Genetic Variability, Heritability and Genetic Advance in Soybean [*Glycine Max (L.) Merrill*] in Northwestern Ethiopia

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ABSTRACT

Eighty-one genotypes were tested in 9×9 simple lattice design to evaluate their genetic variability, heritability and genetic advance for 11 contributing traits at Pawe (main research station) and Dibate substation of Pawe Agricultural Research Center during 2018/2019 cropping season. Based on analysis of variance, most of traits showed highly significant ($p<0.01$) differences except number of nodules per plant, number of pods per plant and number of seeds per pod. The estimates of phenotypic and genotypic coefficients of variations (PCV&GCV) showed that the values of PCV were higher than of GCV. This would be indicated that expression of traits was highly influenced by environmental factors. High GCV and PCV values were observed by number of seeds per plant and grain yield at Pawe and only by grain yield at Dibate implied that the presence of genetic variability for selection in these traits. High heritability coupled with high genetic advance as per cent of mean was recorded by number of seed per plant (82.8% and 56.81%) andgrain yield (89.9% and 45.2%) at Pawe and days to flowering (97.2% and 23.7%) and plant height (96.6% and 33.7%) at Dibate implying selection could be effective for these traits per each location.

Keywords: *Soybean; Genetic advance; Heritability; Variability*

Introduction

Soybean (*Glycine max (L.) Merrill*) is a self-pollinated diploid and has a chromosome number of $2n = 4x = 40$. Soybean is categorized in the legume family, Leguminosae. Soybean is cross compatible with the wild species Glycine soja, but undesirable growth characteristics of Glycine soja are apparent in the progeny.Soybean is the most widely grown leguminous crop in the world and is an important source of protein and oil for food and feed. Soybean seeds are rich in proteins, unsaturated fatty acids, minerals (e.g. Ca and P) and vitamins (e.g. A, B, C and D) which meet the nutritional needs of humans and other animals [1].

Estimation of the magnitude of variation through germplasm introduction for important plant attributes will enable breeders to exploit genetic diversity more efficiently. Effective selection is dependent on the existence of genetic variability. The characterization of this variability in a population is pertinent since genetic diversity within population and within species determines the rates of adaptive evolution and the extent of response in crop improvement. Dissimilarity will always exist among individuals in a population and assessing the origin and magnitude of variability is the key to success in a crop improvement program. The extent of the genetic variability in a specific breeding population depends on the germplasm included in it. Hence, genetic variability is of immense importance to plant breeders because it can be transmitted to the progeny and the proper management of the diversity can produce permanent gain in the performance of the plant [2,3].

Estimations of genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are useful genetic parameters for determination of genetic variability. These parameters enable breeders to select the characteristics to be considered in initial and advanced steps of the breeding program.

The national average production and productivity of soybean increased from 15824.4 tons with productivity of 1.4 tons ha-1 in 2010 to 86467.9 tons with productivity of 2.27 tons ha-1 in 2017. However, it is low compared to the world average productivity potential of 2.7 tons ha-1. In Ethiopia, currently, the demand for soybean product is increasing as a result of increasing population growth, agro processing and urbanization. Though, its production and productivity in Ethiopia remains low due to lack of diversified soybean materials and genetic potential reductions of released varieties (Mesfin Hailemariam and Abush Tesfaye, 2018). There are considerable numbers of introduced soybean materials, which are not systematically characterized under Ethiopian condition. As a result, genotypes that has been introduced from abroad by Pawe agricultural research center of the Ethiopian Institute of Agricultural Research need to be characterized and clustered, because quantitative traits are strongly influenced by environmental factors, to use as a base material for further breeding programs such as breeding for higher yield, wider adaptation, desirable quality and disease resistant. Therefore, the present study was conducted to estimate the variability among genotypes to be used for plant selection in soybean breeding programs [4-6].

Materials and Methods

The experiment was conducted at Pawe Agricultural Research Center main station and Dibate (10o30′ 0″ N, 36o 10′ 0″ E) sub-station during

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main cropping season of 2018/19. Pawe Agricultural Research Center (11018`49.6``N and 036024`29.1``E) in Metekel Zone.

Eighty one introduced soybean genotypes from IITA, USA and Brazil were used for the experiment (Table 1). The experiment was laid out in 9x9 simple lattice designs with plot size of 7.2 meter square (2.4m×3m).Each plot consisted of four rows with 60cm inter row and 5cm intra row spacing. The spacing between plots, blocks and replications were 0.8m, 1m and 2m, respectively. The total net harvestable experimental area for each location was 583.2 m2. The amounts of seed and DAP fertilizer rate per plot were 54g and 72g, respectively. All the cultural practices were applied as per individual location recommendation [7].

Table 1: Mean squares for eight traits of soybean genotypes tested at Pawe in lattice design

Trait	Rep (1)	Geno. Adjusted (80)	Block with in rep adjusted (16)	Error		
				Intra block (64)	RCBD	
					(80)	RE
DF	9.38ns	65.7**	14.11	10.7	17.03	109.9
DM	206.72ns	79.12**	21.9	11.3	24.2	108.4
PHT	299.3ns	321.8**	119.2	80.29	93.7	107
BrP	7.86ns	1.75**	1.15	0.92	0.98	105.8
PdP	3571.1	191.3ns	146.9	47.1	138.2	105.4
SdP	0.29*	0.07ns	0.07	0.03	0.06	106.3
HSW	4.37ns	5.3**	1.6	1.23	2.12	119.7
Protein	3.64ns	12.13**	5.2	3.9	4.2	105.1

Data collected

Data were recorded during the cropping season and after harvesting. Observations which were recorded both on plot and plant bases are listed below. Data on days to 50% flowering, days to 95% maturity, protein content (%), oil content (%) and grain yield (kg) were recorded on plot bases. The grain yield per plot was measured from the middle two rows and converted to hectare bases. All other parameters were recorded on plant basis by taking ten plants randomly from each experimental plot according to Malik.

For determination of the quantity of oil and protein, one hundred fifty grams of dried seed samples from each genotype were grinded using grinder at laboratory room. Then, two to three grams of seed flour was taken using small cups (internal diameter of 35 mm and depth of 8 mm) and scanned by Near infrared spectroscopy (NIRS) monochromator model FOSS 6500 (FOSS NIR Systems, Inc., Silver Spring, Denmark) to estimate the percentage of oil and protein contents. Proximate compositions (list of the parameter) were predicted using plant based global calibration (infra soft international) from the collected spectra [8].

Data analysis

The data were checked for its normal distribution using Shapiro Wilk's test before proceeding to analysis and all data were found normal. Analysis of variance (ANOVA) was done using proc GLM for the traits analyzed based on RCBD and proc lattice procedures of SAS version 9.3 (SAS, 2011) for the traits analyzed based on lattice. Relative efficiency of using lattice over RCBD was checked and found that effective for traits days to flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod and protein content. But, relative efficiency of using lattice over RCBD was ineffective for traits number of nodules per plant, oil content and grain yield; hence ANOVA was carried out based on RCBD design [9].

Analysis of variance

The result of analysis of variance (ANOVA) for eight traits analyzed using lattice design is given in Table 2 and 3 traits analyzed using RCBD is given in (Table 2 and 3). There was highly significant different (P<0.01) among genotypes in days to flowering, days to maturity, plant height, number of branches per plant, hundred seed weight, protein content, protein content and grain yield whereas, number of nodules and number of pods per plant were showed non-significant differences [10].

Table 2: Mean squares for five traits of soybean genotypes tested at Pawe in RCBD

Trait	Rep (1)	Geno (80)	CV (%)
NN	1ns	6.06 ns	12.7
BB	0.00ns	0.15*	25.7
FLS	0.00ns	0.61*	37.4
Oil	0.04ns	2.34**	0.9
Yield	618192**	1252523.9**	7.8
NN= number of nodules per plant, BB= bacterial blight, FLS= frogeye spot, CV= Coefficient of variation.			

Table 3: Mean squares for eight traits of soybean genotypes tested at Dibate in lattice design

Traits	Rep (1)	Geno. Adjusted (80)	Block within rep adjusted (16)	Error		RE over RCBD
				Intra block (64)	RCBD (80)	
DF	26.9ns	131.1**	5.98	1.88	2.7	126.3
NN	25.5ns	15.1ns	79.3	29.3	72.4	108

DM	0.62ns	153.6**	202	140.7	153	110.4
PHt	20.9*	185.33**	5.9	3.5	4	105.4
BrP	7.5ns	1.33**	0.8	0.51	0.58	108.6
PdP	323.9ns	74.31ns	48.6	48	48.6	109.1
Oil	0.02ns	2.41**	0.01	0.01	0.01	108.3
Protein	0.01ns	9.23**	0.02	0.02	0.02	110.1
DE= Days to 50% flowering, NN= number of nodules per plant, DM= Days to 95% maturity, PHT= Plant height, BrP = number of branches per pod, PdP=Number of pods per plant and RE= Relative Efficiency						

Results and Discussion

Variability of genotypes

The result of separate analysis of variance (ANOVA) for eleven traits at Pawe and Dibate are given in (Tables 1 and 2), respectively. There was highly significant different (P<0.01) among genotypes in days toflowering, days to maturity, plant height, number of branches per plant, hundred seed weight, protein content, protein contentand seed yield at Pawe and Dibate indicate the existence of variability among genotypes for these traits.

Similarly, significantly different (p<0.01) results have been reported in soybean for days to 50% flowering, days to maturity, plant height, number of branches per plant and hundred seed weight. Whereas, number of nodules per plant and number of pods per plant were showed none significant difference at both locations. Mean square of number of seeds per pod, bacterial blight and frogeye leaf spot showed significant difference at Pawe and non- significant difference Dibate (Table 4).

Table 4: Mean squares for five traits of soybean genotypes tested at Dibate in RCBD

Trait	Rep (1)	Geno (80)	CV (%)
SdP	0.29*	0.06ns	13.2
BB	3.7ns	1.9ns	46.9
FLS	0.64ns	0.8ns	52
HSW	17.3**	3.9**	8.2
Yield	16265.5ns	245526**	13

"*", **"= significant at 1% and 5% levels, respectively. DF=days to flowering, NN= number of nodules, DM= days to maturity, PH=plant height, BrP= number of branches per plant, PdP= number of pods per plant, SdP= number of seeds per pod, HSW=hundred seed weight, Geno= Genotype and Rep = number of replication

Mean and range values of soybean traits

Range and mean values of eleven quantitative and three qualitative traits are presented in Table 5 at both locations. Genotypes showed wide range of variability for all traits (Table 5). The highest and lowest range values showed that genotypes had different performances in yield, yield related traits and quality traits. The lowest (1586.9g) and highest (2822g) yield per plot were recorded at Pawe. The lowest (844.4g) and highest (2445.2g) yield per plot were recorded at Dibate. Variation for flower color, stem pubescence color and pod pubescence color as qualitative descriptors were recorded. More than half (85.2%) of the genotypes had purple flower color, while 14.8% of the genotypes had white flower color. The genotypes showed two different pubescence colors, brown and white, which accounts for 64.2% and 35.8 %, respectively. All genotypes showed 100% stem and pubescence color [11].

Estimates of genetic parameters

Estimate of phenotypic ($\sigma2p$), genotypic ($\sigma2g$) and environmental ($\sigma2e$) variances and phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are provided in Tables 6 and 7 at Pawe and Dibate, respectively. High $\sigma2g$ and $\sigma2p$ were recorded for grain yield, plant height, number of pods per plant, days to maturity and days to flowering at Pawe, whereas grain yield, plant height, days to maturity and days to flowering showed the highest $\sigma2g$ and $\sigma2p$ at Dibate. Similarly, high genotypic and phenotypic variances have been reported in soybean for grain yield, days to flowering and days to maturity [12,13].

At Pawe, genotypic coefficients of variation (GCV) values ranged from 0.05% for number of nodule per plant to 29.2% for number of seeds per pod, whereas the phenotypic coefficients of variation (PCV) values ranged from 5.1% for oil content to 32.1% for number seeds per pod. The highest GCV value was recorded by number of seeds followed by grain yield. Moderate (10%-20%) GCV values were recorded by number of pods, number of branches, plant height and hundred seed weight. Similarly, moderate GCV values has been reported in soybean for number of pods, number of branches, plant height and hundred seed weight [14].

Table 5: Descriptive statistics for eleven quantitative and four qualitative traits

Traits	Pawe				Dibate			
	Range	Mean ± S.E	CV(%)	R2(%)	Range	Mean± S.E	CV(%)	R2(%)
DF	43-78	57.4±0.23	7.1	88	60-102	69.4± 0.14	2	97
NN	10.8-28.2	17.3 ±3.8	12.7	85.5	2.4-27	13.9± 0.7	15.8	78
DM	98-141	112.6 ±0.25	2.2	85.6	110-150	124.6± 0.2	1.6	96
PHt	41.9-156.6	78.3 ±2.5	9.7	83.7	42-108.6	62.01± 0.59	3	91

Trait	Range	Mean ±SE	CV	R2	Range	Mean ±SE	CV	R2
BrP	1.5-8.1	4.22 ±0.25	18.4	75.8	2.2-7.6	4.1± 0.22	17.4	77.8
PdP	26.7-118.8	55.2 ±2.2	12.7	71.9	14-65.4	31.1± 1.7	18	67
SdP	1-3.7	1.93 ±0.1	13.4	60	0.9-3.48	1.9± 0.1	13	79
HSW	8.5-18	13 ±0.1	6.8	77.4	8.5-15.5	13± 0.1	7.2	90.9
Oil	19.5-24.2	21.2±0.02	0.9	98.5	18.6-23.9	21.3±0.01	0.3	98
Protein	8.6-41.4	35.6±0.2	5.6	76.8	30.2-40.8	36.2 ±0.01	0.3	76.8
Yield	1587-2822	2147 ±166	7.8	83	844-2445	1543± 20.6	14	87.5
Flower color					Purple (85.2%) followed by white (14.8%)			
Pubescence					Present (100% present)			
Stem pubescence color					Brown (64.2%) followed by white (35.8%)			
Pod pubescence color					Descriptive			
SE = Standard Error and DF = days to flowering, NN = number of nodules, DM= days to maturity, PHt = Plant height, BrP= number of branches per plant, PdP = number of pods per plant, SdP = number of seeds per pod, HSW=hundred seed weight, Coefficient of Variation and R2=efficiency of the model.								

At Dibate, genotypic coefficients of variation (GCV) values ranged from 4.4 % for number of nodules per plant to 20.7% for grain yield, whereas the phenotypic coefficients of variation (PCV) values ranged from 5.4% for oil content to 43.4% for number of nodules per plant. Number of nodules, number of branches, number pods and grain yield showed highest phenotypic coefficients of variation (PCV) values. Similarly, highest phenotypic coefficients of variation values have been reported in soybean for grain yield, number of pods, number of nodules and number of branches [15].

Estimation of heritability and genetic advance

Heritability estimate for traits studied at Pawe and Dibate are given in Tables 6 and 7, respectively. At Pawe, broad sense heritability values were ranged from 12% for number of nodules to 96.1 % for oil content. Oil content, grain yield, days to flowering, days to maturity and number of seeds at Pawe had highest broad sense heritability values. At Dibate, broad sense heritability values were ranged from 1% for number of nodule to 97.2% for days to flowering (Table 6). Days to flowering, plant height, oil content, days to maturity and protein content had highest broad sense heritability. In agreement with this result, high heritability for days to flowering and plant height in soybean has been reported by Weber and Moorthy. Conversely, low heritability for protein content in soybean has been reported. Characters with low heritability may be difficult or impractical for selection, due to the masking effect of the environment [16].

Table 6: Variances and Genetic parameters of soybean traits studied at Pawe

Traits	σ²g	σ²e	σ²p	GCV (%)	PCV (%)	H2 (%)	GA	GAM (%)
DF	32.39	5.23	37.6	9.91	10.7	86.14	10.87	18.93
NN	0.65	4.8	5.5	0.05	13.5	12	0.57	3.3
DM	34.6	6.2	40.8	5.2	5.7	84.8	11.2	10.1
PHT	154.6	60.8	215.4	15.6	18.7	71.8	26	33.21
BrP	0.48	0.8	1.28	16.3	26.8	37.3	2	47.4
PdP	114.4	48.9	163.3	19.4	24.6	70.1	22.6	43.62
SdP	0.32	0.07	0.39	29.2	32.1	82.8	1.1	56.81
HSW	1.9	0.8	2.7	10.6	13.1	70.3	2.9	23.29
Oil	1.13	0.04	1.2	4.9	5.1	96.1	2.2	10.2
Protein	4.11	3.92	8.03	5.7	7.9	51.2	5.02	14.1
Yield	246470	27702	274172	23.1	24.4	89.9	969.7	45.2

At Pawe, genetic advance as percent of mean ranged from 0.57% for number of nodules to 56.8% for number of seeds per pods. At this location, the highest genetic advance as percent of mean was recorded by number of seeds per pod followed by number of branches, grain yield, number of pods and plant height. At Dibate, genetic advance as percent of mean ranged from 0.9% for number of nodule to 36% for grain yield (Table 6). Within this range, the highest genetic advance as percent of mean was recorded from grain yield followed by plant height, days to flowering and number of branches. In agreement with this result, high genetic advance as percent of mean in soybean for plant height has been reported.

High heritability estimates along with the high GAM is usually more helpful in predicting gain under selection than heritability estimates alone. The present study showed high heritability coupled with high genetic advance as percent of mean for number of seeds (82.8% and 56.8%) and for grain yield (89.9% and 45.2%) at Pawe. High genetic advance coupled with high heritability offers the most effective condition for selection because of variability and indicates the presence of additive genes in the inheritance of trait. Similarly,

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high heritability coupled with high genetic advance as percent of mean has been reported for plant height, grain yield, number of seeds and number of pods in soybean by various workers.

At Dibate, high heritability coupled with relatively high genetic advance as percent of mean was recorded for days to flowering (97.2% and 23.7%), plant height (96.6% and 33.7%) and grain yield (71.1%

and 36%) (Table 7). Similarly, high heritability with high GAM has been reported for plant height and grain yield in soybean. So, high values of heritability along with high GAM for characters such as days to flowering, plant height and grain yield can be effective for predicting gain under selection. In addition, effective phenotypic selection and high genetic gain from such characters can be achieved.

Table 7: Variances and Genetic parameters of soybean traits studied at Dibate

Traits	$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 p$	GCV (%)	PCV (%)	H2 (%)	GA	GAM (%)
DF	65.6	1.9	67.5	11.67	11.83	97.2	16.44	23.70
NN	0.5	49	49.5	4.4	43.43	1.0	0.15	0.90
DM	75.7	4.1	79.8	6.98	7.16	94.9	17.46	14.00
PHT	99.6	3.5	103.1	16.1	16.91	96.6	20.21	33.70
BrP	0.42	0.5	0.92	15.71	23.33	45.4	0.89	21.80
PdP	14.95	48.5	63.45	12.43	26.01	23.5	3.87	12.63
SdP	0.03	0.09	0.12	9.9	19.8	25	17.8	19.8
HSW	1.49	0.9	2.5	10.2	13.2	59.6	1.9	16.2
Oil	1.2	0.06	1.26	5.23	5.41	95.2	2.20	10.61
Protein	4.6	0.95	5.6	5.64	6.53	83.0	4.04	11.17
Yield	102006.6	41513.5	143520	20.7	24.6	71.1	554.9	36

DF=days to 50% flowering, NN= number of nodules per plant, DM=days to 95% maturity, PH=plant height, BrP= number of branch per plant, PdP= number of pod per plant, SdP= number of seeds per pod, HSW=hundred seed weight, Pro=protein content, σ2g= genotypic variance, σ2e=environmental variance, σ2p=phenotypic variance, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, GA= genetic advance and GAM=genetic advance as percent of mean.

Conclusions and Recommendations

The analysis of variance showed highly significant (p<0.01) differences among the tested genotypes for days to 50% flowering, days to 95% maturity, plant height, number of branches, hundred seed weight, oil and protein contents and seed yield at both locations. High heritability coupled with high genetic advance as percent of mean was observed by number of seeds and grain yield at Pawe and days to flowering and plant height at Dibate.

The soybean genotypes grouped into four distinct clusters at both locations. The first four principal components were found to be significant (with Eigen values greater than one) and accounted for about 63% and 65% of the total variation at Pawe and Dibate, respectively. Therefore, genotypes with traits that had high heritability coupled with high GAM such as number of seeds and grain yield at Pawe and days to flowering and plant height at Dibate would be considered as a selection criterion for further trait improvements in soybean.

Acknowledgment

None

Conflict of Interest

The author's declared that they have no conflict of interest.

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