
Genetic Variability, Heritability and Expected Genetic Advance as Indices for Selection in Soybean [*Glycine max* (L.) Merrill] Varieties

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Abstract: Genetic variability, heritability and genetic advance under selection studies were conducted at Assosa on 49 soybean genotypes. A field study laid out in 7x7 simple lattice design with two replications at Assosa Agricultural Research Center with the objective of estimating genetic variability, heritability, expected genetic advance, and to estimate genetic divergence, thereby, to cluster the test genotypes in to genetically divergent classes. The result of this study indicated variations for all the traits evaluated. The highest heritability value was recorded for days to 50% flowering followed by days to maturity and days to pod setting. Wide range of mean values was observed in all the characters evaluated. This indicates that the characters can be improved through selection. Divergence analysis grouped the 49 soybean genotypes into three. The principal component analysis revealed that five principal components PC1 to PC5 with Eigen values 4.27, 2.53, 1.91, 1.28 and 1.08 respectively, have accounted for 73.81% of the total variation.

Keywords: Divergence Analysis, Genetic Variability, Heritability, Principal Component Analysis

1. Introduction

Soybean *Glycine max* (L.) Merrill] is the world's leading source of oil and protein. It has the highest protein content (40%) of all food crops and is second only to groundnut in terms of oil content (20%) among food legumes. The meal is also rich in minerals, particularly calcium, phosphorus and iron [3, 4, 10, 11]. The crop belongs to the family *Leguminaceae*, subfamily *Papilionoideae*, tribe *phaseolae*, and genus *Glycine*. It is reported to be domesticated in Asia, probably in north eastern China about 2500 B.C. [1, 2, 7, 18].

Soybean breeding in Ethiopia was started in the 1950s on evaluation of introduced varieties with main emphasis of replacing soybean flour import with locally produced soybean flour and introducing the crop in to the existing crop production system and in the diet of the poor farmers [4, 8, 9, 11].

As soybean breeding in Ethiopia is concentrated on plant introductions, which are being used as the only source of new genes, the introductions were evaluated to identify varieties

well adapted to the country, and at the same time to identify potential areas for producing the crop [3-6, 19, 19, 21].

The magnitude of genetic variability present in a population of any crop species is central to crop improvement which must be exploited by plant breeders for yield improvement. Because the crop is grown in diverse agro-ecological environments, variation in genetic constitution do exist among the various genotypes. This implies the potential for utilizing such variability in crop improvement programs [12-14, 17].

Therefore, research is undertaken with the objective of estimating the extent of phenotypic and genotypic variability, heritability and genetic advance expected under selection.

2. Materials and Methods

An investigation study was carried out at Assosa Agricultural Research Center. 49 soybean genotypes were evaluated for their genetic parameter performances. The materials were sown out to the field in simple lattice design with two replications on the main cropping season of 2015.

2.1. The Experimental Site

Assosa Agricultural Research Center is located at latitude 10°03'12" N and longitude: 34° 59'48" E at elevation of 1950 m. a. s. l. in western part of Ethiopia, 656 km away from the capital Addis Ababa. And it is categorized under Hot to warm moist lowland plain, Tepid to cool humid, sub humid lowland plain, Tepid to cool sub humid mountain. The area receives mean annual rainfall of about 950 mm. Maximum and minimum temperatures of the site are 34.4°C and 9°C, respectively. The major soil type of the area is Nitisol with pH of 5.8.

2.2. Experimental Design and Management

The experiment was laid out in a 7X7 simple lattice design with two replications. The plot size was three rows of 4m length with 0.6m row spacing i.e. 4m x 0.6m = 4.8m².

In order to facilitate the nitrogen fixation process of the roots, rhizobia bacteria (*Rhizobium japonicum*) were incorporated into the soil uniformly.

2.3. Data Analyses

The data were subjected to statistical analysis of variance

Table 1. Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variation and genetic advance as per cent of mean for characters of soybean genotypes.

Characters	Range	Mean ± S.E Mean	σ^2_g	σ^2_e	σ^2_p	GCV (%)	PCV (%)	H ² (%)	GA	GA (%)
DF	36.00-75.00	50.06±0.95	245.38	0.95	246.33	31.29	31.35	99.61	23.62	47.18
DPS	65.00-103.00	72.60±0.80	82.51	0.58	83.09	12.51	12.56	99.30	13.63	18.77
DM	94.00-120.00	111.10±0.87	135.22	0.76	135.98	10.47	10.50	99.44	16.97	15.28
PH	20.00-62.00	35.27±1.18	197.7	1.48	199.18	39.87	40.02	99.26	20.62	58.48
PPP	9.00-28.00	15.98±0.91	35.06	0.84	35.90	37.05	37.49	97.66	8.52	53.29
PL	3.50-5.00	4.49±0.26	0.43	0.07	0.50	14.52	15.67	85.86	0.82	18.24
BY	11.00-31.00	14.12±1.33	16.49	1.82	18.31	28.96	30.52	90.06	3.11	22.20
TNPP	4.00-47.00	15.37±0.99	140.08	1.04	141.12	77.02	77.30	99.26	17.92	116.64
ENPP	2.00-25.00	7.79±1.07	49.11	1.25	50.36	90.00	91.14	97.52	10.42	133.86
RV	3.00-13.00	4.96±0.58	4.23	0.36	4.59	41.47	43.20	92.16	2.96	59.76
RDW	3.00-5.00	3.53±0.47	0.38	0.2	0.58	17.87	22.08	65.52	0.29	8.28
RBR	11.11-33.33	25.50±1.93	23.63	3.67	27.30	19.06	20.49	86.55	5.86	22.98
HSW	8.00-22.00	13.68±1.05	13.20	1.17	14.37	26.55	27.70	91.86	5.13	37.48
HI	16.13-71.07	32.79±1.37	262.38	2.08	264.46	49.39	49.59	99.21	23.86	72.74
GY	444.00-2134.00	885.76±30.51	152972.8	979.09	153951.89	44.16	44.30	64.66	593.49	67.01

DF=Days to 50% flowering, DPS=Days to 50% pod setting, DM=Days to maturity, PIH=Plant height, PPP=Pod per plant, PL=Pod length, BY=Biomass yield, TNPP=Total nodules per plant, ENPP=Effective nodules per plant, RV=Root volume, RDW= Root dry weight, RBR=Root to biomass ratio, HSW=Hundred seed weight, HI=Harvest index, GY=Grain yield. S.E. Mean= Standard error of the mean, σ^2_g = Genotypic variance, σ^2_e = Environmental variance, σ^2_p = Phenotypic variance, H² (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) ECV= Environmental coefficient of variation, GA= Genetic advance, GA (%) = Genetic advance as per cent of mean.

Characters such as root to biomass ratio, root volume, pod length and hundred seed weight showed higher values with mean values of 25.50%, 4.96, 4.49cm and 13.68g, respectively. The genotypes such as *HI8*, *Promoveria* and *IAC-6* scored the highest values of root to biomass ratio (32.29%), root volume (12.50cm³) and hundred seed weight (21.50g), respectively. Therefore, if the breeding objective is to improve the above traits the respective genotypes should be given due attention.

as per the simple lattice design for each character by the GLM and ANOVA procedures of SAS version 9.2 [22]. Efficiency of the simple lattice design relative to RCBD was checked and in most of the traits studied the lattice design was found to be more efficient than that of the RCBD. Least Significant Difference (LSD) was used to separate the means.

3. Results and Discussion

3.1. Mean, Range and Estimates of Genetic Parameters

Range and mean values of the 15 characters studied are shown in Table 1. The 49 soybean genotypes showed wide range of variability for all characters; except pod length and root dry weight. The highest grain yield (2134 kg/ha) was recorded from the genotype *TGX-1895-33F* and the lowest yield (444 kg/ha) was obtained from *G00386*. The grand mean of grain yield was 885.76 kg/ha. Earlier days to flowering, days to pod setting and days to maturity was observed with mean values of (37.00), (65.50) and (94.50) days for the genotypes *F81-7636-4*, *FBI-7636* and *H2*, respectively. 46.93 per cent of the genotypes gave above the grand mean of grain yield.

3.2. Estimates of Variance Components

Grain yield, days to 50% flowering, pod number per plant, plant height, total nodules per plant, effective nodule per plant, harvest index, biomass yield, root volume and hundred seed weight have exhibited high genotypic and phenotypic variances. Phenotypic coefficient of variation (PCV) values ranged from 10.50% for days to maturity to 91.14% for effective nodules per plant; whereas the genotypic coefficient

of variation (GCV) ranged from 10.47% for days to maturity to 90.00% for effective nodules per plant. High PCV and GCV values were recorded for grain yield, days to flowering, biomass yield, number of pods per plant, hundred seed weight, plant height, root volume, total nodules per plant, effective nodules per plant, and harvest index indicating the availability of adequate variability for these traits which aids in the improvement of the respective characters. PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium. Based on this delineation, Genotypic coefficients of variation (GCV) and phenotypic coefficient of variation (PCV) values were medium for days to pod setting, days to maturity and pod length. Medium GCV values were recorded for days to pod setting, days to maturity and pod length. High PCV values were recorded for root dry weight and root to biomass ratio.

3.3. Estimation of Broad-Sense Heritability and Genetic Advance

Root dry weight and days to 50% flowering had moderate and high heritability with 65.52% and 99.61% respectively.

All characters except root dry weight and grain yield, 65% and 64.66% respectively, had very high heritability. This indicates that selection will be the best approach to be employed to identify the best soybean genotypes for the traits with high heritability. This is because; there will be a close correspondence between the genotype and the phenotype of the genotypes, due to the relative small contribution of the environment to the phenotype. But, for characters with low heritability, selection may be considerably difficult or virtually impractical, due to the masking effect of the

environment. The magnitudes of heritability for most of the quantitative characters were moderate to high.

Genetic advance as percent of mean ranged from 8.28 for root dry weight to 133.86 for effective nodules per plant (Table 1). Within this range, a relatively high genetic advance was observed for effective nodules per plant (133.86%), total number of nodules per plant (116.64%), harvest index (72.74%), grain yield (67.01%), root volume (59.76%), plant height (58.48) and days to 50% flowering (47.58). Low genetic advance as per cent of mean values were observed for root dry weight (8.28), days to maturity (15.28), pod length (18.24%) and days to pod setting (18.77%). This low estimate of genetic advance as a percent of mean arises from low estimate of phenotypic variance and heritability.

The present study showed high heritability coupled with high expected genetic advance as per cent of mean for effective nodules per plant, total nodules per plant, pod number per plant and harvest index across both locations.

3.4. Cluster Analysis

Divergence analysis was used to categorize genotypes that are similar into one group and others into a different group. D-square statistics (D^2) developed by Mahalanobis (1936), has been used to classify the divergent genotypes into different groups [15].

The genotypes were classified into three clusters (Table 2). Cluster II was the largest cluster with 29 (59.18%) genotypes followed by cluster I which contained 19 genotypes or almost 38.77% of the total population. Cluster III contained only 1 genotype which is 2.04% of the total population.

Table 2. The distribution of genotypes into three clusters based on D^2 analysis for the 49 soybean genotypes.

Cluster	Number of genotypes	Genotypes included
I	19	H10, G00386, Promoveria, IAC-11, H4, Essex, H1, Crowford, PR-41(339), G01892, G00141, AGS-3-1, H14, PR-160-6, G01853, PR-143 (14), F82-7629-2, Clark-63k, V1-1
II	29	AGS-234, AGS-214, HS-82-2136, SR-4-1, H18, PR-149-81-EP7, Davis, FB1-7636, TGX-1895-49-F, G03705, AGS-299-2, H2, H3, H5, TGX-297-6E-1, PR-145-2, JSL-1, G9945, F81-7636-4, Lotus, SR-4-3, Protana, IAC-6, IAC-73-5115, Assosa local check-1, AGS-7-1, AGS-3, Hardee-1, G00391
III	1	TGX-1895-33F

Table 3. Cluster mean for 14 characters in soybean genotypes.

Traits	Cluster I	Cluster II	Cluster III
Days to 50% flowering	48.60*	50.48	65.50**
Days to 50% pod setting	71.52*	73.27	73.50**
Days to maturity	114.21	108.87*	116.50**
Plant height	33.18*	35.72	61.50**
Pod number per plant	14.02*	17.27**	15.50
Pod length	4.56**	4.45	4.00*
Biomass yield	13.42*	14.06	24.00**
Total nodules per plant	15.65	14.68*	29.50**
Effective nodules per plant	8.44	7.24*	11.00**
Root volume	5.00	4.81*	8.50**
Root dry weight	3.42*	3.43	4.50**
Root to biomass ratio	26.14**	25.42	15.71*
Hundred seed weight	12.92*	13.98	19.50**
Harvest index	28.06	36.42**	17.50*
Grain yield	630.78*	1009.67	2130.00**

**= highest value and *= lowest value.

3.5. Genetic Distance Between Clusters

The pair wise generalized squared distance (D^2) among clusters is depicted in table 2. The χ^2 -test for the three clusters (Table 4) indicated that there was statistically significant difference among the clusters except cluster I and III (11.85). The highest cluster distance was recorded between cluster I and cluster III ($D^2=304.36$) followed by cluster I and cluster III ($D^2=224.41$), which revealed that these clusters were genetically more divergent from each other.

Crosses involving parents belonging to most divergent clusters are expected to manifest maximum genetic recombination and variation in genetic architecture.

In most of the cases, genotypes collected from same place of origin fell in to the different clusters and from different places of origin fell in to same cluster. Regarding to genotypes collected from Ethiopia, genotypes from Awassa area are distributed in cluster I (27.77%) and in cluster II (72.23%). Genotypes from Pawe area are distributed in to the three clusters 60% in cluster II, 30% in cluster I and the rest 10% in cluster III. The genotypes from Jimma area are distributed in cluster I (66.66%) and in cluster II (33.34%). The genotype from Assosa area is found in cluster II.

In this study the results showed that there was moderate diversity in soybean genotypes. However, there was no definite relationship between geographic diversity and genetic diversity. It is suggested that selection of parents for hybridization need not necessarily be based on geographic diversity but genetic diversity must form the base for parental selection.

Table 4. Mahalanobis distance between groups of soybean genotypes.

CLUSTERS	I	II	III
I	-	11.85 ^{ns}	304.36**
II		-	224.41**
III			-

$\chi^2=23.68$ and 29.14 at 5%, 1% probability level respectively.

4. Conclusion

Based on the relative squared distance values (D^2) between any two genotypes, the 49 soybean genotypes were grouped into three distinct clusters. This indicates that the soybean genotypes were moderately divergent.

The study generally implied the presence of moderate genetic variability among the tested genotypes. Thus, there is an opportunity to bring about improvement through direct selection or hybridization.

The principal component analysis indicated five principal components (PCs) having eigenvalues between 1.08 and 4.27 explained a cumulative of 73.81% of the total variation among the genotypes. It was also noted that differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather than the small contribution of each character.

Phenotypic coefficient of variability (PCV) values ranged from 10.50% for days to maturity to 91.14% for effective

nodules per plant, whereas the genotypic coefficient of variability (GVC) ranged from 10.47% for days to maturity to 90.00% for effective nodules per plant. The traits such as, grain yield, days to 50% flowering, biomass yield, number of pods per plant, hundred seed weight, plant height, root volume, total nodules per plant, effective nodules per plant, and harvest index had high phenotypic (PCV) and genotypic coefficient of variability (GCV) values.

High heritability coupled with high expected genetic advance was observed for effective nodules per plant, total nodules per plant, harvest index, pod number per plant, biomass yield, plant height and root volume. Thus, these characters can be improved through selection more easily than other characters.

In this study high phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent of mean was recorded for effective nodules per plant, total nodules per plant, harvest index, pod number per plant and plant height.

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