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Research article

Performance, similarity and genetic parameters of agronomical characters of soybean [*Glycine max* (L) Merrill.] germplasms

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Abstract

Plant phenotypic performance does not necessarily reflect the genetic appearance of a plant. Therefore, in addition to plant phenotypic performance, selection on the crossing genotypes should be done based on the relatedness and genetic parameters of the targeted character. Samples of 42 soybean accessions were grown using a randomized complete block design with three replications. Significant differences were found for all observed characters, except for days to flowering (DTF). Two asymmetrically large groups were obtained based on the agronomical characters. One of these two groups consisted of four subgroups. To increase genetic variability in a breeding program, genotypes from different groups can be crossed, especially genotypes with a long distance. Based on the coefficient of correlation, grain yield (YLD) was significantly correlated with plant height (HIG), number of reproductive nodes (NOD), number of filled pods (POF) and number of unfilled pods (POU). Broad genetic variability was found for YLD, POU, NOD, POU, number of branches (BRC) and weight of 100 grains (W100). The characters of HIG, NOD and W100 showed high heritability, while YLD showed medium heritability. Based on the heritability, the selection of a genotype with high YLD through only this character is less effective due to the high role of environmental factors. The high-yielding genotypes should be selected using other characters that are related to YLD. The most suitable character for this purpose is NOD because it was significantly correlated with YLD, had broad genetic variability and had high heritability.

Introduction

The performance of genotypes is very important because it often also describes genetic diversity. However, the same genotype can provide different performance outcomes if grown in different environments, where such differences are due to the genetic, environmental and genetic × environmental factors (Falconer, 1989). Quantitative and qualitative characters in a genotype can be used to differentiate this genotype from others (Smykal et al., 2008). Information on phenotypic diversity as a result of the interaction of genetic and environmental factors can also be used to predict the progress of selection (Hamawaki et al., 2012). Qualitative characters can be easily observed as they are controlled by a few genes, while differentiation of quantitative characters between genotypes is more limited because they are influenced by environmental factors (Perić et al., 2014). Assuming that different characters are caused

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by differences in the genetic constitution, the diversity of a plant genotype expressed in the plant's phenotypes can reflect its genetic diversity, especially for qualitative characters that are not influenced by the environment such as flower color (Sabaghpour, 2000).

In plant breeding programs the prediction of genetic relationships is particularly useful for managing germplasm, cultivar identification, assisting parents for crossbreeding and reducing the number of individuals that are required for sampling with a wide range of genetic diversity (Falconer, 1989; Souza and Sorrels, 1991; Thorman et al., 1994). Plant relationships can be expressed using phenetic and phylogenetic methods. Phenetic methods are based on phenotypic characteristic similarities (morphology, anatomy, embryology, phytochemistry), whereas phylogenetic methods are based more on the evolutionary value of each character (Radford and Caddell, 1986). This evolution can be traced to related plants such as *Arabidopsis thaliana* and *Glycine max* (Ashfield et al., 2014). Classification makes it easier to study and simplify the object of study. Closely related plants have similar anatomy, morphology and physiological processes, with the greater the similarity between living things, the closer the relationship; and vice versa (Rideng, 1989).

Morphological characters can also be used to classify the relationships between the genotypes (Smykal et al., 2008; Mazid et al., 2013). Characterization of morphological properties is also considered to accurately assess agronomical characters and the classification of plant taxonomy (Soenarsih et al., 2012; Jost, 2017). Phenotypic similarity is a relationship based on the analysis of a number of phenotypic characters of an organism. The relatives-relationship between two individuals or the population can be measured on the basis of the similarity of a number of characters with the assumption that different characters are caused by different genetic background. This was similar to Dong et al. (2014) who reported that China has more diverse vegetable soybean germplasms than other areas. Other studies in soybean agro-morphology characters also have been reported such as developing core collections of the soybean germplasm (Oliviera et al., 2010; Kaga et al., 2012), root growth and architecture (Manavalan et al., 2010), leaf morphology and stomatal conductance (Tanaka et al., 2010), and the relationship of agro-morphology characters to yield (Kumar et al., 2015a).

The status of genetic diversity is a major factor in the management and the use of soybean germplasm, where the range and the distribution of genetic diversity may affect the priority of germplasm collection management (Chen and Nelson, 2005). The wide genetic diversity in a population is indicated by the presence of distance relationships, where a close relationship indicates the narrowness of genetic diversity because many of the same traits are shared by each accession. Finally, this leads to consequences on knowledge of the relationship among the accession and the strategy development of genetic diversity in breeding programs (Bretting and Widrlechner, 1995). Relatives-relationship is also closely related to heritability because the magnitude of heritability determines the degree of similarity between the parents and their offspring. High heritability indicates that a character is not much affected by the environment. Heritability is also associated with genetic diversity. Wysmierski and Velo (2013) stated that genetic diversity can be assured through the genetic base concept, and a relative genetic contribution can be calculated through the coefficient of parentage between the ancestors and the cultivars.

The genetic constitution of the plant is not always seen in plant performance. Different populations in the same environment will provide different genetic parameters. Therefore, genetic parameters are needed to predict the genetic constitution and characteristics that are effective for genetic improvement through selection. Usually, selection of certain character is not done on that character only, but also on other supporting characters. Selection will be effective if the selected character has high heritability and wide genetic variability. In addition to genetic parameters, the kinship relationship in the population reflected in similarity also plays an important role, since it can distinguish one line from another. The purpose of this research was to study the similarity and genetic parameters of agronomical characters of soybean reflected in the performance of agronomical characters. The obtained genetic and similarity parameters can be used for soybean selection with high seed yield.

Materals and Methods

Study site and design

The study was carried out at the Jambegede Research Station, Malang, East Java Province, Indonesia, in Dry Season II from August to November 2016. This site is located at 8.174951°S, 112.559634°E, at an altitude of 308 m above sea level. The soil type of this site was associated with Entisols-Inceptisols. A randomized complete block design with three replications was used for the experiment design with 42 germplasm accessions as the plant material. The 42 germplasm samples were from the collection of the Indonesian Legume and Tuber Crops Research Institute. The origins of the germplasm used in this study were from some provinces in Indonesia and other countries (Table 1). These germplasm represent the production center of soybean in Indonesia and the genotype of some countries (Taiwan, Marroco, the USA).

Soil tillage

Before the soil was plowed, the planting area the litter of previous plants was removed. Soil tillage was conducted using a tractor until the soil was lumpy, and then the soil was leveled using a rake. Irrigation/drainage canals were made every 3 m with a 20 cm width and 40 cm depth.

Planting

The plant material consisted of 42 soybean germplasm samples that originated from Indonesian landraces and introduced varieties from other countries. Before planting, the seeds were treated using insecticide with the active compound being carbosulfan. Planting was conducted on 1 August 2016. Every genotype was grown in two rows with 3 m length, where the space between the rows was 40 cm. The space between the hills was 15 cm with 3−4 seeds per hill. After 7 d, the plants were thinned to two plants per hill.

Table 1 Origin of germplasm

Number	Genotype	Origin
1	MLGG 0009	Jember, East Java, Indonesia
2	MLGG 0078	B1312/B317 (Bogor Research Institute for Food Crops)
3	MLGG 0091	GM907SI (Sukamandi Research Institute for Food Crops)
4	MLGG 0092	GM911SI (Sukamandi Research Institute for Food Crops)
5	MLGG 0103	Lee (variety), USA
6	MLGG 0106	Sidoarjo, East Java, Indonesia
7	MLGG 0109	Morocco
8	MLGG 0124	Lampung, Indonesia
9	MLGG 0135	Jember, East Java, Indonesia
10	MLGG 0164	Nganjuk, East Java, Indonesia
11	MLGG 0169	Magetan, East Java, Indonesia
12	MLGG 0173	Madiun, East Java, Indonesia
13	MLGG 0195	AVRDC, Taiwan
14	MLGG 0196	Davros, Indonesia
15	MLGG 0201	Taiwan
16	MLGG 0233	Taiwan
17	MLGG 0276	Banyuwangi, East Java, Indonesia
18	MLGG 0375	Garum, Blitar, East Java, Indonesia
19	MLGG 0488	Gunungkidul, Yogyakarta, Indonesia
20	MLGG 0493	Gunungkidul, Yogyakarta, Indonesia
21	MLGG 0523	Hitam (local variety), Indonesia
22	MLGG 0529	Indonesia
23	MLGG 0564	No. 27 (variety), Indonesia
24	MLGG 0582	B629 (Bogor Research Institute for Food Crops)
25	MLGG 0583	B630 (Bogor Research Institute for Food Crops)
26	MLGG 0650	B1394 (Bogor Research Institute for Food Crops)
27	MLGG 0652	B1396 (Bogor Research Institute for Food Crops)
28	MLGG 0656	Kebumen, Central Java, Indonesia
29	MLGG 0695	B831/B452 (Bogor Research Institute for Food Crops)
30	MLGG 0707	Indonesia
31	MLGG 0714	Indonesia
32	MLGG 0739	Indonesia
33	MLGG 0745	Metro
34	MLGG 0757	B1338 (Bogor Research Institute for Food Crops)
35	MLGG 0760	B1340 (Bogor Research Institute for Food Crops)
36	MLGG 0817	Lombok Tengah, West Nusa Tenggara, Indonesia
37	MLGG 0873	Tabanan, Bali, Indonesia
38	MLGG 0879	Blitar, East Java, Indonesia
39	MLGG 0892	Pasuruan, East Java, Indonesia
40	MLGG 0896	Ponorogo, East Java, Indonesia
41	MLGG 0989	Dompu, West Nusa Tenggara, Indonesia
42	MLGG 1004	Lombok Timur, West Nusa Tenggara, Indonesia

Cultural practices

Application of fertilizers was carried out at the planting time using Zwavelzure Ammonia (75 kg/ha), Super Phosphate (100 kg/ha) KCl (36, 75 kg/ha) and manure fertilizer (1 t/ha). To prevent the weed growth invading the soybean plants, weed control was manually performed at 14 and 28 d after planting (dap). Pests and diseases were intensively controlled by monitoring.

Data analysis

The statistical software package PKBT STAT 1.0 (Bogor Agricultural University, Bogor, Indonesia) was used to perform the analysis of variance and significance was tested at the $p < 0.05$ level. Based on this analysis, the expected mean squares were calculated to estimate the genetic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) according to Singh and Chaudhary (1981). The genetic standard deviation (GSD) was used to classify the genetic variability criteria. Broad genetic variability was determined if GCV ≥ 2GSD, while narrow genetic variability was concluded if GCV < 2GSD. Broad sense heritability was also calculated using GCV and PCV according to Falconer (1989). The similarity was performed using the NCSS 11 statistical software program (NCSS 11 Statistical Software, 2017).

Results and Discussion

Agronomical character performance

The phenological character is important because the plant life cycle depends on it. Of the two phenological characters observed only days to maturity (DTM) was significantly different (Table 2), while days to flowering (DTF) were not significantly different because soybean has different durations of pod filling, resulting in different DTM values (Boerma and Ashley, 1988). Furthermore, in the equatorial region, there is no large annual difference in the length of the day so that DTM is relatively the same. This can be seen in previous research (Kuswantoro et al., 2014b) where the vegetative phase of the subtropical varieties grown in a more tropical area was shorter due to the different daylength and temperature. However, the tested germplasm differed in all the vegetative and reproductive characters. This indicated that based on the observed vegetative and reproductive characters, there was at least one accession different from the others. This difference illustrates the diversity present in soybean germplasm. Liu et al. (2016) also reported rich phenotypic variations in their population, and this variation should be confirmed through the existence of genotype, environment, and genotype × environment interaction.

Table 2 Analysis of variance of agronomical characters of soybean germplasm

	MS replication	MS genotype	MS error
DTF	20.39	16.15	12.89
DTM	163.91**	44.54**	11.51
HIG	14.84	472.21**	18.06
BRC	0.00	0.80**	0.28
NOD	3.61	23.03**	5.57
POF	177.12	186.19**	61.76
POU	2.04	8.21**	3.54
W100	72.53	13.37**	0.49
YLD	3.72**	0.91**	0.31

MS = mean square; DTF = days to flowering; DTM = days to maturity; HIG = plant height; BRC = number of branches/plant; NOD = number of reproductive nodes/plant; POF = number of filled pods/plant; POU = number of unfilled pods/plant; W100 = weight of 100 grains; YLD = grain yield.
** = significant at level of 0.01.

DTF marks the end of the vegetative phase and the early part of the reproductive phase, especially in the determinate type of soybean. Growth in the vegetative phase is required to make useful leaves and to undertake photosynthesis. DTF in this study varied with the highest number of genotypes in 37−38 d (Fig. 1). The range in DTF was 33−45 d. Kuswantoro (2017a) and Kuswantoro (2017b) also reported DTF in two different populations equivalent to this study. In the current study, there were seven accessions that had DTF ≤ 35 d, and only one accession had a DTF of 45 d. DTF is very useful for crop production because with a short DTF a plant will prolong its reproductive duration and that will ultimately increase soybean yield. Therefore, the accession with the shortest DTF can be used as a gene source to extend the reproductive duration.

Harvesting is a major problem in increasing soybean production. An earlier harvest is desirable because it can increase the production per unit time. The faster the harvest, the sooner the land can be used for other cultivation. There was no germplasm tested that had a DTM under 80 d (Fig. 1), but there was germplasm with DTM more than 100 d. Hence, the early gene source was not obtained in this population. Germplasm from subtropical regions will become more mature if grown in tropical regions (Kuswantoro et al., 2014b), and *vice versa* (Kuswantoro et al., 2017).

Plant height (HIG) and number of branches (BRC) are plant characters that are established in the vegetative phase. The HIG of the germplasms tested was largely 72−84 cm (28 of 42 genotypes) as shown in Fig. 2A. Such an HIG range a good for soybean because the soybean plant does not easily collapse. A taller plant will easily collapse due to the wind. Another factor that needs to be considered in taller plants is that assimilates from the photosynthetic activity will be distributed farther to supply the nutrition for growth and development of plant organs. Consequently, some assimilate losses occur during the pod-filling period and the grains become smaller. The HIG of these accessions was similar to the soybeans grown in China that can reach an average of 85.6 cm with a range of 45.8−127.2 cm (Liu et al., 2017).

The number of branches (BRC) ranged from 35 branches per plant. Most of the accessions tested had a mean BRC of about 3.5 branches, which translates to 3−4 actual branches. This result was better than in the studies by Kuswantoro (2017a) and Kuswantoro (2017b) which had averages of only 2.3 and 2.8, with the largest BRC values being 3.2 and 4.2 branches, respectively. There were two accessions having a BRC of 5 (Fig. 2B) which was higher than the BRC reported by Liu et al. (2017) with 0.3−3.4 branches and a mean of 1.2, although they were grown at a wider spacing.

The greatest number of reproductive nodes (NOD) was in the class 21−25, with one accession having 30 nodes (Fig. 3A). Kuswantoro (2017a) and Kuswantoro (2017b) reported that the NOD of soybeans grown under acidic conditions only reached 11 and 17.3 nodes, respectively. The site of the reproductive nodes is where the pods are located. Therefore, NOD is important as a soybean agronomical character because it affects the number of pods produced. Not every node has the same number of pods. Liu et al. (2017) reported a mean NOD of 17 on the main stem with the highest NOD value being 21.4 nodes.

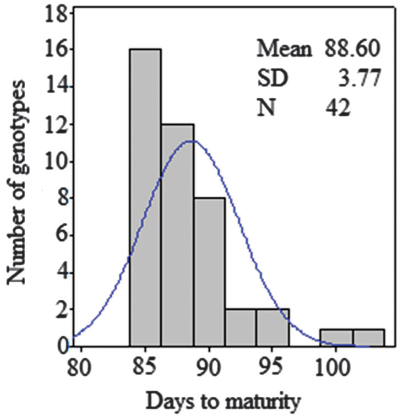
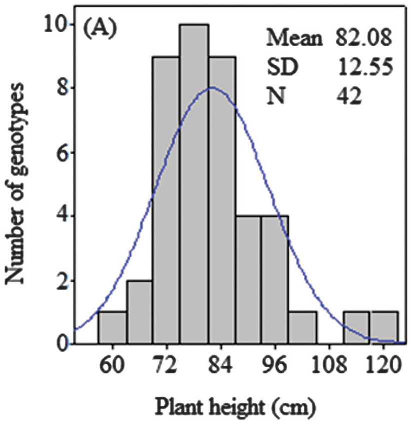


Fig. 1 Days to maturity of soybean germplasm, where N = number of accessions



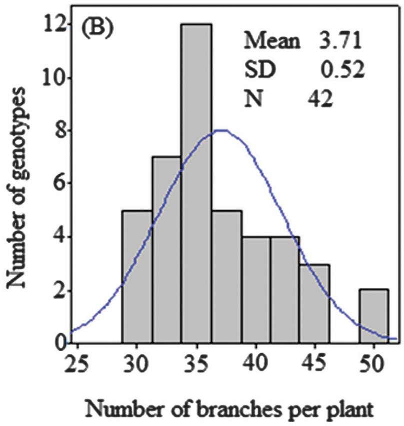


Fig. 2 Soybean germplasm: (A) plant height; (B) number of branches, where N = number of accessions

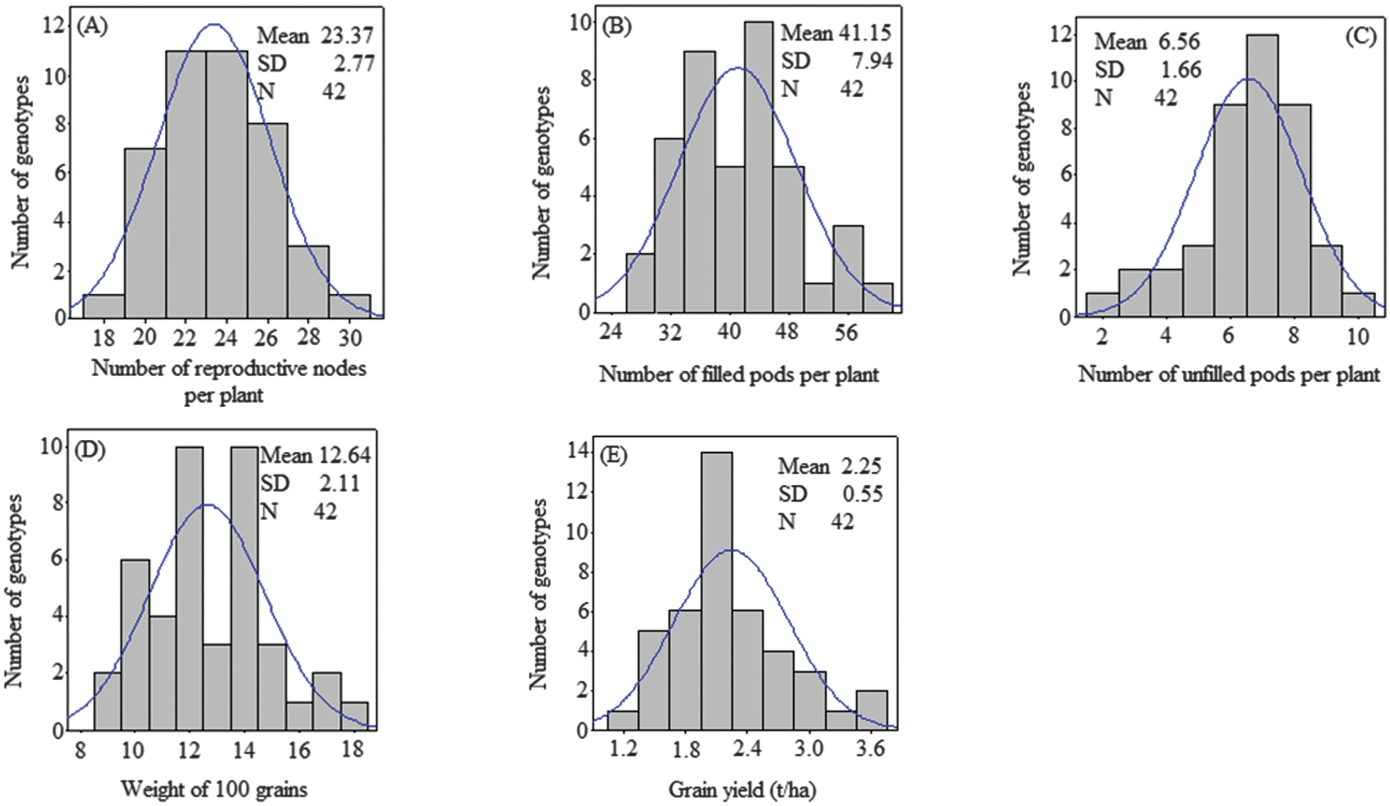


Fig. 3 Reproductive characters of soybean germplasm: (A) number of reproductive nodes per plant; (B) number of filled pods per plant; (C) number of unfilled pods per plant; (D) weight of 100 grains; (E) grain yield, where N = number of accessions

The number of filled pods (POF) and number of unfilled pods (POU) are important components of the yield. Accessions with a large POF were found in the classes of 44 and 36 pods. There were five accessions with a POF of more than 55 pods (Fig. 3B). Most of the POU values in this study were in the class of 6−8 unfilled pods (Fig. 3C). The POF and POU in the current study were better than in Khan et al. (2015), but the POF was lower than for Kumar et al. (2015b). Various factors can affect the occurrence of unfilled pods, such as pest attacks, drought or lack of nutrients. In the current study, cultivation was optimal so the results were assumed to be due to genetic factors.

The yield quantity and the soy product quality are determined by single grain size (Kato et al., 2014). The grain size (weight of 100 grains, W100) of the tested germplasm also varied, being mostly 12–14 g (Fig. 3D). Currently, large grains are preferred by farmers in Indonesia, because such grain is suitable for making tempeh, a typical Indonesian food (Krisdiana, 2007). In Indonesia, a W100 value higher than 15 g is classified as large grain (Adie and Krisnawati, 2013). This classification is different to others country such as Japan where W100 of 20.0 g is still classified as small grain (Kato et al., 2014). Four accessions had W100 greater than 15 g. These can be used as a source of soybean genes for developing large grain varieties. Zhang et al. (2015) reported that the W100 of a genotype could reach up to 40.35 g, and they also found seven genotypes with W100 higher than 30 g. The W100 values in the current study were more comparable to those reported by Khan et al. (2015).

The grain yield (YLD) of the germplasms varied with a mean of 2.25 t/ha. The greatest number of germplasms were in the range 2.0−2.2 t/ha (Fig. 3E). The lowest YLD was 1.2 t/ha, while the highest YLD was 3.6 t/ha. There were two accessions with YLD of about 3.6 t/ha which could be used to improve the soybean grain yield. This condition is almost the same as for soybeans grown in Brazil that had a maximum of about 3.6 t/ha for the 45 genotypes tested (Gomez et al., 2014), and in Bangladesh where the highest yield was 3.76 t/ha (Khan et al., 2015).

Similarity

Similarity is often used in grouping processes by performing a data classification that has similar characteristics. Similarity is one of the methods to compare the distance of similarity of two phenomena. The proximity of germplasms relationships is essential in breeding programs. Based on the dendrogram (Fig. 4), there were two large groups of germplasm that were not symmetrically grouped as one group consisted of only four accessions and the other group consisted of many accessions divided into other four groups. Liu et al. (2016)

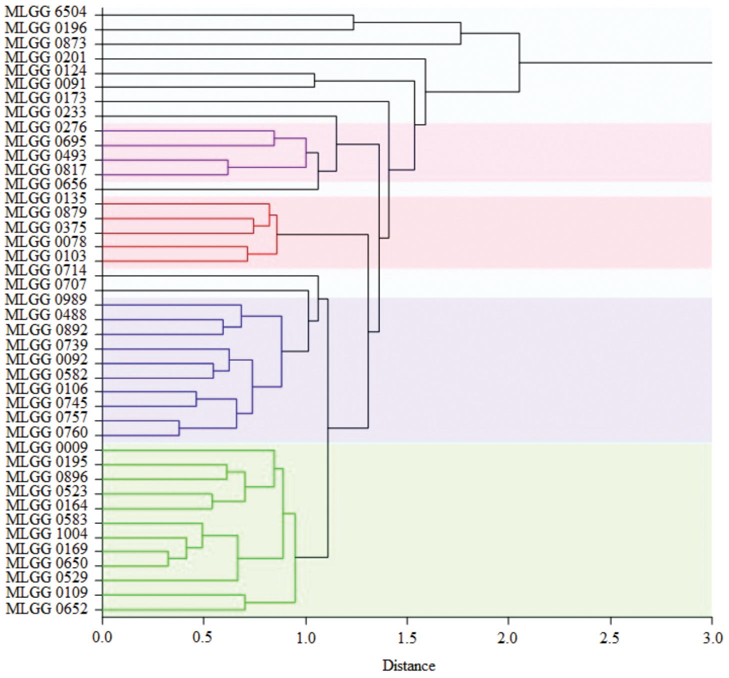


Fig. 4 Relatedness among soybean germplasms (derived using NCSS 11 Statistical Software, 2017)

also obtained two major groups of tested accessions. These two groups also partially reflect the difference in the origin of the accessions. Marconato et al. (2016) reported that the groupings obtained did not necessarily correspond to the geographical origin of the accessions. The first group consisting of four accessions was strictly separated from the second group. These four accessions (MLGG 564, MLGG 0196, MLGG 0873 and MLGG 0201) can be used as parent genotypes to the other 38 accessions. However, high genetic diversity will be obtained if the four accessions are crossed with the green and blue groups (Fig. 4) because they have the greatest distance (Dong et al., 2014). These four accessions had four differentiating characters from other accessions, namely higher values of DTF, DTM and HIG. The YLD in this gray group were also higher, but still lower than the red group. The purple group, if compared to the other three groups, had higher BRC, NOD and POU. The red group compared with the other two groups had a higher POF and YLD. The blue group compared with the green had a small POF, but W100 was larger (Table 3).

The similarity between genotypes is measured by the observed characters. Genotypes with similar characters will cluster in the same group. Correlations between characters contribute to similarity since correlated characters provide identical characteristics in an individual. Positive correlations were achieved between some agronomical characters. However, negative correlation was also present in the current study. There was a significant negative correlation for POU with DTM, HIG, POF and YLD (Table 4). YLD is the most important character in plant breeding because genetic improvement is directed at this character (Fehr, 1978). YLD characters are supported by other characters, especially POF and W100. Positive correlations were obtained for YLD with HIG, NOD and POF, whereas negative correlations were obtained for YLD and POU. In other words, increasing HIG, NOD and POF will increase YLD, but increasing POU will decrease YLD. Similar conditions have also been reported by some authors, where YLD increased with increasing HIG and NOD (Liu et al., 2017), and POF (Kuswantoro et al., 2014a), but YLD decreased with increasing POU (Kumar et al., 2015a).

Table 3 Means of agronomical characters in groups of soybean germplasm

	Gray	Purple	Red	Blue	Green
DTF	39.8 ± 1.7	36.8 ± 2.2	36.8 ± 1.1	35.5 ± 1.6	37.4 ± 0.9
DTM	91.6 ± 5.4	85.8 ± 1.1	89.1 ± 2.3	87.4 ± 1.4	87.3 ± 2.1
HIG	89.0 ± 18.8	70.7 ± 6.1	91.2 ± 8.5	76.0 ± 5.4	84.8 ± 7.0
BRC	3.6 ± 0.6	4.4 ± 0.4	3.5 ± 0.4	3.3 ± 0.2	3.9 ± 0.3
NOD	25.4 ± 3.7	26.3 ± 2.2	24.1 ± 1.2	21.0 ± 1.8	23.0 ± 2.4
POF	45.9 ± 11.2	42.5 ± 3.6	49.2 ± 2.8	34.4 ± 3.8	41.8 ± 6.8
POU	6.0 ± 3.2	8.6 ± 0.5	4.1 ± 0.9	6.9 ± 1.2	7.0 ± 0.6
W100	12.48 ± 3.22	13.04 ± 2.06	12.46 ± 1.51	13.88 ± 1.29	11.03 ± 1.18
YLD	2.3 ± 0.9	2.0 ± 0.3	3.0 ± 0.4	1.9 ± 0.3	2.2 ± 0.3

DTF = days to flowering; DTM = days to maturity; HIG = plant height; BRC = number of branches/plant; NOD = number of reproductive nodes/plant; POF = number of filled pods/plant, POU = number of unfilled pods/plant; W100 = weight of 100 grains; YLD = grain yield.

Table 4 Correlation among agronomical characters of soybean germplasm

	DTM	HIG	BRC	NOD	POF	POU	W100	YLD
DTF	0.177	0.322*	0.007	0.225	0.167	-0.230	-0.041	0.144
DTM		0.461**	-0.297	0.091	-0.041	-0.456**	0.175	0.248
HIG			-0.221	0.422**	0.359*	-0.544**	0.107	0.437**
BRC				0.488**	0.231	0.380*	-0.331*	-0.082
NOD					0.510**	-0.029	-0.037	0.312*
POF						-0.387*	-0.443**	0.379*
POU							-0.246	-0.465**
W100								0.068

DTF = days to flowering; DTM = days to maturity; HIG = plant height; BRC = number of branches/plant; NOD = number of reproductive nodes/plant; POF = number of filled pods/plant; POU = number of unfilled pods/plant; W100 = weight of 100 grains; YLD = grain yield.
** = significant at level of 0.01; * = significant at level of 0.05.

Genetic parameters

Genetic diversity plays an important role in the development of varieties as high genetic diversity allows the selection of genetic material more freely (Kuswantoro, 2017a). For all observed characters, the phenotypic coefficients of variation (PCV) values were higher than the genetic coefficients of variation (GCV) values with various differences between these two parameters (Table 5). Most of the observed characters had farther difference between PCV and GCV. However, three characters had closer values (DTM, HIG and W100). Previous studies also suggested closer values on DTM and W100 (Kuswantoro, 2017a; Kuswantoro, 2017b). The closer values indicate the higher adaptability for these characters, meaning that the expression of the characters was less influenced by the environment (Reni and Rao, 2013). The difference between PCV and GCV had no effect on the genetic variability criteria. This was clearly demonstrated by W100, where the genetic variability criterion was broad, although the difference between PCV and GCV was very small. Wide genetic diversity in the germplasm population was obtained in the BRC, NOD, POU, W100 and YLD characters, whereas for DTF, DTM, HIG and POF it was narrow. The BRC, NOD, W100 and YLD characters were consistently broad-ranging as was also reported in previous studies (Kuswantoro, 2017a; Kuswantoro, 2017b). YLD is the main character target of soybean improvement. YLD with high diversity makes it easier to implement genetic improvement. Indirectly, improvements can be made through an increase in W100 because this also had broad genetic diversity.

Heritability is also very important in breeding programs because if the heritability of a character is high, the genetic improvement can be implemented by selection in early generations. High heritability was obtained in W100, HIG and NOD. Medium heritability was obtained in DTM, BRC, POF, POU and YLD (Table 6). Only DTF had low heritability. High heritability describes that genetic factors play a higher role than environmental factors. Some author reported that heritability of grain weight was also high (Hu et al., 2013; Kuswantoro, 2017a; Kuswantoro, 2017b). Heritability of grain length, grain width and grain thickness have also been reported as high, but the ratio of grain width-to-thickness has been reported as medium (Hu et al., 2013; Niu et al., 2013). Heritability of grain size still needs to be confirmed further because in soybeans grown under acid conditions had a substantial drastic decrease in grain size (Kuswantoro et al., 2014a; Kuswantoro, 2015). The heritability of POF and POU was medium (Table 6), which indicated that selection with these characters would be less effective because the heritability measured in the current study was the broad sense heritability. Therefore, its value must still be reduced by environmental factors. Consequently,

Table 5 Genetic variability of agronomical characters of soybean germplasm

	PCV	GCV	GSD	Criterion
DTF	10.04	2.80	1.82	Narrow
DTM	5.36	3.75	3.44	Narrow
HIG	15.86	14.99	34.00	Narrow
BRC	18.20	11.25	0.07	Broad
NOD	14.44	10.32	1.76	Broad
POF	24.47	15.51	14.99	Narrow
POU	34.39	19.01	0.71	Broad
W100	17.31	16.39	0.96	Broad
YLD	31.79	19.91	0.07	Broad

PCV = phenotypic coefficient of variation; GCV = genetic coefficient of variation; GSD = genetic standard deviation; DTF = days to flowering, DTM = days to maturity; HIG = plant height; BRC = number of branches/plant; NOD = number of reproductive nodes/plant; POF = number of filled pods/plant; POU = number of unfilled pods/plant; W100 = weight of 100 grains; YLD = grain yield.

Table 6 Genetic variance (Vg), phenotypic variance (Vp), environmental variance (Ve) and broad-sense heritability (h^2_{bs}) of agronomical characters of soybean germplasm

	Vg	Vp	Ve	h^2_{bs}	Criterion
DTF	1.09	13.98	12.89	0.08	Low
DTM	11.01	22.52	11.51	0.49	Medium
HIG	151.38	169.44	18.06	0.89	High
BRC	0.17	0.45	0.28	0.38	Medium
NOD	5.82	11.39	5.57	0.51	High
POF	41.48	103.24	61.76	0.40	Medium
POU	1.56	5.10	3.54	0.31	Medium
W100	4.29	4.78	0.49	0.90	High
YLD	0.20	0.51	0.31	0.39	Medium

DTF = days to flowering; DTM = days to maturity; HIG = plant height; BRC = number of branches/plant; NOD = number of reproductive nodes/plant; POF = number of filled pods/plant; POU = number of unfilled pods/plant; W100 = weight of 100 grains; YLD = grain yield.

the narrow sense heritability will be lower. Nevertheless, some authors derived high categories for POF (Kumar et al., 2015b; Kuswantoro, 2017a, Kuswantoro, 2017b) and POU (Kumar et al., 2015b; Val et al., 2017). YLD heritability was classified as medium, indicating that this character is also less effective for the selection of genotype. However, the population in the current was homozygous so that selection can be done at any time, unlike in a segregated population.

It can be concluded that all observed characters, except DTF, were significantly different. Based on these agronomical characters, there were two asymmetrically large groups where the first group consisted of four genotypes and the second group consisted of four subgroups. The genotypes from different groups can be crossed to increase genetic variability. YLD, as the most important character, was significantly correlated with HIG, NOD, POF and POU. YLD also had broad genetic variability as did POU, NOD, POU, BRC and W100. However, YLD had medium heritability, while HIG, NOD and W100 had high heritability. These results suggested that YLD improvement can be done, but the selection should be carried out using NOD that had broad genetic variability and was significantly correlated to YLD.

Conflict of Interest

The author declares that there are no conflicts of interest.

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