	37	91	44.4	3	25	1.791
SSD-E-M6-387-1	**37**	**93**	**50.6**	**2**	**22**	**2.363**
SSD-E-M6-411-25	38	93	49.6	3	28	1.829
SSD-E-M6-418-32	38	91	47.0	4	29	1.426
Bulk-C-M6-458	38	91	42.2	2	26	2.033
Bulk-C-M6-465	37	93	48.7	2	24	2.122
Bulk-C-M6-467	**37**	**93**	**50.7**	**2**	**25**	**2.248**
Bulk-C-M6-470	37	93	53.3	2	26	2.115
Bulk-C-M6-476	37	94	52.8	2	25	2.020
Bulk-C-M6-493	**38**	**95**	**53.6**	**2**	**26**	**2.269**
Bulk-C-M6-497	38	91	50.7	3	27	2.198
Bulk-C-M6-499	38	95	46.4	2	30	2.178
Bulk-C-M6-501	37	93	44.4	2	21	2.010
Bulk-D-M6-503	37	93	44.8	2	26	2.127
Bulk-D-M6-504	38	92	47.9	2	25	1.868
Bulk-D-M6-506	39	97	49.5	2	25	1.869
Bulk-D-M6-507	**37**	**93**	**51.7**	**2**	**23**	**2.238**
Bulk-D-M6-508	38	92	48.5	2	25	1.960
Bulk-D-M6-534	37	92	50.7	2	23	2.134
Bulk-D-M6-537	37	93	49.1	3	24	2.036
Bulk-E-M6-557	38	93	37.2	3	36	2.192
Bulk-E-M6-561	38	93	48.9	2	27	1.804
Bulk-E-M6-562	38	93	51.9	2	23	1.983
Bulk-E-M6-567	**38**	**93**	**46.1**	**3**	**29**	**2.339**
Bulk-E-M6-580	38	93	50.2	2	22	2.114
Mo (F10G.10428 × Panderman)	36	93	53.0	2	23	2.470
G.10428	37	93	47.8	1	14	2.418
Panderman	37	98	52.8	2	37	1.640
Anjasmoro	42	93	65.3	2	29	2.182
Mean	38	93	49.4	2	25	2.094
LSD 0.05 (%)	1	1	5.4	1	9	0.410

DF = days to flowering (days), DM = days to maturity (days), PH = plant height (cm), NB = number of branch/plant, PN = number of pod/plant.

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Table 2. Yield and agronomic characters of M_7 selected mutant lines in advanced yield trial at Pamijahan, Bogor (2017).

Genotypes	DM	PH	NB	NP	NN	100 SW	Yield (t/ha)
SSD-C-M7-338-6	88	45.4	1	24	7	23.74	1.707
SSD-C-M7-342-10	**89**	**47.7**	**1**	**23**	**6**	**24.89**	**2.334**
SSD-C-M7-350-18	**91**	**43.1**	**2**	**17**	**5**	**25.99**	**2.536**
SSD-C-M7-353-21	89.	50.3	2	16	5	23.87	2.298
SSD-D-M7-360-2	89	42.4	2	26	7	21.37	2.231
SSD-D-M7-372-14	**88**	**48.9**	**2**	**24**	**7**	**22.94**	**2.482**
SSD-E-M7-387-1	**91**	**50.1**	**1**	**21**	**7**	**25.56**	**2.460**
Bulk-C-M7-458	**89**	**48.0**	**1**	**23**	**7**	**24.79**	**2.425**
Bulk-C-M7-465	89	46.8	1	26	7	24.49	2.279
Bulk-C-M7-493-1	**90**	**47.6**	**1**	**27**	**7**	**24.37**	**2.346**
Bulk-C-M7-497	87	47.2	1	23	7	24.20	2.089
Bulk-D-M7-503	90	46.9	2	24	7	23.83	2.077
Bulk-D-M7-507	89	50.0	2	23	7	24.26	2.259
Bulk-D-M7-534	89	50.1	2	25	7	22.75	2.057
Bulk-C-M7-493-20	**89**	**40.7**	**2**	**29**	**6**	**23.76**	**2.525**
SSD-D-M7-374-16	89	46.5	1	20	7	25.32	2.130
Bulk-C-M7-499	**88**	**46.6**	**1**	**22**	**7**	**24.45**	**2.320**
SSD-C-M7-358-26	88	38.6	1	26	7	20.81	1.976
Bulk-C-M7-478	88	46.4	2	26	7	22.42	1.920
SSD-E-M7-404-18	**88**	**44.5**	**1**	**21**	**6**	**24.54**	**2.451**
Mo:(G10428 × Pand)-10-1	93	44.4	2	28	7	28.41	2.070
G.10428	91	32.6	1	18	5	34.08	1.534
Panderman	91	44.1	1	32	8	18.34	2.015
Anjasmoro	87	55.6	1	34	7	16.48	1.925
Mean	89	46.0	1.48	24.10	6.63	23.99	2.185
LSD 0.05	2	5.2	NS	8	NS	2.14	0.424

DM = days to maturity (days), PH = plant height (cm), NB = number of branch/plant, NP = number of pod/plant, NN = number of fertile nod, 100 SW = seed weight (g/100 seeds).

Table 3. Yield and agronomic characters of M_7 selected mutant lines in advanced yield trial at Pamijahan, Bogor (2017).

	DM (X1)	PH (X2)	NB (X3)	NP (X4)	NN (X5)	100 SW (X6)
PH	0.143^{ns}					
NB	0.192^{ns}	0.042^{ns}				
NP	-0.247^{ns}	-0.337^{ns}	0.010^{ns}			
NN	-0.284^{ns}	0.124^{ns}	-0.284^{ns}	**0.588****		
100 SW	**0.464***	0.398^{ns}	-0.319^{ns}	**-0.546***	-0.327^{ns}	

DM = days to maturity (days), PH = plant height (cm), NB = number of branch/plant, NP = number of pod/plant, NN = number of fertile nod, 100 SW = seed weight (g/100 seeds).

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4. Conclusions

In preliminary yield trial, nine mutant lines produced higher yield compared to check varieties. Of those nine lines, two M_6 lines produced the best yield and better agronomic characters. Those two lines were SSD-C-M6-338-6 and SSD-C-M6-342-10. In advanced yield trial, 9 of 20 selected M6-mutant lines produced higher yields, 15−26% higher than Panderman and 20−31% higher than Anjasmoro), and better agronomic characters. Those nine lines were SSD-C-M7-342-10, SSD-C-M7-350-18, SSD-D-M7-372-14, SSD-E-M7-387-1, Bulk-C- M7-458, Bulk-C-M7-493-1, Bulk-C-M7-493-20, Bulk-C-M7-499 and SSD-E-M7-404-18. The nine selected soybean lines need to be tested in multilocation and seasons in order to select one or more of the best selected promising lines (high potential and yield, and other excellent agronomic characters) will have opportunity to be released as newly improved varieties.

5. References

[1] Sudaryanto T and Swastika D K S 2007 Ekonomi kedelai di Indonesia *Forum Agro Ekon.* **12** 1–27

[2] Asadi 2014 Pendayagunaan kedelai introduksi dalam perbaikan varietas *War. Biog.* **10** 8–10

[3] Fehr W.R 1987 *Principles of Cultivar Development: Theory and Technique* (USA: Macmillian Publishing Company)

[4] Asadi, Soemartono, Woerjono M and Jumanto H 2004 Keefektifan metode seleksi modifikasi bulk dan pedigri untuk karakter agronomi dan ketahanan terhadap virus kerdil (SSV) galur-galur F_7 kedelai *Zuriat* **15** 64–76

[5] Acquaah G 2007 *Principles of Plant Genetic and Breeding* (USA: Blackwell Publishing)

[6] Carsono N 2008 Peran pemuliaan tanaman dalam meningkatkan produksi pertanian di Indonesia *Seminar on Agricultural Sciences, Januari 2008* (Tokyo) pp 1–8

[7] Miladinović J, Burton J W, Tubić S B, Miladinović D, Djordjević V and Djukić V 2011 Soybean breeding: comparison of the efficiency of different selection methods *Turkish J. Agric. For.* **35** 469–80

[8] Arefrad M, Nematzadeh G, Jelodar N B and Kazemitabar S K 2012 Improvement of qualitative and quantitative traits in soybean (*Glycine max* [L.] Merrill) through gamma irradiation *J. Plant Mol. Breed.* **1** 10–5

[9] Aminah, Nur A, Abdullah, Tahir N, Edy and Nuraeni 2015 Improving the genetic diversity of soybean seeds and tolerance to drought irradiated with gamma rays *Int. J. Curr. Res. Acad. Rev.* **3** 105–13

[10] Ulukapi K and Nasircilar A G 2015 Developments of gamma ray application on mutation breeding studies in recent years *International Conference on Advances in Agricultural, Biological & Environmental Sciences* (London: International Institute of Chemical, Biological, and Environmental Engineering) pp 31–4

[11] Beyaz R and Yildiz M 2017 The use of gamma irradiation in plant mutation breeding *Plant Engineering* ed S Jurić (INTECH) pp 33–46

[12] Asadi 2012 Sidik lintas karakter agronomi dan ketahanan hama pengisap polong terhadap hasil plasma nutfah kedelai *Bul. Plasma Nutfah* **18** 1–8

[13] Silva A, Sediyama T, Silva F, Bezerra A and Ferreira L 2015 Correlation and path analysis of soybean yield components *Int. J. Plant, Anim. Environ. Sci.* **5** 177–9

[14] Machado B Q V, Nogueira A P O, Hamawaki O T, Rezende G F, Jorge G L, Silveira I C, Medeiros L A, Hamawaki R L and Hamawaki C D L 2017 Phenotypic and genotypic correlations between soybean agronomic traits and path analysis *Genet. Mol. Res.* **16** 1–11