

## AGRONOMIC PERFORMANCE AND GENETIC PARAMETERS OF SOYBEAN (*GLYCINE MAX* (L.) MERR.) LINES IN TIDAL SWAMP LAND

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**Abstract.** This study aimed to find out the agronomic performance and genetic parameters of soybean lines in tidal swampland. A total of 100 soybean lines were planted in the tidal swampland using a randomized complete block design. The results showed that the broad genetic diversity was reflected in plant height (HGT), number of branches (BRC), number of productive nodes (NOD). Number of filled pods (POF), number of unfilled pods (POU), 100-seed weight (SEW), and seed yield (YLD). Those seven characteristics also had high heritability, except for YLD. Phenotypic correlations were found in all characters except for SEW with POF, POU, and YLD, while genotypic correlations were only found between NOD with BRC and POF, and YLD with POF. The moderate heritability of YLD results in measurement bias when used as the single selection criterion. Therefore, it is necessary to have other characters with significant genetic correlation with YLD as supporting characters in the selection of soybean lines for high YLD. POF as a character that had a significant correlation with YLD can be used to select soybean lines for high YLD.

**Keywords:** *genetic variability, phenotypic variability, genotypic correlation, phenotypic correlation, heritability*

### Introduction

Plants need water for growth and development, but excess water can reduce productivity and affect their survival. Flash floods or high tide cause plants to completely submerge. Plants that grow in tidal areas experience multiple stresses, especially when they sink due to the high tides. These stresses include low oxygen levels, low light intensity, nutritional deficiencies, and a high risk of disease infection. Then as the floodwaters recede, submerged plants are suddenly exposed to higher oxygen concentrations and greater light intensity, which can lead to post-drowning injuries caused by oxidative stress, high light, and dehydration (Tamang and Fukao, 2015).

Improvements in the characteristics of high productivity soybean and tidal swampland adaptive are still to be done. The study on genetic variability, phenotypic variability, and interactions between genotype and environment will assist the selection process to obtain adaptive soybean varieties in tidal swamplands. Agronomic characters are influenced by variances of genetics, the environment, and interactions between the

genotype and the environment (Kuswanto et al., 2020). The wide genetic and phenotypic variabilities help plant breeders to identify parents for the hybridization program and to obtain the desired offspring with a higher degree of heterosis (Kumar et al., 2018).

The selection of genetically diverse parents is a prerequisite for a plant trait improvement program because it increases the chances of a better selection of offspring for various characters. Selection criteria are very important for determining the selection of adaptive lines for tidal fields. Physiological, morphological, and agronomic characters can be used to identify resistance mechanisms that are owned by the selected genotype. According to Kuswanto (2010), the selection criteria for adaptive tidal land genotypes that can be used practically in the field are chlorosis, necrosis, and leaf defoliation.

Study on genetic diversity, phenotypic diversity, and heritability has been carried out in soybean plants (Aditya et al., 2011; Akram et al., 2016; Baraskar et al., 2014; Dilnesaw et al., 2013; Ghodrati, 2013; Reni et al., 2013; Malek et al., 2014). Liu et al. (2017) revealed that genetic diversity in soybean germplasm can be determined by several methods including pedigree information, phenotypic observation, and low-density polymorphism markers. Meanwhile, biochemical methods, plant morphology, and plant agronomic characters can be used to determine the phenotypic diversity between soybean cultivars from China and North America. The heritability value can be used as a predictive value for the phenotype, whether the trait displayed is caused by genetic factors or environmental factors. The high heritability value for agronomic characters such as 50% flowering age, plant height, number of branches per plant, number of pods per plant, pod length, the 100-seed weight, harvest index, and seed weight per plant can indicate that genetic factors have a greater influence than the environmental factors. These characters can be used for initial selection (Reni and Rao, 2013). According to research by Baraskar et al. (2014), genetic factors are more influential than environmental factors on the character of protein content and oil content in addition to other agronomic characters. Malek et al. (2014) identified and separated the diversity of 27 mutant soybean genotypes and 4 parent genotypes into 5 clusters based on the diversity of morphological characters and it was found that the environmental effect was lower than the genetic effect on all observed morphological characters.

## Materials and methods

### *Plant materials and experimental design*

A total of 100 soybean lines were planted in Barito Kuala Regency, South Kalimantan, Indonesia, with coordinates 1°11'50", 140°4'9", 17 m above sea level. Planting was carried out on May 8, 2019. The experimental design used was a randomized block design, repeated twice. Each line was planted on a plot measuring 1.6 m × 3 m, spacing 40 cm × 15 cm, two plants per hill. Soil analysis was carried out on soil samples taken before planting. The soil properties are presented in *Table 1*.

### *Cultural practice*

Fertilization was done using 125 kg of urea, 250 kg SP36, and 150 kg KCl. Fertilization was carried out in stages, namely at the time of planting as much as 40% Urea + 100% SP36 + 100% KCl/ha, while the rest (60% Urea) was given when the

plants approaching flowering. Soil tillage was carried out optimally to obtain an ideal soil structure for the growth of soybean plants. Making drainage channels was done before planting and herbicides were applied.

**Table 1.** Soil properties

Soil properties	Value
pH	4.8 <sup>A</sup>
N (%)	0.14 <sup>L</sup>
P <sub>2</sub> O <sub>5</sub> (ppm)	58.5 <sup>H</sup>
C-Org (%)	1.8 <sup>L</sup>
SO <sub>4</sub> (ppm)	58.1 <sup>L</sup>
Cu (ppm)	0.86 <sup>VH</sup>
Mn (ppm)	6.39 <sup>VH</sup>
Fe (ppm)	341.41 <sup>VH</sup>
Zn (ppm)	2.36 <sup>H</sup>
K (Cmol <sup>+</sup> /kg)	0.19 <sup>VL</sup>
Ca (Cmol <sup>+</sup> /kg)	0.09 <sup>VL</sup>
Mg (Cmol <sup>+</sup> /kg)	1.05 <sup>VL</sup>
CEC (Cmol <sup>+</sup> /kg)	8.46 <sup>L</sup>
Al <sub>ex</sub> (Cmol <sup>+</sup> /kg)	0.42
H <sub>ex</sub> (Cmol <sup>+</sup> /kg)	1.99

A = acid, L = low, VL = very low, H = high, VH = very high

### Observation

Before the plants were harvested, a sample of 10 plants was taken. Observations were done on plant height (HGT), number of branches (BRC), number of filled pods (POF), number of empty pods (POU), number of productive nodes (NOD), 100-seed weight (SEW), seed yield (YLD).

### Data analysis

The expected mean square was used for calculating phenotypic and genotypic variability coefficient and broad-sense heritability (Singh and Chaudary, 1985). The significance of genotypic variability was determined using the genetic standard deviation. Phenotypic and genotypic correlations were calculated according to Singh and Chaudary (1985). A t-test was performed to determine the phenotypic and genotypic correlation significance (Dabi et al., 2016). Analysis of variance was performed using PKBT STAT 3.1. Phenotypic and genotypic correlation were calculated using MS Excel.

### Results and discussion

Tidal land is acid soil with the main problems of micronutrients poisoning and the lack of macronutrients. In this study, macronutrients such as N, P, and K were classified as low, high, and very low, respectively. The other macronutrients, Ca and Mg, were

also very low. All micronutrients were at high levels, where Zn was classified as high, while Cu, Mn and Fe were very high (Table 1).

All the agronomic characters observed were significantly different between the tested lines (Table 2). This shows that all tested lines had differences in the observed characters. Character differences between the lines tested can also be seen in Figures 1-7 describing the large ranges.

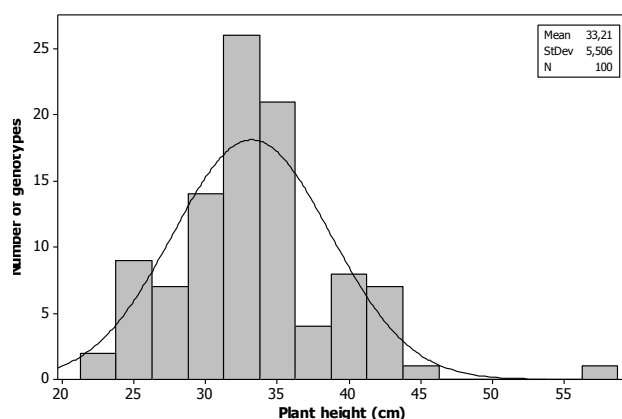
**Table 2.** Mean square of agronomic characters

	Replication	Genotype	Error
HGT	4.91	60.63 **	1.61
BRC	2.69 **	0.65 **	0.05
NOD	3.26 *	15.82 **	0.59
POF	74.57 **	81.97 **	1.84
POU	23.33 **	0.94 **	0.14
SEW	68.86 **	7.39 **	0.09
YLD	11.51 **	0.64 **	0.27

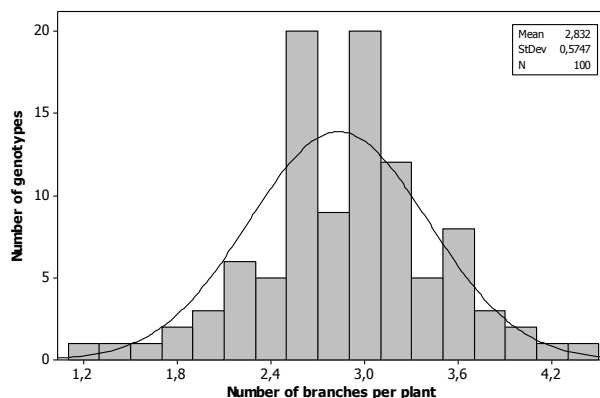
HGT = plant height (cm), BRC = number of branches per plant, NOD = number of productive nodes per plant, POF = number of filled pods per plant, POU = number of unfilled pods per plant, SEW = 100 seeds weight (g), YLD = seed yield per plot (t/ha), \* = significant at 0.05, \*\* = significant at 0.01

The 100 lines tested had an average plant height (HGT) of 33.21 cm. The largest distribution of lines had HGT around 30-35 cm. The lines that had HGT above 55 cm were less than 5 lines. According to Felici et al. (2019), the soybean genotype is strongly influenced by the environment. Knowing the interactions between the genotype and the environment will help identify an adaptive and stable genotype. Peter et al. (2019) reported that plants with high plant posture, a large number of filled pods on the main branch, and each pod containing 3 soybeans had high yields. Soybean plants that had an HGT below 48 cm may be caused by off-season planting or they are grown in suboptimal conditions that affect the growth process.

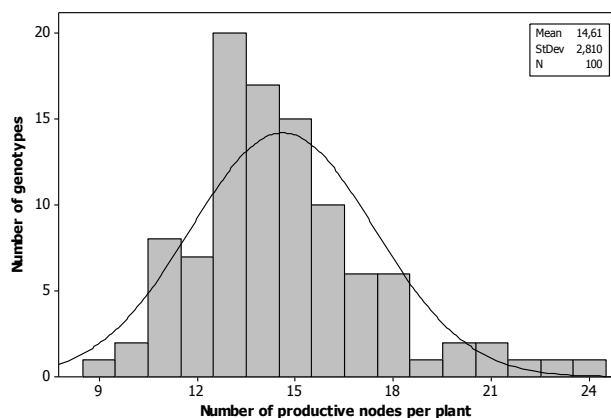
The number of branches per plant (BRC) ranged from 1.2 to 4.2 branches per plant with an average BRC of 2.8 branches per plant. Based on Figure 2, the largest distribution of BRC was 2.6-3.0 branches per plant. Less than 50% of the genotypes had BRC above 3 branches per plant. The lines with BRC 4.2 branches per plant were less than 5 genotypes. According to Kareem et al. (2015), soybean yields had a positive correlation with leaf number, seed weight, and had a strong correlation with BRC.



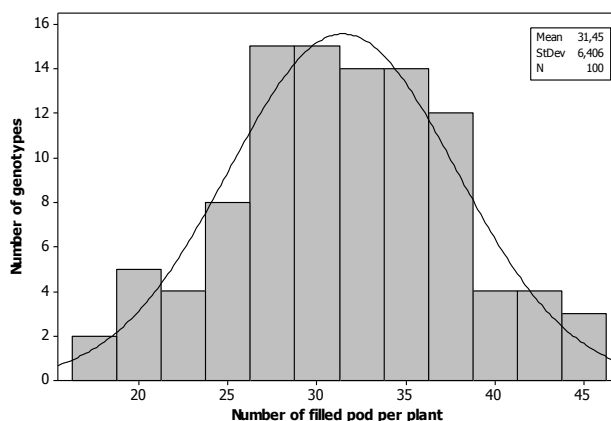
**Figure 1.** Plant height of soybean lines



**Figure 2.** Number of branches per plant of soybean lines



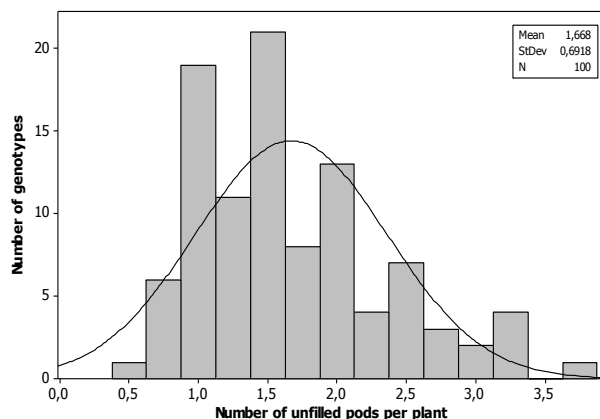
**Figure 3.** Number of productive nodes per plant of soybean lines



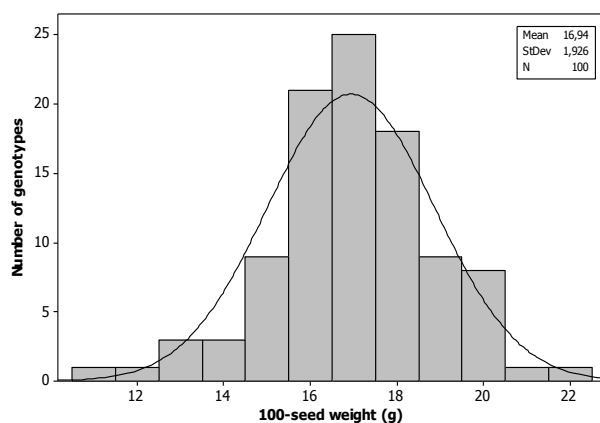
**Figure 4.** Number of filled pods per plant of soybean lines

The number of productive nodes per plant (NOD) of the 100 lines tested ranged from 9-24 nodes with an average of 14.6 nodes. Of the 100 soybean lines tested, the most number of lines had 13 NOD. Soybean lines that had more than 20 NOD were less than 10 lines. According to Peter et al. (2019) that HGT can affect NOD formation.

The average number of filled pods (POF) of the 100 soybean lines tested was 31.45 POF. The highest distribution of lines was in 27.5-30 filled pods, followed by 32.5-35 filled pods. Soybean lines that had filled pods above 25 pods per plant were more than lines that had POF below 25 pods per plant. Soybean lines that had POF above 40 were less than 15 lines. There were about two soybean lines that had POF below 20 pods. Malek et al. (2014) also reported that the number of pods and number of seeds was the main characters that affected yield. High yields of soybeans are obtained with pods containing 2-3 seeds per pod. Hakim et al. (2014) reported that NOD can be used to identify the soybean genotype with high seed yield.



**Figure 5.** Number of unfilled pods per plant of soybean lines

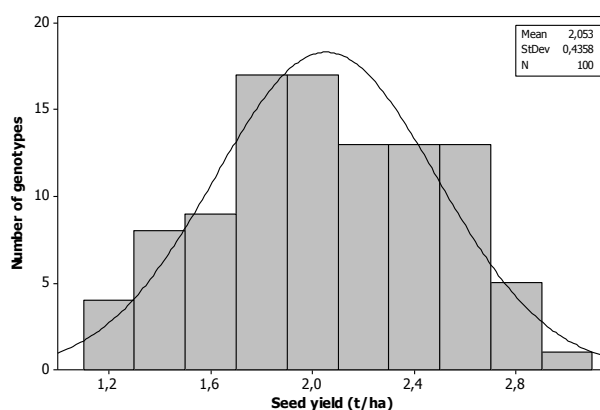


**Figure 6.** 100-seed weight of soybean lines

The average number of unfilled pods per plant (POU) was 1.6 pods. The highest POU was around four pods. There were less than five soybean lines that had more than 3.5 POU. Of the 100 tested soybean lines, the most number of lines had 1.5 POU reached 20 soybean lines.

The average 100-seed weight (SEW) was 16.94 g/100 seeds. Based on the SEW results, all tested lines had medium to large seed sizes. *Figure 6* describes that more soybean lines had SEW higher than 14 g/100 seeds. Less than 15 lines had SEW larger than 20 g/100 seeds. Most soybean lines had SEW of 17 g/100 seeds, which was about

25 soybean lines. Jin et al. (2010) stated that an increase in soybean yields was correlated with an increase in the number of pods, while the size of seeds and the number of seeds per pod were not very influential at any time. Hakim et al. (2014) and Aditya et al. (2011) stated that seed size characters had high heritability values on plant height (HGT), maturity, and the number of pods per plant.



**Figure 7.** Seed yield of soybean lines

The average seed yield (YLD) was 2 t/ha with the range of 1.00-3.57 t/ha. Seed yield positively correlated with plant population, HGT, number of leaves per plant, stover weight, number of pods per plant, number of seeds per pod, number of seeds per plant, and negatively correlated with SEW and harvest index. The characters that can be used to select superior soybean genotypes include the number of seeds per pod, number of pods per plant, and weight of stover (Ali et al., 2013). In line with Jin et al. (2019) YLD correlates with the number of pods per plant. Akram et al. (2016) stated that YLD had a positive correlation with BRC, number of pods per plant, number of seeds per plant and SEW. Mahbub et al. (2015) stated that the characters of the number of seeds per pod, SEW, pod length, maturity, and HGT showed a direct positive effect on YLD.

The genetic variance of all observed characters was lower than the phenotypic variance because the phenotypic variance was the result of both genetic variability and environmental variability. In general, the observed characters had relatively small differences in PCV-GCV, except for POU and YLD. However, all character's genetic diversity observed were broad (Table 3). It is confirmed that the difference of PCV-GCV does not affect the genetic diversity determined by GSD. In other words, genetic diversity is not determined by PCV, but by GCV and GSD.

Broad genetic diversity is very useful in the development of superior varieties because it allows for high genetic advances. With the broad genetic diversity of all observed characters, selection can be made based on each of these characters. Broad genetic diversity was also reported by Kuswantoro (2017 a, b) in BRC, NOD, SEW, and YLD, but narrow genetic diversity in HGT.

Heritability describes the proportion of genetic variance to phenotypic variance. Similar to PCV and GCV, the genetic variance is lower than phenotypic variance because phenotypic variance is the sum of genetic variance and environmental variance. All of the seven characters observed were genetic variance in the high category except YLD (Table 4). This means that the appearance of the six characters is more influenced

by genetic factors than environmental factors. Therefore, selection based on these six characters can avoid errors due to environmental influences. Chandrawat et al. (2017) reported that the seven characters observed in this study also had high heritability except for NOD which was not observed. Getnet (2018) also reported that YLD also had high heritability. This difference occurs because the plant materials are different. Differences can also occur due to differences in an environment so that the tested lines do not show their genetic potential optimally.

**Table 3.** Phenotypic and genotypic coefficient variation of agronomic characters

	PCV	GCV	GSD	Category
HGT	16.81	16.37	4.27	Broad
BRC	21.04	19.48	0.05	Broad
NOD	19.63	18.91	1.11	Broad
POF	20.60	20.14	5.77	Broad
POU	44.69	38.47	0.07	Broad
SEW	11.42	11.28	0.52	Broad
YLD	26.04	15.04	0.03	Broad

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), PCV = phenotypic coefficient variation, GCV = genotypic coefficient variation, GSD = genetic standard deviation

**Table 4.** Heritability of agronomic characters

	Vp	Vg	Ve	H bs	Category
HGT	31.12	29.51	1.61	0.95	High
BRC	0.35	0.30	0.05	0.86	High
NOD	8.21	7.62	0.59	0.93	High
POF	41.91	40.07	1.84	0.96	High
POU	0.54	0.40	0.14	0.74	High
SEW	3.74	3.65	0.09	0.98	High
YLD	0.29	0.10	0.19	0.33	Medium

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), Vp = phenotypic variance, Vg = genotypic variance, Ve = environment variance, Hbs = broad sense heritability

YLD is a character that is controlled by many genes so that it is influenced by environmental factors. Thus, selection based on YLD will be more difficult because the genotype obtained does not necessarily have the genetic structure desired. Therefore, the other characters are necessary to support the selection of a line with high YLD so that it is not biased by environmental factors. The phenotypic correlations on the agronomic characters were all significant, except between SEW with POF, POU, and YLD (Table 5). The significant YLD relationship with BRC was also reported by Kumar et al. (2018) but the relationship between YLD with POD and HGT was not significant. Although almost all agronomic characters had significant phenotypic correlations, while genotypic correlations were only found in the correlations between NOD with BRC and POF, and POF with YLD. Genotypic correlation is very important because environmental factors that cause bias in the phenotypic correlation have been



eliminated. Kumar et al. (2018) also did not find any genotypic correlation between agronomic characters.

The selection of YLDs with moderate heritability needs to be supported by other characters that had significant genotypic correlation. Although there was a significant phenotypic correlation between YLD with HGT, BRC, NOD, POF, and POU, this correlation still involves environmental factors that can provide a bias in the assessment of lines. In this study, POF had a significant genotypic correlation to YLD. Thus, selection for high-yielding lines can be done based on POF. A high POF will result in a high YLD as well.

**Table 5.** Phenotypic correlation and genotypic correlation of agronomic characters

	<b>BRC</b>	<b>NOD</b>	<b>POF</b>	<b>POU</b>	<b>SEW</b>	<b>YLD</b>
HGT	0.395** 0.430	0.449** 0.480	0.435** 0.455	0.265** 0.314	-0.328** -0.341	0.269** 0.483
BRC		0.795** 0.814*	0.722** 0.756	0.296** 0.363	-0.205* -0.222	0.361** 0.669
NOD			0.855** 0.874**	0.458** 0.506	-0.209* -0.219	0.399** 0.707
POF				0.470** 0.541	-0.124 -0.134	0.500** 0.887*
POU					0.033 0.032	0.372** 0.811
SEW						-0.080 -0.165

Upper = phenotypic correlation, Lower = genotypic correlation, 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), \* = significant at 0.05, \*\* = significant at 0.01

## Conclusion

The genetic diversity of the agronomic characters of the soybean lines tested was broad, allowing for the selection of these lines easily. YLD as a character that is influenced by other characters as a component of the yield had moderate heritability which can provide bias during selection, so it is necessary to have other characters associated with YLD. POF was a character that had a genetic correlation with YLD, so POF can be used as a selection criterion to obtain soybean lines with high YLD. Counting filled pods are more laborious than a yield measurement, so the proposed approach could be applied at an early phase of breeding.

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