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Genetic Variability, Heritability and Genetic Advances of Soybean (*Glycine max* (L.) Merrill) Varieties Grown at Bako Tibe in Western Ethiopia

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ABSTRACT

Sixteen soybean genotypes were evaluated in randomized complete block design with three replication in 2015/2016. Data were collected on Days to50% flowering, Days to pod setting, Days to 95% maturity, plant height and number of branch per plant, number of pods per plant, number of seeds per pod, pod length, Leaf Area Index, Biological yield, hundred seed weight, Grain yield and Harvest index. Computed mean values were used to estimate characters Genotypic and Phenotypic Variance, Genotypic coefficient of variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability and genetic advance percent of mean were estimated for each trait. All characters show significant variation and the coefficient of variation were relatively low. Heritability was greater than 70% for all characters studied except number of branch per plant, leaf area index, harvest index and days to flowering whereas expected genetic advance percent of mean ranged from low (1,98%) in Harvest index to high (42.2%) in biological yield in ton/ha. High heritability and high genetic advance percent of mean for biological yield followed by pod length and plant height indicates the presence of additive genes in the trait and suggests reliable soybean improvement through selection of the trait. In this studies high heritability with high genetic advance as percent of mean were found for plant height (84.59%, 21.3), pod length (89.2%, 35.3) and biomass yield (94.46%, 42.2), respectively. Whereas high heritability was associated with moderate genetic advance were found for number of pod/plant (89.8%, 11.43%) and days to 95% maturity (91.46 %, 9.96), respectively.

Keywords: Genetic variation, Genetic advance, Heritability, Soybean, Selection intensity, Traits

Abbreviations: ANOVA: Analysis of Variance; BARC: Bako Agricultural Research Center; CSA: Central Statistical Agency; GAM: Genetic Advance as Percent of Mean; GCV: Genotypic Coefficient of Variation; Hb: Heritability in Broad Senses; LAI: Leave Area Index; GLM: General Linear Model; SNK: Student-Neuman Keuls Test; PCV: Phenotypic Coefficient of Variation; RCBD: Randomized Complete Block Design

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a member of Papilionaceae family and believed to have originated in North Eastern China and distributed in Asia, USA, Brazil and Argentina. The crop has a fairly wide range of climatic condition for adaptation and mostly cultivated on rain fed land. Soybean was introduced to Ethiopia in 1953 and the current national production of the country is estimated at 11, 261 hectares with a total productivity of 1,582 tons/hectares [1]. It has highest protein (42%), oil (24%), rich in lysine, vitamins A and B and free from cholesterol [2]. Many developing country in the tropics show interests in the production of soybean due to raised demands for use in animal feed, regulating soil fertility and reducing the cost of nitrogen fertilizer and increasing demands of protein and vegetable oil [3]. Soybean production in Ethiopia is very important to overcome malnutrition and substitutes domestic animal products. The area of production of soybean in the country is increased due to increasing demands of soy cooking oil, soy fortified food, animal feed, and improving human nutrition and soil fertility [4]. However its cultivation is still not spread much and its average yield is very low as compared to other crop grown during the same season [1].

This low productivity of this crop is due to various reasons, but, the major reason is lack of improved varieties, limited knowledge on its potential as food, difficulty in processing (knowledge and technology) and difficulty in marketing the crop [5]. Development of high yielding varieties with desired plant characters and duration of maturity of paramount important for any crop improvement program. So that, genotypes with suitable plant types are to be selected from a diverse pool for their future utilization as parents in the hybridization program. Therefore germ plasma collection and assessments of genetic variability is the basic steps in any crop improvement program.

Yield is a complex characters controlled by many genes and influenced by environment [6]. Therefore variability for these characters is the result of genetic effect and environmental effect. Hence it is necessary to partition the observed variability in to heritable and non- heritable components measured as Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability and Genetic Advance expressed as percent of Mean. Many farmers still unable to distinguish Soybean (*Glycine max* (L.) Merrill) from common bean (*Phaseolus vulgaris*) in Bako-Tibe district that located in western Showa zone Oromia regional states western Ethiopia, about 223 km away from Addis Ababa and lies at a latitude of 906'N longitude 3709'E and at an altitude of 1650 m above sea level. The annual temperature of the site ranges from 13.5-29.7°C with average annual rain fall of 1237 mm. The specific soil type of the site is reddish-brown in color well drained Niti soil with the pH value ranges from 5.5-5.6 and there was no studies on genetic variability of soybean have conducted in western Ethiopia Bako-Tibe district. Therefore, there is a scarcity of information regarding genetic variability, genetic advance and heritability in Ethiopia in general and at Bako Tibe in particular. Hence the present studies were conducted to attain the following objectives:

- To estimates genetic variability of Soybean genotypes.
- To estimates heritability and Genetic Advance of traits among the seed yield and yield contributing characters of Soybean genotypes.

MATERIALS AND METHODS

Sixteen Soybean genotypes (eight released and eight pipe line) (Table 1) were planted in RCBD design with three replications. Genetic materials were obtained from Bako Agricultural Research Center (BARC) in 2015/2016 and planted in plot size of 2 m and 1.5 m width with 1 × 1.5 m net plot size, with 4 rows on each plot and, the spacing between block, plot, row and plants were 1.5 m 1 m, 40 cm and 10 cm, respectively. Planting was done during main cropping season of 2015/2016 at Bako Tibe district in side Farmers Training Center (FTC) under rain fed. All the recommended agronomic packages were applied.

Data were collected for: days to 50% flowering, days to 50% pod setting, days to 95% maturity, plant height, leaf area index, number of branch per plant, number of pods/plant, pod length, biological yield ton/hectares, grain yield ton/hectare, hundred seed weight, number of seed /pod and harvest index. The data obtained for selected different characters were statistically analyzed using GLM procedure of SAS software 9.0 versions [7] and the treatment mean that exhibited significance difference were separated using student Neumankeulls test (SNK) at 5% level of significance [7]. RCBD ANOVA was computed using the following model

Table 1: Name of genotypes, pedigree, sources and attributes of soybean genotypes used

No.	Genotypes	Seed sources	Adaptation	Pedigree	Genotypes (released/pipeline)
1	BOSHE	BARI/OARI	Intermediate and long rain fall	IAC-13-1	RELEASED
2	AWASSA-95	BARI/OARI	Intermediate and long rainfall	AG-2261	RELEASED
3	NVT-P41	BARI/OARI	-	-	PIPLINE
4	NVT-P11	BARI/OARI	-	-	PIPLINE
5	NVT-P28	BARI/OARI	-	-	PIPLINE
6	CHARI	BARI/OARI	Intermediate and long rain fall	IPB-81-EP-7	RELEASED
7	BELESSA-95	BARI/OARI	Intermediate and long rain fall	PR-149	RELEASED
8	ETHIO	BARI/OARI	Intermediate and long rain fall	YUGOSLAVIA	RELEASED
9	DIDESSA	BARI/OARI	Intermediate and long rain fall	PR-149-81-EP-7-2	RELEASED
10	JALALE	BARI/OARI	Intermediate and long rain fall	AGS-217	RELEASED
11	NVT-P32	BARI/OARI	-	-	PIPLINE
12	AWASSA-O4	BARI/OARI	Intermediate and long rain fall	-	RELEASED
13	NVT-P36	BARI/OARI	-	-	PIPLINE
14	NVT-P23	BARI/OARI	-	-	PIPLINE
15	NVT-P22	BARI/OARI	-	-	PIPLINE
16	NVT-P42	BARI/OARI	-	-	PIPLINE

$$Y_{ij} = \mu + r_j + g_i + \mu_{ij}$$

Where, Y_{ij}=the response of trait y in the i^{th} genotype and the j^{th} replication, μ= the grand mean of trait y, r_j=the effects of the j^{th} replication, g_i=effect of the i^{th} genotype and μ_{ij}=experimental error effect

Estimation of genetic parameters

Variance components

Phenotypic and Genotypic coefficient of variation were computed according to the methods suggested by Burton and de vane [8] as follows:

Environmental variance $(\sigma^2 e)$=Mse

$$Genotypic\ variance(\sigma^2 g) = \frac{Msg - Mse}{r}$$

$$Phenotypic\ variance\ (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

$$Genotypic\ coefficient\ of\ variation\ (GCV) = \frac{\sigma^2 p}{\overline{X}} \times 100$$

$$Genotypic\ coefficient\ of\ variation\ (GCV) = \frac{\sigma^2 p}{\overline{X}} \times 100$$

Where $\overline{X}$ is a grand mean of a character

Heritability

Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance $(\sigma^2 g)$ to the phenotypic variance $(\sigma^2 p)$ was estimated on genotype mean basis as described by Alard [9] as:

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where, $\sigma^2 p$=phenotypic standard deviation, $\sigma^2 g$=Genotypic standard deviation

Genetic advance

Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johansson [10] as:

$$GA = K\sigma p h^2$$

$$GAM = \frac{GA}{\overline{X}} \times 100$$

Where, GA=Genetic advance under selection,

$\sigma^2 p$=phenotypic standard deviation, h^2=heritability in broad sense, k=is selection intensity and $\overline{X}$ grand mean.

RESULTS AND DISCUSSION

Variance components

The analysis of genotypic variance of the characters studied resulted in highly difference at $(p \le 0.01)$ probability level for biological yield tone per hectare, pod length, plant height, number of seed per pod and grain yield tone per hectare. Significance difference at $(p \le 0.05)$ probability level for days to 50% flowering, days to 95% maturity and number of branch per plant were observed. Among treatment mean yield comparisons significant variation were observed at $(p \le 0.05)$ probability level with mean yield value ranges from 0.42-61.3 kg/ha. Table 2 showed the means, coefficients of variation (CV), ranges and mean squares of 13 characters of Soybean genotypes. Significant variation existed (at $P=0.05$) in all the characters.

Phenotypic and genotypic coefficient of variation

High Genotypic Coefficient of Variation (GCV) were recorded for Bytha (21.13) while, Low Genotypic Coefficient

Table 2: Mean value, coefficient of variation, range and mean squares of some yield contributing traits of 16 Soybean genotypes

Characters	Mean	CV (%)	Range		Mean squares	
			Minimum	Maximum	Genotypes df=15	Error df=30
DF 50%	68.1	2.84	61.3	72.3	19.72**	3.74
DP 50%	76.5	1.81	70.0	80.0	16.93**	1.92
DM 50%	136.5	4.80	122.0	145.0	79.33**	2.39
PH	57.5	4.81	49.9	71.91	0.079**	0.022
NBPP	3.8	6.17	2.5	4.5	134.0**	7.67
NPPP	61.3	3.21	46.2	68.2	0.66**	0.55
PODL	2.6	6.35	2.0	3.2	107.13**	3.89
Gytha	4.4	3.69	3.7	5.0	0.72**	0.028
Bytha	10.3	2.06	8.9	12.3	14.49**	0.278
HSW	11.2	2.97	10.1	12.4	0.47**	0.026
NSPP	3.1	6.01	2.5	3.4	1.61**	0.278
LAI	3.5	4.24	3.3	3.92	0.32**	0.034
HI	0.42	2.66	0.4	0.43	0.0003**	0.00012

**Significant at P=0.01

Where, DF: Days to 50% flowering; DP: Days to 50% initiate pod setting; DM: Days to 50% maturity; PH: Plant Height; NBPP: No. of Branch/ Plant; NPPP: No. of Pods/Plant; PDL: Pod Length; Gytha: G. yield/ton/hectare; Bytha: B. yield/ton/hectare; HSW: Hundred Seed Weight; NSPP: No. Seed/Pod; LAI: Leaf Area Index; HI: Harvest Index; CV: Coefficient of Variation

of Variation (GCV) was recorded for Days to flowering 50% (3.39), Days to pod setting 50% (2.92), and Days to maturity 95% (3.71), Leaf area index (3.95), Number of branch per plant (5.01), Gytha (8.82), Number of seed per pod (9.94) and Harvest index (1.74) (). High Phenotypic Coefficient of variation (PCV) were also recorded for Bytha (21.74), but moderate PCV were recorded for Plant height (12.25), Number of pod per plant (10.10), pod length (19.26) and number of seed per pod (11.59), whereas low PCV were recorded for Days to flowering 50% (4.42), Days to maturity 95% (3.88), Days to pod setting 50% (3.44), Leaf area index (5.8), Gytha (9.57) and Hundred seed weight (7.57) (Table 3), as stated by Shivasubramanian S and Menon [11] the GCV and PCV value are ranked as low, medium and high with 0-10%,10-20% and >20%, respectively.

High Genotypic Coefficient of variation (GCV) and Phenotypic Coefficient of variation (PCV) indicated that selection may be effective based on these traits and their phenotypic expiration would be good indication of their genetic potential. Similarly high GCV and PCV were reported for biological yield by Zaraf et al. [12] in soybean. The comparison of traits as regards to the extents of the genetic variation could be essential through estimation of genotypic coefficient of variation in relation to their phenotypic coefficient of variation. As indicated in Table 3, difference between GCV and PCV were observed for traits Number of branch per plant, Harvest index, Hundred seed weight, Leaf area index and Number of seed per pod and this traits were small that indicates less influence of the environment on the traits.

Heritability

Heritability ranged from 6.25% to 94.46% and high heritability value were recorded for biological yield tone/hectare (94.46%), Days to maturity 95% (91.48%), plant height (84.59%), number of pod/plant (89.84%) (), whereas, low heritability value were recorded for number of branch /plant (6.25%), while harvest index (30.77%), leaf area index (46.34%) and days to flowering (58.75%), were resulted in moderate heritability values (Table 3). Heritability value are categorized as low (0-30%), moderate (30-60%) and high (above 60%) as stated by Robinson et al. [13] and Basavaraja [14] also reported high heritability for plant height as similar as the current work. According to Beebe et al. [15], high heritability percentage reflects the large heritable variance that may offers possibility of improvement through selection. A measure of variability and an understanding of the genetic constituents of a crop is very important for any crop improvement program [16]. Phenotypic, genotypic and environmental variances as well as their coefficients of variation are presented in Table 3. Similarly, heritability and expected genetic advance are presented in the table.

Genetic advance and genetic advance percent of mean

Genetic advance measures the expected genetic progress that resulted from selecting the best performing genotypes to a given characters [9]. The genetic gain that obtained from particular traits through selection is the product of its heritability, phenotypic and genotypic standard deviation and selection differential [8]. High genetic advance as percent of mean were recorded for plant height (21.30), pod length (35.32) and biological yield tone /hectare (42.23) (Table 3). Whereas, moderate genetic advance as percent of mean were recorded for number of pod/plant (18.19), grain yield tone/hectare (16.73) and number of seed/pod (17.54) (Table 3). While low genetic advance as percent of mean were obtained for days to flowering 50% (5.34), days to pod setting 50% (5.11), days to maturity 95% (7.30),

Table 3: Estimation of genotypic variation, phenotypic variation, genotypic coefficient of variation, phenotypic coefficient of variation, heritability in broad sense, expected genetic advance and genetic advance as percent of mean

Characters	Σ^2_e	σ^2_g	σ^2_p	Gm	δg	EFNO 4.6 1.8 6.0 20.19 NENO 2.6 1.0 CV 5.4 2.6	h²b (%)	GA	GAM	GCV	PCV
DF	3.74	5.33	9.07	68.12	2.31	2.84	58.75	3.64	5.34	3.39	4.42
DPS	1.92	5.00	6.92	76.5	2.24	1.81	72.27	3.91	5.11	2.92	3.44
DM	2.39	25.65	28.04	136.5	5.06	4.80	91.48	9.96	7.30	3.71	3.88
LAI	0.02	0.02	0.04	3.49	0.14	4.81	46.34	0.19	5.53	3.95	5.80
PH	7.67	42.1	49.8	57.60	6.49	6.17	84.59	12.2	21.3	11.27	12.25
NBPP	0.55	0.04	0.59	3.82	0.19	3.21	6.25	0.10	2.58	5.01	20.05
NPPP	3.89	34.4	38.30	61.30	5.87	6.35	89.84	11.4	18.6	9.57	10.10
PODL	0.03	0.23	0.26	2.64	0.48	3.69	89.18	0.93	35.3	18.19	19.26
Bytha	0.28	4.74	5.02	10.30	2.18	2.06	94.46	4.35	42.2	21.13	21.74
Gytha	0.03	0.15	0.17	4.36	0.38	2.97	85.06	0.73	16.7	8.82	9.57
HSW	0.28	0.44	0.72	11.23	0.67	6.01	61.50	1.07	9.57	5.93	7.57
NSPP	0.03	0.10	0.13	3.10	0.31	4.24	73.64	0.54	17.5	9.94	11.59
HI	0.00	0.00	0.00	0.42	0.01	2.66	30.77	0.01	1.98	1.74	3.13

Where, DF: Days to 50% flowering; DP: Days to 50% initiates pod setting; DM: Days to 50% maturity; PH: Plant Height; NBPP: No. of Branch/ Plant; NPPP: No. of Pods/Plant; PDL: Pod Length; Gytha: G. yield/ton/hectare; Bytha: B. yield/ton/hectare; HSW: Hundred Seed Weight; NSPP: No. Seed/Pod; LAI: Leaf Area Index; HI: Harvest Index; CV: Coefficient of Variation; σ_g: Genotypic Variation, σ_p: Phenotypic Variation, GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; H²b: Heritability in Broad Sense; EGA: Expected Genetic Advance; GAM: Genetic Advance as Percent of Mean

Leaf area index (5.53) and hundred seed weight (9.57),(Table 3). Genetic advance as percent of mean were classified as low (0-10%), moderate (10-20%) and high (above20%) as stated by Johansson et al. [10]. Also Rashed et al. [3], Hinacavsar [17] and Parameshwar [18] were reported similar result as the current work. High heritability for the plant height, pod length, biological yield tone/hectare and number of pod/plant were associated with high genetic advance indicating additive gene action in the inheritance of these traits. Therefore high genetic gain was expected from selection of such traits [19].

CONCLUSION

Soybean is emerging as an important feed, food as well as raw material for producing high-quality protein and oil products in the world and in Africa including Ethiopia. Therefore, development of adapted and high yielding soybean varieties is necessary in Ethiopia. The present experiment was conducted during summer season in 2015/2016 at Bako Tibe district of Western Showa zone of Oromia regional State, to elucidate information on Genetic variation, the nature and magnitude of heritability and genetic advance in soybean.The16 soybean genotypes were planted in randomized complete block design with three replications. All 16 soybean genotypes showed wide range of variation, heritability and genetic advance for thirteen selected yield contributing characters. High heritability with moderate genetic advance indicates that characters were less influenced by environment but, governed by additive and none additive gene action.

It can be concluded that high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) coupled with high heritability indicates that there is a lesser influence of environment in the expression of characters which are amenable for selection. The character days to 50% flowering, days to 95% maturity and days to 50% initiates pod setting showed high heritability but low level of variability; hence these characters are not amenable for selection in the present studies. Based on heritability and genetic advance study AWS-04 and AWS-95 were identified as early in maturity, hence these can be used for developing early maturing type. Genotype Jalale, Belessa, Chari, Ethio and NVT22 had high number of heritability for branch per plant hence these varieties can be used for developing plants with many branches. Varieties AWS95, AWS04, Ethio, Chari, Belessa and NVT42 have high heritability for number of nodules per plant; hence these can be used for developing more modulating varieties for tropical biological nitrogen fixation.

RECOMMENDATION

It is important to determine how the essential trait leads to improvement of soybean cultivars through inheritance and genetic advance for future breeding program and it should utilize the studied accessions that based on heritability of traits and their genetic advance, so that hybridization should be carried out between genotypes having highly heritable treats. Therefore improvement in seed yield could be achieved by direct or indirect selection of traits that are highly heritable with high genetic advance.

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