

Performance of Agronomic Characters of Soybean Lines Derived from Different Crossing

Keragaan Karakter Agronomi Galur-galur Kedelai dari Beberapa Persilangan Berbeda

Purwanto, Sutrisno, Heru Kuswantoro

Research Center for Food Crops, Research Organization for Agriculture and Food
National Research and Innovation Agency, Cibinong Science Center-Botanical Garden
Jl. Raya Jakarta-Bogor Km. 46 Cibinong, Bogor Regency, 16911
*E-mail: purwantorosp@gmail.com

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ABSTRACT

High productivity has always been a top priority in current soybean plant breeding activities. The availability of high yielding varieties would considerably increase the national soybean production and have a positive impact on farmers' income and welfare. This study aimed to evaluate selected soybean characters supporting high yield in several genotype crosses. The study was conducted in 2017 using 26 soybean lines derived from crosses among different parents. A randomized block design was used with three replications. The results showed that the soybean lines tested showed differences in days to flowering, days to maturity, plant height, number of branches per plant, number of productive nodes per plant, number of filled pods per plant, 100-seed weight, and seed yield per plot. The lines with the same days to maturity were related to selection process. Seed yield was significantly correlated with the number of productive nodes per plant, and the number of filled pods per plant. The parent of the cross had an effect on the grouping. There were two major groups with Tgm/Anj-773 as a separate group. The highest number of filled pod was achieved by Grb/Lwt-17, while the highest seed yield was noted in Tgm/Anj-773. In addition to the highest seed yield, Tgm/Anj-773 also had early days to flowering, as well as many number of branches, productive nodes and filled pods, thus this genotype is promising to be released as a variety with high yield potential.

Keywords: clustering, crossing, genotypic correlation, phenotypic correlation, soybean

ABSTRAK

Produktivitas tinggi selalu menjadi prioritas utama dalam kegiatan pemuliaan tanaman kedelai saat ini. Dengan diperolehnya varietas unggul maka peluang peningkatan produksi kedelai nasional dapat dicapai, dan hal ini akan berdampak positif terhadap pendapatan dan kesejahteraan petani. Penelitian ini bertujuan untuk mengevaluasi beberapa karakter terpilih yang mendukung hasil tinggi pada beberapa genotipe hasil persilangan. Penelitian dilakukan pada tahun 2017 menggunakan 26 galur kedelai yang berasal dari persilangan antar tetua yang berbeda. Penelitian menggunakan rancangan acak kelompok dengan tiga ulangan. Hasil penelitian menunjukkan bahwa galur-galur yang diuji menunjukkan

perbedaan umur berbunga, umur masak, tinggi tanaman, jumlah cabang per tanaman, jumlah buku produktif per tanaman, jumlah polong isi per tanaman, bobot 100 biji, dan hasil biji per tanaman. Galur dengan umur masak yang sama terjadi karena proses seleksi. Hasil biji berkorelasi nyata dengan jumlah buku per tanaman, dan jumlah polong isi per tanaman. Tetua persilangan memiliki pengaruh pada pengelompokan. Ada dua kelompok besar dengan Tgm/Anj-773 sebagai kelompok yang terpisah. Jumlah polong isi tertinggi dicapai oleh Grb/Lwt-17, sedangkan hasil biji tertinggi dicapai oleh Tgm/Anj-773. Selain hasil biji tertinggi, Tgm/Anj-773 juga memiliki umur berbunga genjah, jumlah cabang, buku subur dan polong isi yang banyak, sehingga berpeluang untuk dilepas sebagai varietas dengan potensi hasil tinggi.

Kata kunci: kedelai, korelasi fenotipik, korelasi genotipik, persilangan, pengelompokan

INTRODUCTION

High productivity has always been a top priority in current soybean breeding activities. By obtaining high yielding varieties, an increase in national soybean production can be achieved, and this will have a positive impact on farmers' income and welfare. The acquisition of high productivity soybean varieties can be done through crosses of soybean varieties that have superior traits and wide genetic variation (Jhilick *et al.* 2022). Therefore, the potential for achieving the combination of desired genetic traits is higher.

The characteristics of high yields are actually controlled by many factors, such as genetic and environmental factors, and the interaction between these two factors, making it difficult to determine the determinants of the yield. From a genetic point of view, the high yielding capacity of a variety is controlled by many genes. The selection of candidate varieties of soybeans with high yields needs to be studied more deeply on the single characteristic that is more dominant in controlling it. Approach

to the selection process of high yielding varieties can be done by observing the supporting factors of plant yields, especially vegetative and generative characters (Zhou *et al.* 2011). Some of the characters that support high productivity include plant height, number of pods per plant, number of seeds per pod, and seed size (Brensha *et al.* 2017). However, superior characters are rarely gathered in one variety (Eskandari *et al.* 2013, Silva *et al.* 2015). Plants that have large seed characters sometimes have a small number of seeds (Kuswantoro *et al.* 2021).

Identification of a single determinant of soybean yield can be done by classifying or grouping certain characters that are more dominant in determining high yields. Grouping was carried out on various lines resulting from crosses from parents with certain characters and then related them to the yields obtained (Vu *et al.* 2013). Certain characters that most dominantly affect yields can be determined as the dominant characters determining high yields (Malek *et al.* 2014). Several crosses between two lines or varieties have been carried out to combine unique traits that are thought to be associated with

high yields. This study aims to evaluate several selected characters supporting high yields in several lines crosses.

MATERIALS AND METHODS

Twenty-six soybean lines were used as the plant materials. The 26 soybean lines were derived from crosses among different parents (Table 1). These parents were germplasms collection of Indonesian Legume and Tuber Crops Research Institute (ILETRI). Those 26 soybean lines were grown in 2017 at Ngale Agricultural Technology Research and Assessment Installation (7°24'23.43" S 111°22'22.83" E with Vertisols soil type and 83 m above sea level).

The experiment used a randomized complete block design with three replicates. Each line was planted in two rows of three meters per row. The planting space was 40 cm x 15 cm with two plants per hill. The plants were fertilized using 75 kg/ha Urea, 100 kg/ha SP36, and 75 kg/ha KCl. To prevent seedling flies, 12.5 g carbosulfan was applied to every 1 kg seed. Weed controls were carried out at three, six, and nine weeks following planting.

Table 1. The 26 soybean lines derived from crosses among different parents

Code	Line	Crossing
G1	Anj/MLGG 0511-20	Anjasmoro x MLGG 0511
G2	Anj/MLGG 0511-29	Anjasmoro x MLGG 0511
G3	Brg/MLGG 0511-29	Burangrang x MLGG 0511
G4	Brg/Myp-14	Burangrang x Menyapa
G5	Brg/Myp-3	Burangrang x Menyapa
G6	Grb/Lwt-12	Grobogan x Lawit
G7	Grb/Lwt-17	Grobogan x Lawit
G8	Grb/Lwt-22	Grobogan x Lawit
G9	Grb/Myp-65	Grobogan x Lawit
G10	Mlbr/MLGG 0927-15	Malabar x MLGG 0927
G11	Sby/Pdm-651	Sibayak x Panderman
G12	Snb/MLGG 1087-147-2-2	Sinabung x MLGG 1087
G13	Snb/ MLGG 1087-147-2-7	Sinabung x MLGG 1087
G14	Snb/ MLGG 1087-148-2-1	Sinabung x MLGG 1087
G15	Snb/ MLGG 1087-148-2-10	Sinabung x MLGG 1087
G16	Snb/ MLGG 1087-148-2-3	Sinabung x MLGG 1087
G17	Snb/ MLGG 1087-210-1-1	Sinabung x MLGG 1087
G18	Snb/ MLGG 1087-210-4-12	Sinabung x MLGG 1087
G19	Tgm/Anj-743	Tanggamus x Anjasmoro
G20	Tgm/Anj-744	Tanggamus x Anjasmoro
G21	Tgm/Anj-773	Tanggamus x Anjasmoro
G22	Tgm/Anj-778	Tanggamus x Anjasmoro
G23	Tgm/Anj-871	Tanggamus x Anjasmoro
G24	Tgm/Anj-908	Tanggamus x Anjasmoro
G25	Tgm/Brg-558	Tanggamus x Burangrang
G26	Tgm/Brg-599	Tanggamus x Burangrang

The observation was conducted on days to flowering (DTF), days to maturity (DTM), duration of reproductive phase (DUR), plant height (HGT), number of branches per plant (BRC), number of productive nodes per plant (NOD), number of filled pods per plant (POF), number of unfilled pods per plant (POU), 100 seeds weight (SEW), and seed yield per plot (YLD). The data were analyzed using PKBT-STAT 3.1, and a dendrogram was done using Minitab 14. The phenotypic and genotypic correlations were estimated based on Singh and Chaudary (1985), and the significance was determined according to Dabi *et al.* (2016).

RESULTS AND DISCUSSION

The analysis of variance showed that all characters were significantly different (Table 2). It indicates that the genotypes were significantly different in all observed characters. Thus there is a variability of lines tested based on these characters. The variability of crosses, which is the genetic background of the tested lines, is thought to affect this significance.

Days to flowering had an average of 35 days with a range of 34-37 days. The earliest days to flowering was reached by Tgm/Anj-773, followed by Brg/Myp-14, Brg/Myp-3 and Snb/ MLGG 1087-148-2-1 (Figure 1). The lines with the longest days to flowering were achieved by Grb/Lwt-12 and Grb/Lwt-17. Soybean development towards early maturity is important because it can prevent plants from pests and environmental stresses. The line with the longest days to flowering was achieved by a line from Grobogan and Lawit crossing. In these lines, the days to flowering come from Lawit. Crosses Tanggamus x Anjasmoro resulted in various days to flowering.

Table 2. Analysis of variance of agronomic characters

Characters	MS Replication	MS Genotype	MS Error
DTF	12.17**	2.87**	0.53
DTM	17.23*	19.07**	5.28
DUR	42.63**	15.10**	6.03
HGT	236.75**	74.07**	19.62
BRC	0.39	1.05**	0.44
NOD	0.73	1.29**	0.55
POF	39.74	177.15**	49.25
POU	0.65*	0.46**	0.20
SEW	1.06	6.26**	1.68
YLD	0.25	0.53**	0.21

* = significant at 0.05, ** = significant at 0.01, DTF = days to flowering, DTM = days to maturity, DUR = duration of reproductive phase, HGT = plant height (cm), BRC = number of branches per plant, NOD = number of productive nodes per plant, POF = number of filled pods per plant, POU = number of unfilled pods per plant, SEW = 100 seeds weight (g), YLD = seed yield per plot (t/ha)

It seems that Tanggamus has earlier days to flowering than Anjasmoro because the lines with Anjasmoro as female parental cross (Anj/MLGG 0511-20 and Anj/MLGG 0511-29) had longer days to flowering. Days to flowering in this study is equivalent to the experiment of Kuswantoro *et al.* (2020). Differences in altitude affect flowering days, whereas higher places with lower temperatures resulted in longer days to flowering (Abugalieva 2016).

Days to maturity ranged from 77-85 days, with an average of 79 days. In general, the tested lines had early days to maturity. There were 17 lines with 77 days to maturity (Figure 2). These lines had the potential to be released as new superior varieties of early maturing soybean. However, it

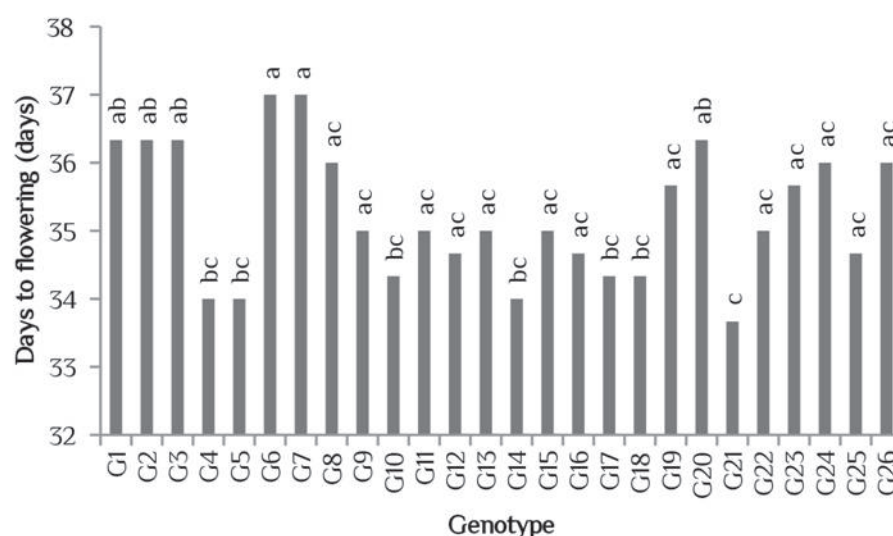


Figure 1. Days to flowering of soybean lines. The bars followed by the same letter were not significantly different at α 0.05.

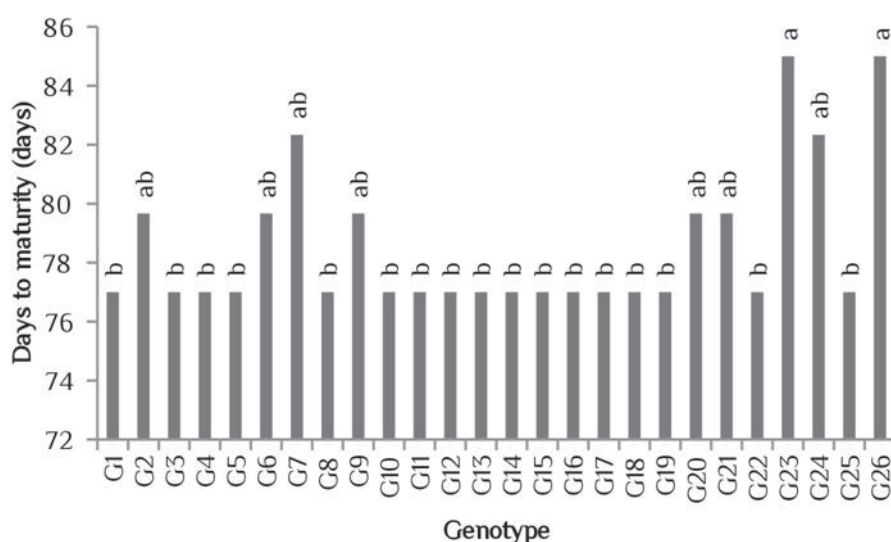


Figure 2. Days to maturity of soybean lines. The bars followed by the same letter were not significantly different at α 0.05.

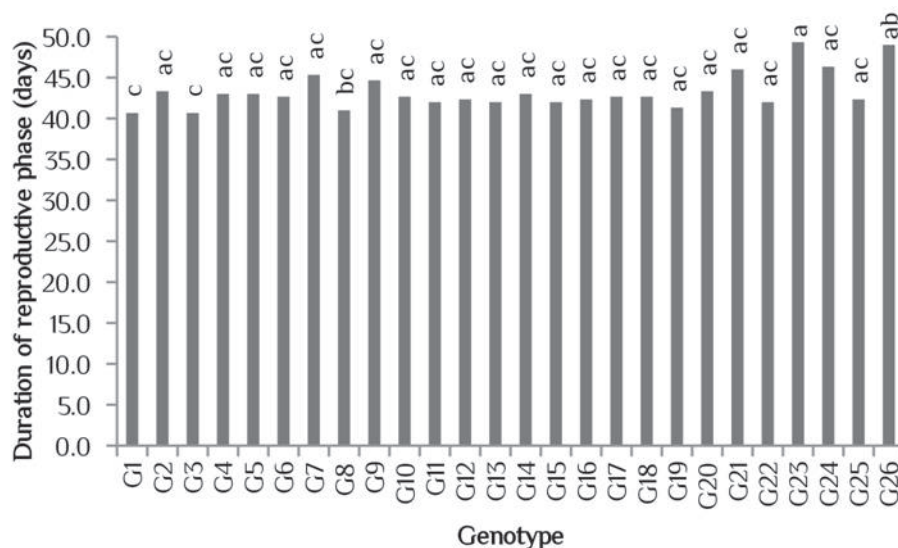


Figure 3. Duration of reproductive phase of soybean lines. The bars followed by the same letter were not significantly different at α 0.05.

seemed that environmental conditions such as were more influential than genetic factors, water conditions and soil type. The water availability was low, and the Vertisols was easy to crack when the soil water content was low. The line with the longest days to flowering did not show the longest days to maturity (Figure 2). Lines with the longest days to maturity generally came from crosses between Tanggamus and Anjasmoro. The days to maturity in this study were longer than those of Kuswanto *et al.* (2020), which used different crossbreeds where Korean varieties caused early days to flowering. The altitude or temperature of planting site affects days to maturity (Abugalieva 2016; Kuswanto *et al.* 2017).

The reproductive duration of soybean lines varied from 40.7-49.3 days (Figure 3). The lines with the shortest reproductive duration were Anj/MLGG

0511-20 and Brg/MLGG 0511-29. It is suspected that the short duration came from male parent MLGG 0511. The line with the longest reproductive duration was Tgm/Anj-871 followed by Tgm/Brg-599. The reproductive phase in this study is almost the same as Kuswanto *et al.* (2014) which reached 39-56 days, where Argomulyo and Anjasmoro reached 45 days. Reproductive duration allows soybeans to develop the reproductive organs, namely pods and seeds. He *et al.* (2018) states a correlation between growth period and plant height, pods per plant, pod length. However, in this study, there was no correlation between reproductive duration and other characters (Table 3).

Plant height (HGT) ranged from 52.8-72.0 cm with a mean of 59.1 cm. The highest HGT was

achieved by Brg/Myp-3 followed by Tgm/Anj-908 and Tgm/Anj-744, while the shortest was achieved by Tgm/Anj-743, followed by Mlbr/MLGG 0927-15 and Brg/Myp-14 (Figure 4). Plant height is very important because taller plants are easier to lodge, while the shorter plant may be resulted from waterlogging by the presence of heavy rains. Plant height in Brg/Myp-3 was more influenced by Menyapa, while at G20 (Tgm/Anj 744) it was influenced by Tanggamus and Anjasmoro. However, environmental factors can significantly affect plant height, because Tgm/Anj-743 which is the result of a cross between Tanggamus and Anjasmoro, shows the shortest plant height. In Mlbr/MLGG 0927-15 and Brg/Myp-14, plant height was more influenced by genetic factors, as Malabar and Burangrang are soybean varieties with relatively short plant figures. The plant height of this study was higher than that of Kuswanto *et al.* (2017a) and Kuswanto *et al.* (2020). The Tgm/Anj cross gave different plant heights at other locations (Kuswanto *et al.* 2017b).

The number of branches ranged from 1.9 to 4.5 with an average of 3.3 (Figure 5). Based on the characteristics of the parents, the Tanggamus and Anjasmoro lineage had more branches than that of Tanggamus but were still lower than Anjasmoro. The number of branches of the Tanggamus variety is between 3-4 while Anjasmoro

has 4-6 branches (Iletri 2016). These results indicate that male parents may control the number of branches in these lines because differences in male parents appear to significantly affect differences in the number of branches of the lineages. The mean of number of branches in the Tanggamus/Anjasmoro lineages in this study was higher than that reported by Kuswanto *et al.* (2014) but lower than Kuswanto *et al.* (2017b). The number of branches in the crosses between Grobogan/Lawit and Burangrang/Menyapa or Burangrang/MLGG 0927-11 also seems to be controlled by the male parent because there is a quite significant variation when the female parent is crossed with different male parents. Other conditions occurred in the lines with Sinabung as a female parent with relatively the same branches even though using different male parents. In the Sinabung lineage, the number of branches may be controlled by the female parent.

The number of productive nodes was relatively homogeneous in all tested lines, with variations between 8-10 nodes per plant (Figure 6). The highest number of productive nodes was produced by the Brg/Myp-3 line, while the least number was produced by the Anj/MLGG 0511-29 and Brg/Myp14 lines. The different parents, both male and female, seemed to produce relatively the same number of productive nodes. The Brg/Myp-3 and Brg/Myp-14 lines had

Table 3. Phenotypic and genotypic correlations among agronomic characters

	DTM	DUR	HGT	BRC	NOD	POF	POU	SEW	YLD
DTF	0.297	-0.070	0.110	-0.190	-0.057	0.337	0.337	-0.326	0.196
	0.621	0.257	0.343	-0.455	-0.078	0.624	0.670	-0.450	0.355
DTM		0.932**	0.095	-0.034	-0.017	0.053	0.057	0.023	0.062
		0.917*	0.382	-0.097	-0.020	0.130	0.197	0.023	0.167
DUR			0.057	-0.055	-0.013	0.023	0.029	0.052	0.047
			0.296	-0.263	-0.013	0.080	0.153	0.091	0.159
HGT				-0.140	0.304	0.059	0.003	-0.033	0.066
				-0.426	0.473	0.087	0.017	-0.094	0.097
BRC					0.617**	0.432*	0.036	0.001	0.036
					0.482	-0.001	0.117	-0.021	0.027
NOD						0.628**	0.037	-0.067	0.433*
						0.636	0.074	-0.208	0.494
POF							0.287	-0.080	0.683**
							0.742	-0.184	0.785
POU								-0.025	0.281
								-0.192	0.534
SEW									0.016
									-0.019

Upper = phenotypic correlation, Lower = genotypic correlation, * = significant at 0.05, ** = significant at 0.01, DTF = days to flowering, DTM = days to maturity, DUR = duration of reproductive phase, HGT = plant height (cm), BRC = number of branches per plant, NOD = number of productive nodes per plant, POF = number of filled pods per plant, POU = number of unfilled pods per plant, SEW = 100 seeds weight (g), YLD = seed yield per plot (t/ha)

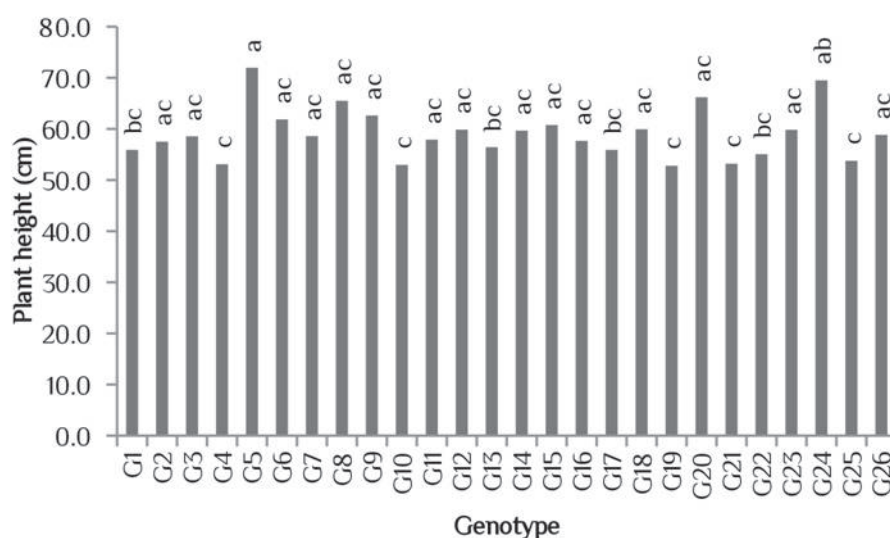


Figure 4. Plant height of soybean lines. The bars followed by the same letter were not significantly different at α 0.05.

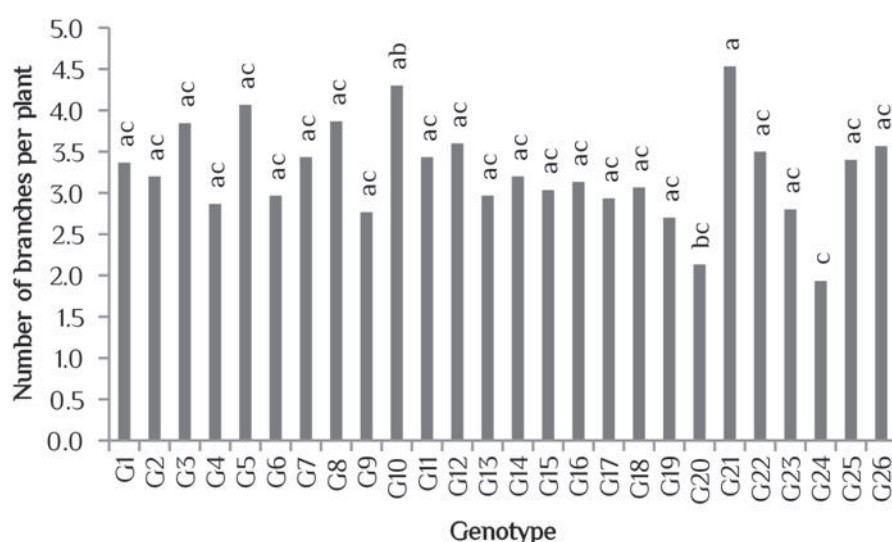


Figure 5. Number of branches of soybean lines. The bars followed by the same letter were not significantly different at α 0.05.

a different number of productive nodes even though the parents are the same. It happens because Brg/Myp-3 had characteristic similar to Menyapa with many productive nodes (Artari and Kuswanto 2017), while Brg/Myp-14 was similar to Burangrang with a few productive nodes (Iletri 2016).

The number of filled pods was significantly different among the tested lines, with the highest number of filled pods achieved by Grb/Lwt-17 which reached 55 pods, followed by Anj/MLGG 0511-20 with 52 pods (Figure 7). The lowest number of pods was achieved by Tgm/Brg-558 with 26 pods followed by Brg/Myp-14 with 28 pods. It is suspected that the small number of filled pods is caused by the female parent of Burangrang because Burangrang has large seeds. In general, large-seeded

soybeans have fewer filled pods than small or medium-seeded soybeans. Badiaraja *et al.* (2021) reported a maternal effect on the number of filled pods. The number of filled pods with Sinabung/MLGG 1087 crosses in this study was lower than the study of Artari and Kuswanto (2017). This is due to the different growing seasons, so that the availability of water during the study was lower than that in the study of Artari and Kuswanto (2017).

The least number of unfilled pods was achieved by Snb/MLGG 1087-210-1-1 followed by Snb/MLGG 1087-147-2-7. These two lines came from the same parent, namely Sinabung and MLGG 1087. The highest number of unfilled pods was achieved by Tgm/Brg-599 and Brg/MLGG 0511-29 (Figure 8). It is suspected that many unfilled pods

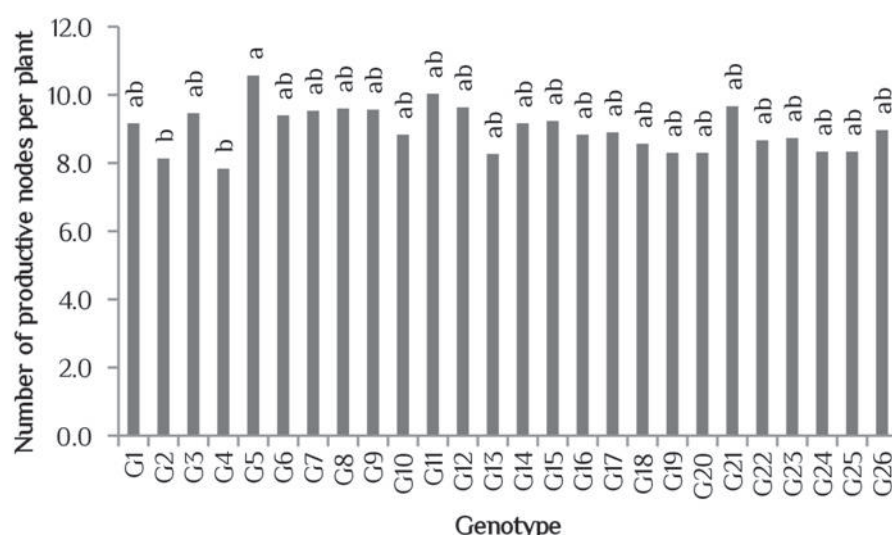


Figure 6. Number of productive nodes of soybean lines. The bars followed by the same letter were not significantly different at α 0.05.

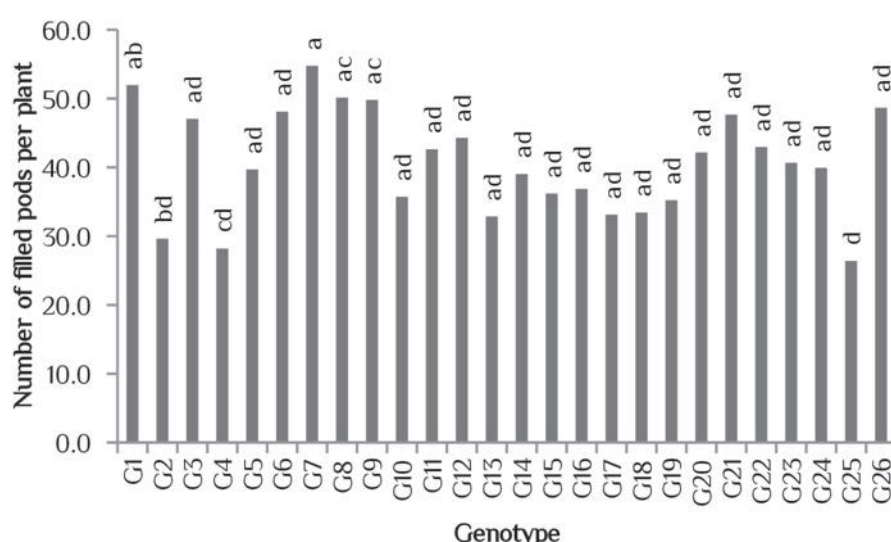


Figure 7. Number of filled pods of soybean lines. The bars followed by the same letter were not significantly different at α 0.05.

were produced by the parent of Burangrang because one of the parents of Brg/MLGG 0511-29 and Tgm/Brg-599 was Burangrang. Badiaraja *et al.* (2021) reported no maternal effect on the number of unfilled pods. The number of unfilled pods in this study was less than study of Kharel and Singh (2019), which reached eight pods. The unfilled pod was positively correlated with Cd and Zn content (Pirdashti 2017). The number of unfilled pods can also be caused by pod-sucking pests that reach an average of 44 pods (Kuswanto *et al.* 2019).

Seed size was measured based on SEW. The largest SEW was achieved by Mlbr/MLGG 0927-15 followed by Brg/Myp-14, while Grb/Lwt-17 followed by Grb/Lwt-12 achieved the smallest SEW. The average SEW is 12.68 g with a range of 9.87-

15.78 g (Figure 9). In general, the size of seeds is classified as medium, and only Mlbr/MLGG 0927-15 has a large seed size. Malabar is a large-seeded soybean variety so that its Mlbr/MLGG 0927-15 was also large-seeded. In contrast, Grb/Lwt-17 and Grb/Lwt-12 were similar to the parent of Lawit, who has small seeds. Crosses with small-seeded parents generally produce small seeds. Therefore, even though Grobogan is a parent with large seeds, because Lawit has small seeds, the descendants produce mostly small seeds. Badiaraja *et al.* (2021) also reported a maternal effect on seed size. Besides genetic factors, the environments such as low concentrations of Cd and Fe (Pirdashti 2017) and soil water availability (Wei *et al.* 2018; Wijewardana *et al.* 2019) may increase the seed sizes.

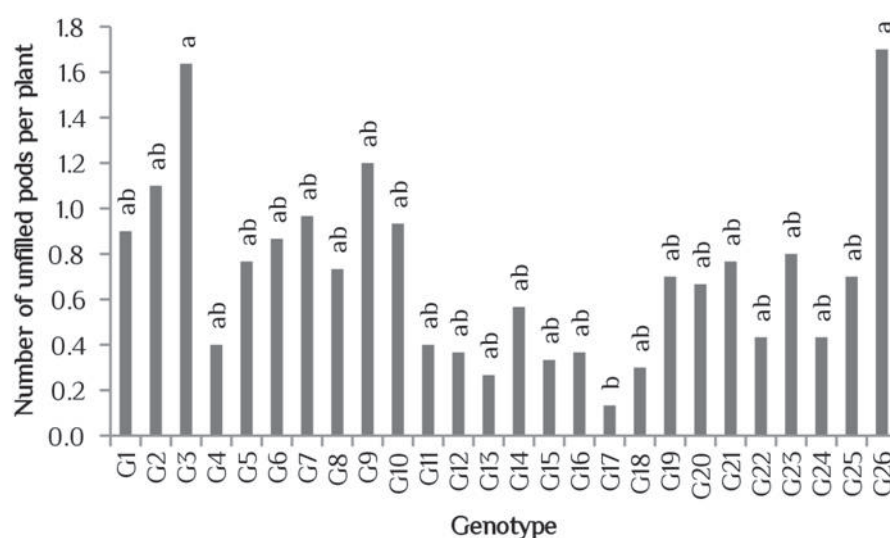


Figure 8. Number of unfilled pods of soybean lines. The bars followed by the same letter were not significantly different at α 0.05.

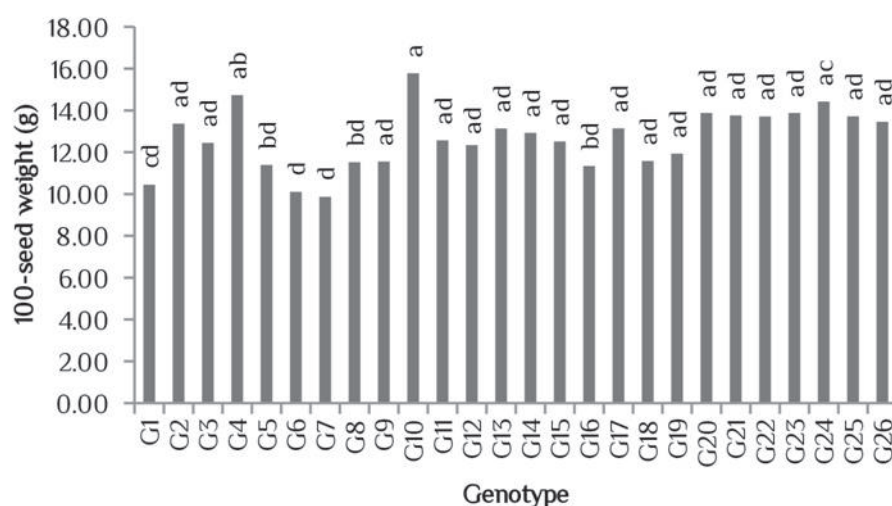


Figure 9. 100-seed weight of soybean lines. The bars followed by the same letter were not significantly different at α 0.05.

Seed yield ranged from 1.23-2.96 t/ha with a mean of 2.26 t/ha. The highest YLDs were achieved by Tgm/Anj-773 and Tgm/Anj-744 (Figure 10). These two lines are lines that come from the same cross. The lowest YLD was achieved by Tgm/Brg-558. The line with the highest YLD Tgm/Anj-773 and Tgm/Anj-744 was the progeny of a cross between Tanggamus and Anjasmoro. Tanggamus originated from a cross of Kerinci x No. 3911, while Anjasmoro was introduction variety from Mansuria. Therefore, there is no kinship between Tanggamus and Anjasmoro. The background of the cross is different from the two previous lines, so that Tgm/Brg-558 did not show a high YLD. Genetic and environmental factors may affect Tgm/Brg-558. At higher temperatures, the yield is also higher (Abugalieva 2016). Increased of soil water availability also increases seed yield (Wei *et al.* 2018;

Wijewardana *et al.* 2019). Nutrient content also affects seed yield (Taliman *et al.* 2019).

Significant phenotypic correlations were shown by DTM with DUR, BRC with NOD and POF, NOD with POF and YLD, and POF with the YLD. However, the genotypic correlation was only shown by DTM with DUR (Table 3). The significance of phenotypic and genotypic correlation suggest that these DTF had no effect on DTM. The DTM was more affected by the DUR. The significance of phenotypic correlation between YLD and NOD and POF suggest that YLD depend on NOD and POF. Balla and Ibrahim (2017) reported that YLD was correlated with number of pods. Mustofa *et al.* (2021) also stated that NOD was correlated with YLD. The direct effect of NOD on seed YLD was reported by Kumagai and Takahashi (2020). The correlation of YLD with NOD may be influenced

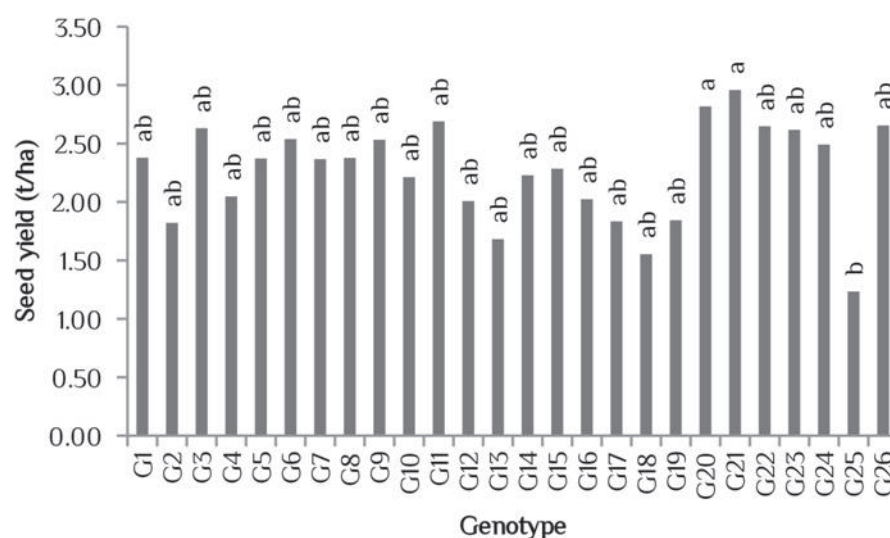


Figure 10. Seed yield of soybean lines. The bars followed by the same letter were not significantly different at α 0.05.

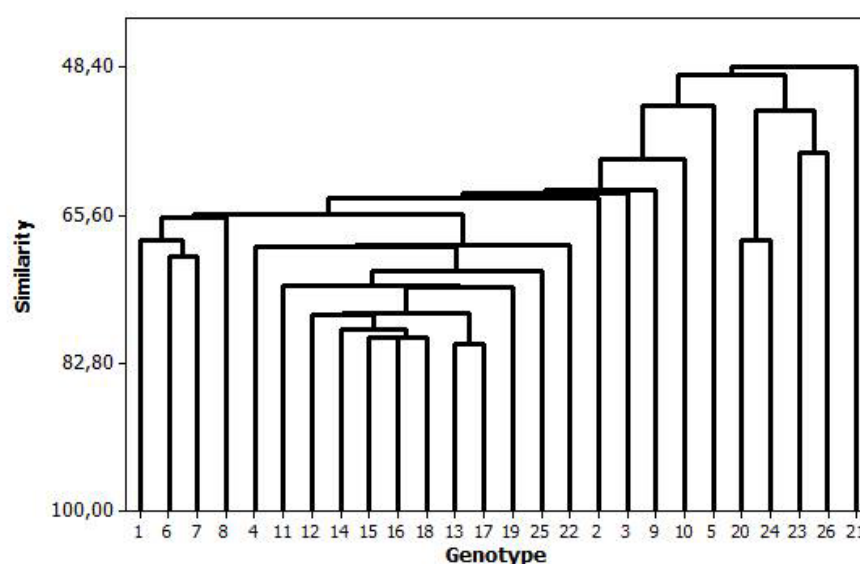


Figure 11. Dendrogram of soybean lines based on the agronomic characters

by the correlation of POF with NOD (Table 3). The indirect effect of NOD through POF was also reported by Mustofa (2021). The more NOD, the more POF. Mathematically, POF and SEW are the main components that affect YLD, but POF is often negatively correlated with SEW. Machado *et al.* (2017) and Mofokeng and Mashingaidze (2018) also reported a correlation between YLD and total pods. In this study, the genotypic correlation was only shown by DTM with DUR. With different plant materials, Kuswantoro *et al.* (2021) reported significant genotypic correlations between HGT and NOD, BRC and POF, and NOD and SEW. With the same plant materials, Balla and Ibrahim (2017) reported inconsistent genotypic correlation in two planting seasons. It suggest that the plant materials and environments affect genotypic correlation.

Based on Figure 11, there were two major groups.

The first group consisted of 25 lines, while the second group consisted of one line where Tgm/Anj-773 differed from the other 25 lines. Thus, Tgm/Anj-773 had a different character scale from the others, namely high seed yield, early flowering age, and higher number of branches, reproductive nodes, and pods. In another group with 25 members, this group was further divided into two smaller groups. The first group consisted of 21 lines, and the second group consisted of four lines. The group consisting of four lines had higher DTM, DUR, HGT, POF, SEW, and YLD than the group consisting of 21 lines. The grouping of lines is influenced by the character values of each line (Badiaraja *et al.* 2021b; Kuswantoro *et al.* 2020), and individuals in a group have similarities (Leite *et al.* 2018). Thus, the selection of a genotype in a particular group has implications for the selection

of a line with characteristics in that group.

CONCLUSION

All of the observed characteristics differed between the tested lines. The preceding selection resulted in a high number of lines with the same days to maturity. The number of productive nodes and pods were all found to be strongly correlated with seed yield per plot (t/ha). The parent had an impact on the grouping of the offsprings. Tgm/Anj-773 was a different group from the other two big groups. Tgm/Anj-773 had high seed yield, early flowering age, as well as many branches, productive nodes, and filled pods. Therefore, Tgm/Anj-773 can be used as a gene source with good agronomy characteristics and can be released as a superior variety after further assessment.

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