Original Research Article

Genetic variability and Heritability of medium maturity group's Soybean(*Glycine max* (L.)) Genotypes at Oromia, Ethiopia

ABSTRACT

Field experiment was conducted to assess the extent of genetic variability and heritability in soybean genotypes for yield and its related traits. A total of thirty six soybean genotypes were evaluated using simple lattice design at Fedis eastern Ethiopia. Data were recorded for major quantitative traits and analyzed using appropriate statistical R-software. Analysis of variance revealed that the genotypes were highly significant for all the traits studied, indicating the existence of considerable magnitude of variability. High broad sense heritability estimate coupled with relatively high genetic advance as percentage of mean were computed for pods/plant, plant height, grain yield and primary branches/plant. Moderate to high genetic advance as percent of mean was estimated from the present result days to maturity, primary branches/plant, plant height, pods/plant, seeds/pod, hundred seeds weight and grain yield were recording high genetic advance as percent of mean, while days to flowering and secondary branches/plant estimated moderate genetic advance as percent of mean. High values of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (H^2*), and genetic advance as percent of mean (GAM) were estimated for plant height, primary branches per plant, pod per plant, seeds per pod, and grain yield indicating the ease of direct selection for the improvement of these traits. Hence, selection for these traits is likely to be effective as high heritability values were associated with high genetic advance as percent of means in the improvement of the performance of the soybean genotypes. As a result breeder can improve the tested soybean genotypes through plant height, number of pods/plant, number of primary branches/plant and grain yield.*

Keywords: Genetic variation, Genetic advance, Heritability and Selection intensity

1. INTRODUCTION

Soybean (*Glycine max* (L.)) is considered as one of the most important legumes produced in the world for human and animal feeding due to its high protein content and vegetable oil ([1]).The higher a heritability, the greater the chance that the breeder will be able to make successful selections for targeted traits causing a genetic change in the trait of interest.Higher estimates of heritability coupled with better genetic advance confirm the scope of selection in developing new genotypes with desirable characteristics ([6]). High heritability coupled with high genetic advance as percent of mean which indicates the operation of additive gene action in the inheritance of traits and improvement in these traits is possible through simple selection ([7]). A number of studies have been conducted to determine the heritability for different traits of different crops particularly; many heritability studies have been conducted on soybean for seed yield, protein concentration, and oil concentration. The higher heritability guides the plant breeders as it increases chance of selection for targeted traits causing a genetic change in the trait of interest.

Therefore, this study was initiated to assess genetic variability among soybean genotypes with the objective of to estimate variance components, heritability and genetic advance for different traits.

2. MATERIALS AND METHODS

The study was conducted at Fadis Agricultural Research Center, Eastern Hararghezone. Fadis, is located at the latitude of 09^{o} 07’ North and longitude of 042^{o} 04’ East (Fig 1).

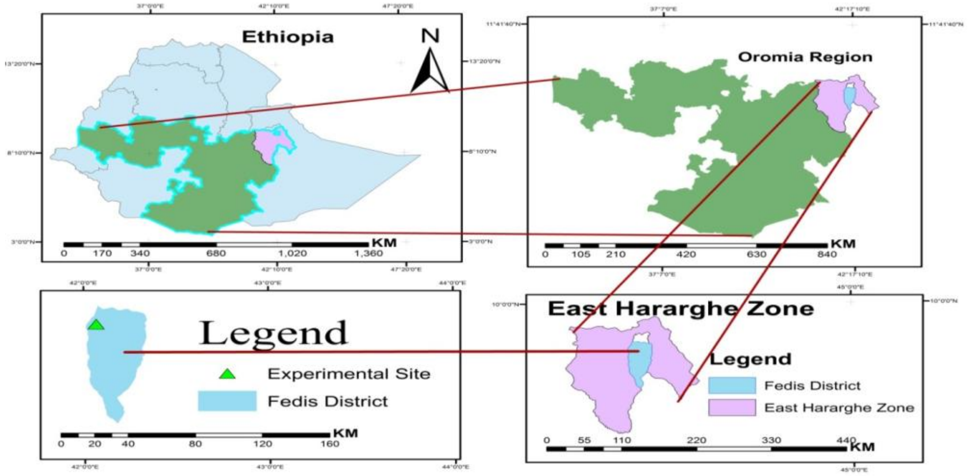

Fig 1. Map of the study area eastern Ethiopia

The field experiment was laid out in 6 * 6 simple lattice designs.All the recommended agronomical practices such as fertilizer application, weeding, hoeing, harvesting and threshing were undertaken to raise the healthy crop. Genotype name and source is listed in below table (Table 1).

Table 1. List of soybean genotypes used for evaluation at Fedis, eastern Ethiopia

No.	Genotypes	Source	No	Genotypes	Source
1	TGX-1990-95F	IITA	19	JM-PR142-H3-15-SB	IITA
2	TGX-1989-75FNF	IITA	20	JM-CLK/CRFD-15-SD	IITA
3	TGX-1989-53FN	IITA	21	JM-DAV/PR142-15-SA	IITA
4	TGX-1989-11F	IITA	22	TGX-1990-8F	IITA
5	TGX-1990-107FN	IITA	23	BRS-286	IITA

6	TGX-1993-4FN	IITA	24	PI-471904	IITA
7	TGX-110F	IITA	25	PI-567025A	IITA
8	TGX-1989-42F	IITA	26	PI-605829	IITA
9	TGX-1990-111FN	IITA	27	PI-605891B	IITA
10	TGX-1990-114FN	IITA	28	PI-567061	IITA
11	(M) TGX-1990-8F	IITA	29	Clark 63	BARC
12	TGX-1990-106FN	IITA	30	PI-230970	IITA
13	TGX-1989-45F	IITA	31	PI-567190	IITA
14	DAV/ALM-15-SA	IITA	32	Korme	BARC
15	JM-CLK/CRFP-15-SA	IITA	33	Awasa04	BARC
16	JM-ALM/PR142-15-SC	IITA	34	Keta	BARC
17	JM-ALM/H3-15-SC-1	IITA	35	Didessa	BARC
18	JM-PR142-SLK-15-SC-2	IITA	36	Awasa95	BARC

Source: BARC

Days to flowering, to maturity, Hundred Seed weight, Grain yield per hectare, Plant height (cm), Primary branches per plant, Pods per plant and Seeds per pod: were recorded and analyzed for interpretation.The genetic parameters like genotypic and phenotypic coefficients of variation were calculated according to the formula given by (2).

Genotypic variance ($\sigma^2 g$) = (Mg-Me)/r Where Mg= mean square of genotypes, Me= mean square of error, and r= number of replications;
Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$, where $\sigma^2 g$= genotypic variance and $\sigma^2 e$= mean square of error;
Phenotypic coefficient of variation (PCV) = (Phenotypic standard deviation)/ (mean) *100
Genotypic coefficient of variation (GCV) = (Genotypic standard deviation)/ (mean) *100
Phenotypic Standard deviation = √ (phenotypic variance)
Heritability in the broad sense was calculated using (3) as follows: $H^{2} = (\sigma^{2} g)/(\sigma^{2} p)$ x100

The heritability was categorized as low (0-30%), moderate (30-60%) and high (60% and above) as given by (5).
Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated and categorized as low (0-10%), moderate (10-20%) and high (20% and above) as illustrated by (4):

$$GA = k * \sigma p * H^2$$

k =selection intensity (= i) (standardized selection differential)
e. g. k=2.063 for 5% selection intensity
σp = phenotypic standard deviation
H^2 = heritability of the trait under selection
Genetic advance (as % of mean) =GA/ (grand mean) x100

3. RESULTS AND DISCUSSION

The genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability in broad sense (H^2), genetic advance and genetic advance as percent of the means (GAM) for yield and yield related traits of soybean genotypes were estimated (Table 2).

Table 2. Estimation of genotypic and phenotypic variance, coefficient of variation, heritability in broad sense, genetic advance and genetic advance as percent of mean for quantitative traits of soybean

Traits	Mean	GV	PV	GCV	PCV	H^2	GA	GAM
Days to flowering	59.00	27.38	30.98	8.86	9.43	88.38	10.14	17.20
Days to maturity	119.00	184.62	188.76	11.38	11.51	77.80	27.72	23.23
Primary branches/plant	4.63	0.91	1.17	20.59	23.30	78.13	1.74	37.56
Secondary branches/plant	0.18	0.12	0.14	18.60	20.46	85.33	0.64	19.42
Plant height	52.80	225.92	235.74	28.46	29.07	95.83	30.35	57.48
Pods/plant	64.98	401.65	464.70	30.84	33.17	86.43	38.43	59.15
Seeds/pod	2.16	0.09	0.13	14.27	16.53	74.45	0.54	25.40
Hundred seed weight	14.38	5.59	6.85	16.43	18.19	81.58	4.40	30.63
Grain yield (tons/ha)	2406.93	47.96	54.51	28.77	30.67	87.99	1340.20	55.68

Comment [A1]: Please mention units

Comment [A2]: Please mention units

Key: sd= standard deviation GV=genotypic variance, PV=phenotypic variance, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, H^2=heritability in broad sense,GA=genetic advance and GAM=genetic advance as percent of mean

Comment [A3]: Where is sd in this table ?

Higher magnitude of variation was estimated for genotypic variance ranges from 0.09 for seeds/pod to 401.65 for pods/plant. Similarly phenotypic variance ranges from 0.13 for seeds/pod to 464.70 for pods/plant. Genotypic coefficient of variation ranges from 8.86% for days to flowering to 30.84% for pods/plant and phenotypic coefficient of variation ranged from 9.43 for days to flowering to 33.17% for pods/plant indicating that the presence of wide range of variation among the genotypes for these traits.

The highest genotypic coefficient of variation 30.84% was observed for pods/plant followed by grain yield (28.77%), plant height (28.46%) and primary branches/plant (20.59%) which indicated the possibility to further improve these traits. High phenotypic coefficient of variation was estimated for pods/plant (33.17%), grain yield (30.67%), plant height (29.07%), primary branches/plant and secondary branches/plant (20.46%).

The highest heritability 95.83% was estimated for plant height, followed by days to flowering (88.37%), grain yield per hectare (87.98%), pods/plant (86.43%), secondary branches /plant

(85.33%), hundred seeds weight (81.58%), primary branches/plant (78.13%), days to maturity (77.80%), and seeds/pod (74.44%), indicating that traits have high selection response.Similarly, ([8, 9, 10, 11, 12, 13])agreed with the present result that high estimates of heritability were estimated for the number of days to flowering, days to maturity, hundred seeds weight, grain yield, plant height, and pods/plant.

High genetic advance were estimated for grain yield, pods/plant, plant height and days to maturity indicating that could provide the best image of the amount of advancement to be expected through selection. Grain yield, days to maturity, plant height and pods/plant exhibited high broad sense heritability and high genetic advance that can be considered as favorable morphological traits for soybean improvement through effective direct selection that can bring the desired improvement in these traits.Similarly ([14, 15]) reported that plant height and pods/plant exhibited high broad sense heritability coupled with high genetic advance, indicating the presence of additive gene action and improvement of these traits through selection.

Moderate to high genetic advance as percent of mean was estimated from the present result (Table 2). Days to maturity, primary branches/plant, plant height, pods/plant, seeds/pod, hundred seeds weight and grain yield were recording high genetic advance as percent of mean, while days to flowering and secondary branches/plant estimated moderate genetic advance as percent of mean. Similarly ([7, 16])noted high heritability coupled with high genetic advance as percent of mean was estimated for plant height, primary branches/plant and grain yield per plant.

High heritability with moderate genetic advance as percent of mean was estimated for days to flowering and secondary branches/plant. This indicates that these traits are highly influenced by environment and they may be conditioned by both additive and non additive gene actions. Hence, selection based on phenotypic observations alone may not be effective for these traits. Similar work done by ([14]) high heritability coupled with moderate genetic advance recorded for hundred seed weight, days to 75% maturity, days to 50% flowering and branching ability suggesting that the expression of these traits are controlled by both additive gene action and non additive gene action.

In the present study, high heritability coupled with high genetic advance as per cent mean were estimated for days to maturity, primary branches/plant, seeds/pod, hundred seeds weight, plant height, pods/plant and grain yield indicating that the operation of additive gene action in the inheritance of these traits and improvement in these traits is possible through simple selection. Hence, selection for these traits is likely to be effective as high heritability values were associated with high genetic advance as percent of means in the improvement of the performance of the soybean genotypes. Contrary to the present result ([17]) reported low genetic advance and GAM for plant height (0.87%) and pods per plant (4.36%)

4. CONCLUSION

High broad sense heritability estimate coupled with relatively high genetic advance as percentage of mean were computed for pods/plant, plant height, grain yield and primary branches/plant. This indicated that these traits are controlled by additive genetic factors and less environmental influence in the phenotypic expression. Therefore, the breeder can improve the tested soybean genotypes through plant height, number of pods/plant, number of primary branches/plant and grain yield.

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