

# 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, 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 (<sup>1</sup>). 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 (<sup>6</sup>). 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 (<sup>7</sup>). 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 Hararghe zone. Fadis, is located at the latitude of 09° 07' North and longitude of 042° 04' East (Fig 1).

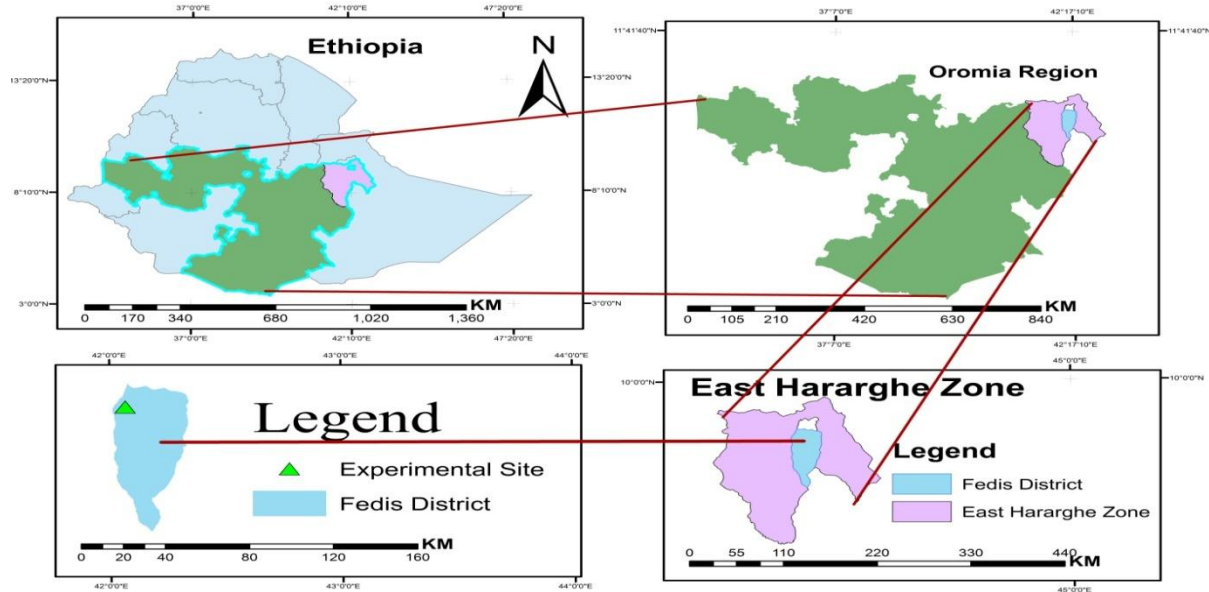


Fig 1. Map of the study area eastern Ethiopia

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 Fadis, eastern Ethiopia

| N <sub>o</sub> . | Genotypes      | Source | N <sub>o</sub> | 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 <sup>(2)</sup>.

Genotypic variance ( $\sigma^2g$ ) = (Mg-Me)/r Where Mg = mean square of genotypes, Me = mean square of error, and r = number of replications;

Phenotypic variance ( $\sigma^2p$ ) =  $\sigma^2g + \sigma^2e$ , where  $\sigma^2g$ = genotypic variance and  $\sigma^2e$  = 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 =  $\sqrt{\text{phenotypic variance}}$

Heritability in the broad sense was calculated using <sup>(3)</sup> as follows:  $H^2 = (\sigma^2 g) / (\sigma^2 p) \times 100$

The heritability was categorized as low (0-30%), moderate (30-60%) and high (60% and above) as given by <sup>(5)</sup>.

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 <sup>(4)</sup>:

$$GA = k * \sigma_p * H^2$$

k =selection intensity (= i) (standardized selection differential)

e. g. k=2.063 for 5% selection intensity

$\sigma_p$  = phenotypic standard deviation

H = 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(cm)         | 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(g)   | 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  |

Key: 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

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, (<sup>8, 9, 10, 11, 12, 13</sup>) 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 (<sup>14, 15</sup>) 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 (<sup>7, 16</sup>) 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 (<sup>14</sup>) 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 (<sup>17</sup>) 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.

#### REFERNECE

1. Lima, I., Bruzi A., Botelho F., and Zambiazzi E., 2015. Performance of conventional and transgenic soybean cultivars in the South and Alto Paranaíba Regions of Minas Gerais, Brazil. *American Journal of Plant Science*. 6: 1385
2. Falconer, D. 1981. *Introduction to quantitative genetics*. Oliver Boyd, London. pp 340.
3. Hallauer, A. and Miranda, J. 1988. *Quantitative Genetics in Maize Breeding*. 2<sup>nd</sup> edition. Iowa State University Press, Ames. 468.
4. Johnson, R. and Comstock, 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* 47: 314-318.
5. Robinson, H., Comstock, R. and Harvey, P. 1949. Estimates of heritability and degree of dominance in corn. *Agronomy Journal* 41:353-359.
6. Talla, R., Sujatha P., Jhansi R. and Ramesh T. 2018. Genetic variability and divergence of morphological and seed quality traits of soybean (*Glycine max* L. Merrill.) *Research Journal of Agricultural Sciences*.
7. Bhakuni, V. Shukla P., Singh K. and Vikash Kumar Singh. 2017. Morphological characterization and assessment of genetic variability in soybean varieties. *International Journal of Current Microbiology and Applied Science*. 6(3): 361-369.
8. Ramteke, R., Kumar, V., Murlidharan, P. and Agarwal, D. 2010. Study on genetic variability and traits interrelationship among released soybean varieties of India [ *Glycine max* (L.) Merrill ], 1(6): 1483–1487.
9. Badkul, A., Shrivastava, B., Rajani, B. and Stuti, M., 2013. Genetic variability, association and path analyses in advanced generation fixed lines of soybean [*Glycine max* (L.) Merr]
10. Teixeira, F., Hamawaki, O., Hamawaki, R., Jorge, G. and Hamawaki C. 2017. Genetic parameters and selection of soybean lines based on selection indexes, 16(3): 1-17.
11. Bizari, E., Val, B., Pereira, E., Mauro, A., and Unêda, S. 2017. Selection indices for agronomic traits in segregating populations of soybean. *Revista Ciência Agronômica*, 48(1):110-117
12. Joshi, P., Kamendra S. and Sneha A., 2018. Study of genetic parameters in soybean germplasm based on yield and yield contributing traits. *International Journal of Current Microbiology and Applied Sciences* 7(1): 700-709.
13. Shruti, K. and Basavaraja, G. 2019. Genetic variability studies on yield and yield toment Traits of soybean. *International Journal of Current Microbiology and Applied Science*. 8(02): 1269-1274.

14. Wanderi, S., Githiri, J. and Muthomi, J. 2013. Assessment of genetic variability among Kenyan soybean (*Glycine max* (L.) Merrill) accessions and other introductions. Joint proceedings of the 27<sup>th</sup> Soil Science Society of East Africa and the 6<sup>th</sup> African Soil Science Society.
15. Deresse Hunde, 2017. Genetic variability, heritability and genetic advances of soybean (*Glycine max* (L.) Merrill) varieties grown at Bako Tibe in Western Ethiopia. *Asian Journal of Plant Science and Research*
16. Nutan, P. and Gabriel M. 2016. Study on genetic variability and character association in soybean [*Glycine max* (L.) Merrill] germplasm at vindhyan zone of Uttar Pradesh. *Agricultural Science Digestion*. : 69-71
17. Sunday, O., and Omolara, O., 2014. Quantitative genetic variation, heritability and genetic advance in the segregating F3 populations in soybean (*Glycine max* (L.) Merrill). *International Journal of Advanced Research*.