AJBS
Asian Journal of
Biological
Sciences

OPEN ACCESS

Assessment of Genetic Variability, Heritability and Genetic Advance in Soybean (*Glycine max* (L.) Merrill) Genotypes at Assosa, Western Ethiopia

[1]Wakjira Getachew Fufa and [2]Gudeta Nepir

[1]Assosa Agricultural Research Center, Ethiopian Institute of Agricultural Research P.O. Box 65, Addis Ababa, Ethiopia
[2]Ambo University, P.O. Box 552, Ambo, Ethiopia

ABSTRACT

Background and Objective: Soybean is a highly nutritious diet that can play a major role in the human body, but soybean production in Ethiopia faces challenges like pests and diseases, limited to improved seeds, resulting in low productivity, Hence, this experiment assessed the genetic variability, heritability and genetic advance in soybean genotypes. **Materials and Methods:** The 49 soybean genotypes were evaluated using a simple lattice design with two replications at Assosa Agricultural Research Center during the main cropping season of 2020/21. The various agronomic characteristics of days to maturity, plant height (cm), number of pods, number of seeds, fresh weight of biomass (g), dry weight of the plant (g), pod length (cm), number of nodules per plant, oil content (percentage) content, 100 seed weight (g) and grain yield were recorded using random sampling techniques. **Results:** The phenotypic coefficients of variation ranged from 8.7 to 46.21% and the genotypic coefficients from 6.92 to 32.94%. Traits like yield, biomass weight, plant height and seed count showed high heritability and genetic advancement, suggesting potential for improvement through selection. Cluster analysis identified five groups, with the largest distance between Clusters 2 and 5 and the smallest between Clusters 1 and 3. Clusters III and IV had the highest intra-cluster distances. The first five principal components explained 79% of the total variation. **Conclusion:** The research revealed that there was adequate variability among the genotypes studied, as well as the possibility of increasing grain and oil yield by selecting superior genotypes. As a result, pre-breeding practices could be made among sub-clusters and between distant clusters to generate further variability.

KEYWORDS

Genetic variability, genotypic variance, heritability, euclidian distance, cluster

INTRODUCTION

Soybean *Glycine max* (L.) Merrill is a globally significant leguminous crop, valued for its protein and oil content, serving both human and animal nutrition needs[1]. It offers substantial health benefits and disease prevention properties[2]. The crop is classified under the family Leguminacae, subfamily Papilionoideae,

ISSN: 1996-3351 (Print)
https://doi.org/10.3923/ajbs.2025.83.92

Received: 01 Jun. 2024
Accepted: 01 Oct. 2024
Published: 31 Mar. 2025

tribe Phaseolae and genus *Glycine*[3]. It is believed to have been domesticated in Asia, most likely in North Eastern China[4]. The initiation of soybean breeding in Ethiopia dates back to the 1950s, focusing primarily on assessing introduced varieties. The main objective was to enhance the production of soybean flour and integrate the crop into the existing production system, thereby enriching the diets of impoverished farmers[5].

Despite its significant importance, soybean breeding in Ethiopia focuses predominantly on the introduction of new genes; evaluations are conducted to identify varieties suitable for the country and potential areas for crop production[6]. Therefore, expanding genetic diversity through germplasm introduction is vital for enhancing soybean breeding[7]. Genetic characteristics that are essential for successful breeding programs include heritability, genetic advance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). Grasping the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance of a trait are essential for applying efficient selection techniques. This knowledge enables plant breeders to anticipate the genetic improvement of any quantitative traits[8].

The narrow genetic base of soybean production impacts grain yield and oilseed quality, leading to a decline in production over time[9]. This decline is aggravated by a lack of improved varieties, along with factors such as poor agronomic practices, insect pests and diseases in Ethiopia[10]. To address these challenges, identifying adaptable and stable genotypes with desirable agronomic traits, high yield potential and resistance to stresses is crucial. So genetic variability is essential for breeding programs to enhance soybean production quality and meet industry standards[9]. Hence, comprehensive research was conducted to meticulously assess the degree of phenotypic and genotypic variability, heritability and the genetic advance anticipated through selection processes.

MATERIALS AND METHODS

The experimental study was carried out at Assosa Agricultural Research Center. The 49 soybean genotypes were evaluated for their genetic parameter performances. The materials were sown out to the field in a simple lattice design with two replications during the main cropping season of 2020/21.

Experimental site: The study site is Assosa Agricultural Research Center on a station located at Latitude of 9°30' to 11°39"N and Longitude of 34°20' to 36°30"E. It is 660 km from Addis Ababa to the west of the country and 1550 m above sea level (masl). It also has an unimodal pattern of rainfall beginning at the end of April and lasting until mid-November, with maximum rainfall occurring in June, July and August. The overall average annual Assosa rainfall is 1275 mm. The temperatures of minimum and maximum are 17 and 28°C, respectively. The dominant soil type of Benishangul Gumuz Region is Nitosols while the experimental site also included this type of soil with pH of 5.0 to 6.0 ranges.

Experimental design and management: The experiment consists of 49 soybean genotypes along with check varieties (Bellesa 95 and Gishama and SCS 1) were evaluated in this experiment. Using 7×7 simple lattice designs, the field experiment was carried out. Four rows of plants were planted in a plot measuring 3 m in length, with regular spacing of 5 cm between plants and 60 cm between rows. Two seeds were carefully placed in each hill to guarantee the first germination and thinning was done 1-2 weeks after emergence. During sowing, NPS fertilizer was applied at the recommended rate of 122 kg/hectare and the remaining agronomic management was carried out in accordance with the recommendation. The following significant agronomic characteristics were recorded using random sampling techniques: Days to 50% flower initiation, days to maturity, plant height (cm), branch per plant, number of pods per plant, number of seeds per pod, total number of seeds per plant, fresh weight of biomass (g), dry weight of the plant (g), number of primary branches per plant, number of pods per primary branches per plant, number of seeds per primary branches per plant, pod length (cm), number of nodules per plant, oil content (%), 100 seed weight (g) and grain yield (kg/ha). The center two harvestable rows served as the source of all the data.

Statistical analysis: All the data were analyzed using Analysis of Variance (ANOVA) and mean separation was tested with the least significant difference (LSD) at a 5% probability level, following the method of Gomez and Gomez[11] with SAS 9.2 software. Genotypic and phenotypic variances were determined using the formulas provided by Miller *et al.*[12]. Genotypic, phenotypic and environmental coefficients of variability were calculated for each studied trait, based on the methodology outlined by Burton and Devane[13]. The heritability coefficient (h^2), representing the ratio of genotypic variance to phenotypic variance, was computed according to the method described by Allard[14]:

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

Where:

h^2b = Heritability in a broad sense
σ^2p = Phenotypic variance and
σ^2g = Genotypic variance

Genetic advance (GA) for each character studied was calculated as given by Johansson *et al.*[15]:

$$GA = h^2\ KP$$

Where:

h^2 = Heritability
P = Phenotype and
K = Selection differential which is equal to 2.06 at 5% intensity of selection[16]

Genetic advance as percent of mean (GAM):

$$EGA = K\sigma^2 x_p H^2$$

Genetic advance at 5% selection intensity was estimated as following[14]:

$$GAM = \frac{EGA}{\text{Grand mean}} \times 100$$

Where:

GAM = Genetic advance per population mean and
EGA = Estimates of expected genetic advance

Genetic divergence and clustering: Clustering was done for 49 genotypes after standardization mean values of each trait.

Genetic distance: Phenotypic genetic distance was computed using MINITAB 17[17]. Software based on phenotypic data collected from 49 soybean genotypes using average Euclidean distance (ED) as follows[18]:

$$EDjk = \sqrt{\sum_{i=1}^{n} (xij - xik)^2}$$

Where:

Edjk = Distance between genotypes j and k
xij, xik = Value of phenotypic trait of the ith character for genotypes j and k, respectively
N = Number of phenotype traits used to calculate the distance
W, D^2p = Total generalized distance based on p characters, Xi and Xj are the p mean vectors of 49 test genotypes i and j, respectively
S-1 = Pooled error variance and co-variance matrix

RESULTS AND DISCUSSION

Mean, range and estimates of genetic parameters: Range and mean values of the 17 characters studied. The 49 soybean genotypes showed highly significant ($p<0.01$) variations among the genotypes for all traits studied. As indicated in (Table 1) mean values of seed yield, 100 seed weight and oil content ranged from 0.5 to 2.8, 100 seed weight 6.3 to 15.7 oil content and 15.0 to 22.8 with mean values of 1.4, 11.1 and 18.6. The maximum plant height was recorded for Tgx-2010-12F (91.3 cm), followed by Tgx-2010- 3F (91.2 cm), Tgx-1990-55F (77.8 cm) and Tgx-1990-59p (69.9 cm) while the minimum plant height was recorded for T34-15-T73-16-SD1 (45.7 cm), JM-ALM/H3-15-SG (48.2) and JM- ALM/H3-15-SF-2 (50.1 cm). About 40.8% of the genotypes were found greater than an average value (66.92 cm) of plant height and 59.2% of the genotypes were found less than an average value.

The genotypes Tgx-2007-11F (2.8 t/ha, PB-12-4 (2.6 t/ha), PB-12-6 (2.6 t/ha) Tgx-1987-68F (2.5 t/ha) had superior seed yield performances. On the other hand, maximum oil yield was recorded from PB-12-6 (23.2%), 5002T (20.9%), PB-12-4 (21.1%) and PM12-12 (20.2%) had superior oil content of which PB-12-4 is high yielder of both seed and oil yield whereas the minimum oil yield was recorded from PM12-11 (15.7%), Tgx-1987-10F (16.6%), Tgx-1448-2F (17%) and Tgx-1990-57F (17.2%).

The maximum number of branch per plant was recorded for Tgx-2011-3F (5.5 no) followed by Tgx-1989-19F (5.3 no), T44-15-T105-16-sc1 (5.1 no), T47-15-T126-16-SF1 (5.1 no), PB-12-6 (5 no), while the minimum number of branch per plant was recorded from Tgx-2008-2F (2.5 no), JM- T34-15-T73-16-SD1 (2.6 no) and ALM/H3-15-SG (3 no). The maximum pod length was recorded for PB-12-6 (4.6 cm) and PB-12-5 (4.6 cm) while the minimum pod length recorded from Tgx-1935-10F (2.9 cm), Tgx-1987-10 F (2.9 cm) and pb-12-2 (2.9 cm).

The present results revealed that 65, 43 and 18% of the test genotypes were earlier in the total number of days to maturity relative to when compared with the standard checks (Gishamam, Belessa-1 and SCS-1), respectively. For the number of days to 50% flowering, 63, 47 and 59% of the test genotypes were earlier than (Gishama, Belessa-1 and SCS-1), respectively. For seed yield, 91.8, 61.2 and 57.1% of these genotypes

Table 1: Estimation of genetic parameters, range and mean of soybean genotypes

Traits	Range	Mean±SE	GV/σ^2g	σ^2e	PV/σ^2p	PCV	GCV	H^2 (%)	GA	GAM (%)
DF	57.00-90.00	71.9±0.7	40.96	8.34	9.30	13.21	9.76	83.08	12.03	16.73
DM	96.00-153.00	126.6±16	212.90	14.54	27.44	16.57	11.91	93.61	29.08	0.22
PH	43.00-97.9.00	65.6±1.32	123.78	4.69	128.47	24.22	751	96.35	22.50	34.31
NBPP	1.9.00-6.2.00	4.0±0.09	0.29	0.27	0.56	22.63	18.38	51.69	0.80	19.57
NSPP	1.9.00-2.8.00	2.1±0.02	0.02	0.02	0.04	12.03	9.59	57.33	0.24	11.32
NPPP	15.2.00-55.00	28.8±0.77	29.92	6.48	36.40	28.24	20.92	82.20	10.22	35.42
TNSPP	29.5.00-95.7.00	53.8±1.51	156.15	12.47	168.62	33.46	24.11	92.60	24.77	45.99
NDPP	23.6.00-83.5.00	57.5±1.41	124.13	23.71	147.83	28.66	21.13	83.96	21.03	36.55
FWT	196.89-685.16.0	376.9±11.17	152.68	196.72	9349.40	36.08	25.65	97.90	195.00	51.73
DWT	57.3.00-182.4.00	117.2±3.40	939.79	41.78	981.57	37.39	26.73	95.74	61.79	52.72
PLTH	2.6.00-4.9.00	3.6±0.04	0.07	0.08	0.16	13.36	10.99	47.75	0.39	10.81
NPB	1.9.00-6.2.00	4.0±0.09	0.29	0.27	0.56	22.63	18.38	51.69	0.80	19.57
NPPBR	.3.00-31.7.00	15.7±0.55	19.11	3.25	22.35	40.99	30.10	85.48	8.33	53.00
NSPPBP	8.7.00-58.1.00	28.9±0.07	82.05	8.66	90.71	45.45	32.94	90.46	17.75	61.37
OILC	15.00-23.00	18.6±0.0	0.96	0.70	1.65	8.70	6.92	57.86	1.53	8.25
HSWT	6.3.00-15.7.00	11.1±0.17	1.18	1.05	2.23	16.70	13.50	52.98	1.63	14.74
SYTPH	0.5.00-2.8.00	1.4±0.0	0.21	0.01	0.22	46.21	32.81	98.30	0.95	66.45

DF: Days to flower, DM: Days to maturity, PH: Plant height (cm), NBPP: Number of branch per plant, NSPP: Number of seeds per pod, NPPP: Number of pod per plant, TNSPP: Total number of seed per plant, NDPP: Number of nodule per plant, FWT: Fresh weight of biomass (gm), DWT: Dry weight (gm), PLTH: Pod length (cm), NPB: Number of primary braches per plant, NPPBR: Number of pods per primary branches per plant, NSPPBP: Number of seeds per primary branches per plant, OILC: Oil content, HSWT: Hundred seed weight(gm), SYTPH: Seed yield tone per hectare, Mean±SE: Standard error of the mean, σ^2g: Genotypic variance, σ^2e: Environmental variance, σ^2p: Phenotypic variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, H^2: Heritability, GA: Genetic advance and GAM: Genetic advance as percent of mean were superior relative to (Gishama, Belessa-1 and SCS-1), respectively and 40.8% were superior to the trial mean. All characters showed wide ranges of variability which could be utilized in breeding programs. So, traits with the highest ranges significantly contributed to the overall variability of soybean varieties. This suggests the potential for selecting these traits for future breeding efforts. Consistent with this finding by researchers[9,19-22] reported a wide range of variability was found among the tested genotypes for the 49 traits. In general, the range of data demonstrates ample potential for enhancing desired traits, with the mean range indicating significant genetic and morphological variability among the tested genotypes. However, there remains limited information on the extent and patterns of soybean genetic variability concerning desirable traits. To address these challenges, it is crucial to identify genotypes with desirable traits, high yield potential and information for the next step breeding program.

Estimation of variance components: The yield and yield-attributing traits of soybean were shown in Table 1 along with the estimated genotypic (GV,σ^2g), phenotypic and environmental (σ^2e) variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2b), genetic advance (GA) and genetic advance as a percentage of the means (GA%). For every characteristic under study, the phenotypic variance values were greater than the matching genotypic variance values.

Dry weight, fresh weight of biomass, days to maturity, total number of seeds per plant, number of nodules per plant, plant height, number of seeds per primary branches per plant, days to flowering, seed yield and the number of pods per primary branches per plant have demonstrated high genotypic and phenotypic variances. Similar findings in soybean have been documented by Adity *et al.*[9] Tesfate *et al.*[21] and Getnet[23]. The presence of such substantial genotypic and phenotypic variances indicates sufficient variability among the genotypes for these traits.

The fresh weight of biomass exhibited the highest phenotypic variance (9349.40), while the number of seeds per pod showed the lowest (0.04). Similarly, the fresh weight of biomass displayed the highest genotypic variance (9152.68), with the number of seeds per pod having the lowest value (0.02). Seed yield, number of pods per plant, total number of seeds per plant, number of nodules per plant, fresh weight of biomass (gm), dry weight (gm), number of pods per primary branches per plant and number of seeds per primary branches per plant recorded the highest PCV and GCV values, indicating ample variability for these traits, which facilitates enhancement in their respective characteristics.

The PCV and GCV values exceeding 20% are classified as high, while those below 10% are deemed low and values falling between 10 and 20% are considered medium. According to this classification system, the genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were categorized as medium for hundred-seed weight, days to maturity and pod length. This classification aligns with the moderate PCV values reported by Getnet *et al.*[23], as well as findings by Guleria *et al.*[24]. Similarly, medium GCV values were observed for the number of branches per plant, number of primary branches per plant, hundred-seed weight and days to maturity, as documented by Adity *et al.*[9] and Guleria *et al.*[24]. High PCV values were recorded for the number of pods per primary branches per plant, number of seeds per primary branches per plant and seed yield.

Estimation of heritability and genetic advance: Heritability values are classified as very high ($\geq$60%), moderate (30-60%) and low ($\leq$0-30%)[25]. The range of heritability values varied from 47.75% for pod length to 98.30% for yield. Most of the traits exhibited high heritability. In agreement with this result, high heritability for dry weight[9] for plant height, seed yield[26], for days to maturity, number of nodules per plant and number of pods per plant[22]. Moderate heritability was observed in traits such as the number of branches per plant, number of seeds per pod, pod length (cm), number of primary branches per plant, oil content and hundred seed weight (gm). Contrarily, traits with low heritability, selection may be impractical due to the masking effect of the environment.

Genetic advance as a percentage of the mean varied from 0.24% for the number of seeds per pod to 66.45% for seed yield. The highest genetic advance percentage was observed in seed yield, followed by the number of seeds per primary branch per plant, the number of pods per primary branch per plant, dry weight, fresh biomass weight, total number of seeds per plant, number of nodules per plant and number of pods per plant. Similarly, a high genetic advance percentage for plant height in soybeans has been reported[23], for the number of pods per plant[27] for the total number of seeds per plant[28] for seed yield and fresh weight of biomass[21,29].

High heritability estimates coupled with a high GAM are typically more useful than heritability estimates alone in predicting benefit under selection[14]. High heritability coupled with high genetic advance as percent of the mean for yield (9 8.3 and 66.45%) for the fresh weight of biomass (97.3 and 51%), plant height (96 and 34%), dry weight (95 and 52%), total number of seed per plant (92 and 45.99%), number of seeds per primary branches per plant (90 and 61%), number of pods per primary branches per plant (85 and 53%), number of nodule per plant (83 and 36%) and number of pod per plant.

Presence of high genetic advance along with high heritability is the most important to implementing selection[30], indicating that additive genes play a role in trait inheritance. Similarly, high heritability coupled with high genetic advance as percent of mean has been reported, for dry weight[9] for plant height, grain yield, number of seeds, number of pod and number of nodules per plant[23-31] for fresh weight of biomass[20]. As a result, high heritability values combined with high GAM for characters like plant height, number of seeds and grain yield will help to predict benefit under selection. Furthermore, such characters can be used to achieve successful phenotypic selection and high genetic benefit.

Cluster analysis and grouping of soybean genotypes: Cluster analysis is a multivariate technique whose primary goal is to group individuals or things based on shared qualities, allowing individuals with similar statistically descriptions. Cluster analysis for 49 soybean genotypes shows that distribution of genotypes into five clusters presented in Cluster I comprised 4 genotypes, accounting for 8.1% of the total. Cluster II represented 10.2% with 5 genotypes. Cluster III was the most extensive, consisting of 29 genotypes, making up 59.1% of the population. Cluster IV had teen genotypes, contributing 20.4%, while Cluster V had one genotype, representing 2.0%. These results indicate a significant level of divergence among the genotypes in Table 2.

Cluster mean analysis revealed distinct trait characteristics within each cluster. Genotypes in Cluster I exhibited the highest mean values for several traits, including the number of seeds per pod and the second highest for the number of branches per plant, total seed yield per plant, number of primary branches per plant and number of seeds per primary branch per plant. However, they displayed the lowest mean value for hundred-seed weight, suggesting better yield and oil content. Thus, selecting based on Cluster I criteria could lead to the development of high-yielding genotypes with favorable oil content. In contrast, Cluster II genotypes generally displayed lower mean values for most traits, except for the number of seeds per pod. Further identification and evaluation are necessary for genotypes in this cluster.

Table 2: Distributionof 49 genotypes into 5 cluster based Eucdidean analysis

Clusters	No. of genotypes pear each cluster	List of genotypes per each cluster
C I	4	T44-15-T105-16-sc1, Tgx-2011-3F, Tgx-1989-19F and TgX-1987-68F
C II	5	PI417089A,JM-ALM/H3-15-SG,JM-ALM/H3-15-SF-2, T34-15-T73-16-SD1 and PB-12-7
C III	29	PI471904, JM-CLK/CRFD-15-SD, T47-15-T126-16-SF1,T34-15-T72-16-Sc1, T34-15-T74-16-SE1,Belessa-95(STCH),PM12-9, JM-ALM/H3-15-SB-2, PB-12-8,PM12-12,PM12-10, Tgx-1990-57F,JM-HAR/ALM-15-SB,SCS-1,JM-ALM/H3-15-SE1,PB-12-October 8, 20242,PM12-11,PB-12-3, PB-12-1, Tgx-1990-59p,5002 T,Tgx-2004-13F,Tgx-1987-10F, Tgx-2010-3F,Tgx-2010-11F,JM-PR142/CLK-15-SE,PB-12- 5, PB-12-6 and Tgx-2007-11F
C IV	10	Tgx-2008-4F, Tgx-1935-10F, Tgx-2004-3F,Tgx-1448-2F,Tgx-1990-78F, Gishama (Check),Tgx-2006-3F,Tgx-1990-55F and Tgx-2010-12F and Tgx2008-2F
C V	1	PB-12-4

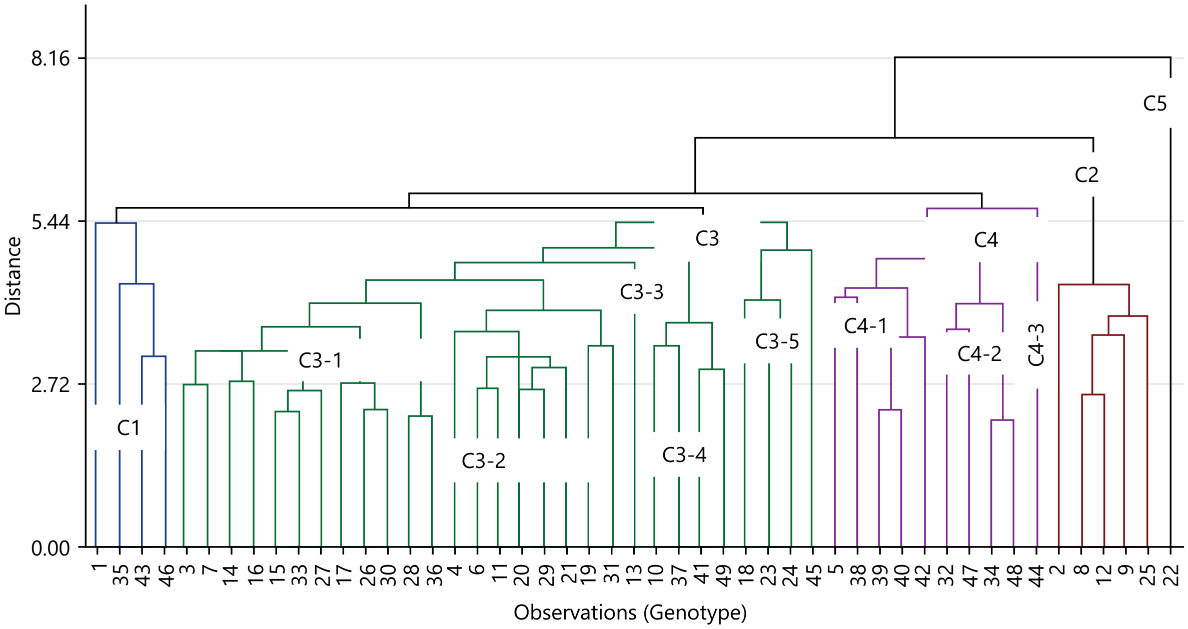

Fig. 1: Dendrogram with average linkage and Euclidean distances using 17 phenotypic traits

Table 3: Cluster numbers, numbers of genotypes, proportion, average distance from centroids for 49 soybean genotypes for 17 traits

Clusters	No. of genotypes	Within cluster sum of squares	Average distance from centroid	Maximum distance from centroid
C I	4	34.330	2.881	3.690
C II	5	30.699	2.431	3.068
C III	29	309.264	3.185	4.877
C IV	10	101.187	3.098	4.332
C V	1	0.000	0.000	0.000

C: Cluster

Table 4: Euclidean distance between cluster based on 17 phenotypic traits in soybean

	C I	C II	C III	C IV	C V
C I		8.102	3.71	6.025	5.299
C II			5.481	5.083	11.731
C III				3.609	6.662
C IV					9.007
C V					9.007

C: Cluster

Genotypes in Cluster III showed the highest mean values for plant height, pod length, days to flowering, number of pods per plant, nodule number, fresh biomass weight, seed yield and oil content, with the lowest mean value for hundred-seed weight. This cluster presents an opportunity to develop shorter genotype types for breeding programs.

Cluster IV genotypes exhibited the highest mean values for days to flowering, maturity, dry weight, oil content, plant height and hundred-seed weight, making them a favorable option next to Cluster III for plant height. Finally, Cluster V genotypes displayed the highest mean values for all traits except days to flowering, suggesting potential for enhancing soybean genotypes, especially in terms of yield components. These clusters offer opportunities for improving soybean genotypes, with Cluster V presenting a comprehensive array of traits conducive to enhancement. Similar findings regarding high grain yield in soybean genotypes have been reported by Malik *et al.*[32].

Cluster distance of soybean genotypes: A maximum Euclidean distance (4.877) from the average distance (4.877) among genotypes of the same cluster was recorded from Cluster III which had 29 genotypes. This cluster also showed a maximum intra cluster sum of squares (309.264). Similarly, Cluster IV had the next maximum distance (4.332) from the average distance of genotypes (3.098) grouped in this cluster and intra-cluster sum of squares (101.187). On the other hand Cluster V was solitary (Table 3).

The inter cluster Euclidean distances of genotypes are presented in (Table 4). Maximum Euclidean distances (11.731) were recorded between Cluster II and Cluster V followed by Cluster IV and V (Euclidean distance = 9.007). A contrarily minimum distance (3.609) was recorded between Cluster I and III as shown in Fig. 1.

CONCLUSION

In the current study, over 40.8% of soybean genotypes surpassed check cultivars in grain yield. Phenotypic coefficients of variation (PCV) ranged from 8.7% for oil content to 46.21% for seed yield, while genotypic coefficients of variation (GCV) ranged from 6.92% for oil content to 32.94% for seeds per branch. Heritability values varied from 47.75 to 98.30%. Significant variability was observed in traits like seed yield and pod count. The 49 genotypes were grouped into five clusters, with notable variability potential between distant clusters. Promising seed and oil yield enhancement genotypes include Tgx-2007-11F, Tgx-1987-68F, PB-12-4, PB-12-6 and 5002T, which could be harnessed in future soybean breeding programs.

SIGNIFICANTEC STATEMENT

This study identified significant genetic variability among soybean genotypes. Soybean productivity in Ethiopia is low due to limited improved varieties and a narrow genetic base. Developing high-yielding, adapted varieties is crucial. Understanding genetic variation, heritability and genetic advance is key for productivity enhancement. Traits positively associated with seed yield can guide selection criteria. Traits with strong genotypic associations with seed and oil yield may be influenced by linked genes. High heritability, GCV and GAM in many traits suggest potential for improvement through recurrent selection. Genotypes Tgx-2007-11F, Tgx-1987-68F and PB-12-4 are promising for seed yield, while PB-12-6, PB-12-4 and 5002T are suitable for high oil yield. The study shows sufficient variability for future breeding.

ACKNOWLEDGMENT

The author expresses gratitude to the Ethiopian Institute of Agricultural Research for providing the necessary resources and facilities to conduct this research.

REFERENCES

1. Sharma, S., M. Kaur, R. Goyal and B.S. Gill, 2014. Physical characteristics and nutritional composition of some new soybean (*Glycine max* (L.) Merrill) genotypes. J. Food Sci. Technol., 51: 551-557.
2. Hea, F.J. and J.Q. Chen, 2017. Consumption of soya bean: The link to decreased breast cancer incidence. Oilseeds Focus, 3: 34-37.
3. Hymowitz, T., 2004. Speciation and Cytogenetics. In: Soybeans: Improvement, Production, and Uses, Shibles, R.M., J.E. Harper, R.F. Wilson and R.C. Shoemaker (Eds.), American Society of Agronomy, Crop Science Society of America, and Soil Science Society of America, Madison, Wisconsin, ISBN: 9780891182665, pp: 97-136.
4. Sileshi, Y., M. Yirga, M.H. Mariam and B. Atero, 2020. Performance of released soybean varieties at Jimma, South Western Ethiopia. J. Biol. Agric. Healthcare, 10: 12-15.
5. Jeong, S.C., J.K. Moon, S.K. Park, M.S. Kim and K. Lee *et al*., 2019. Genetic diversity patterns and domestication origin of soybean. Theor. Appl. Genet., 132: 1179-1193.
6. Arshad, M., N. Ali and Abdul Ghafoor, 2006. Character correlation and path coefficient in soybean *Glycine max* (L.) Merrill. Pak. J. Bot., 38: 121-130.
7. Jahufer, M.Z.Z. and F.I. Gawler, 2000. Genotypic variation for seed yield components in white clover (*Trifolium repens* L.). Aust. J. Agric. Res., 51: 657-663.

8. Jandong, E.A., M.I. Uguru and E.C. Okechukwu, 2020. Estimates of genetic variability, heritability and genetic advance for agronomic and yield traits in soybean (*Glycine max* L.). Afr. J. Biotechnol., 19: 201-206.
9. Aditya, J.P., P. Bhartiya and A. Bhartiya, 2011. Genetic variability, heritability and character association for yield and component characters in soybean (*G. max* (L.) Merrill). J. Cent. Eur. Agric., 12: 27-34.
10. Berhanu, H., B. Tesso and D. Lule, 2021. Correlation and path coefficient analysis for seed yield and yield related traits in soybean (*Glycine max* (L.)) genotypes. Plant, 9: 106-110.
11. Gomez, K.A. and A.A. Gomez, 1984. Statistical Procedures for Agricultural Research. 2nd Edn., John Wiley & Sons Inc., New York, ISBN: 9780471870920, Pages: 704.
12. Miller, P.A., J.C. Williams, H.F. Robinson and R.E. Comstock, 1958. Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. Agron. J., 50: 126-131.
13. Burton, G.W. and E.H. Devane, 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron. J., 45: 478-481.
14. Allard, R.W., 1960. Principles of Plant Breeding. Wiley, Hoboken, New Jersey, ISBN: 9780471023104, Pages: 485.
15. Johnson, H.W., H.F. Robinson and R.E. Comstock, 1955. Estimates of genetic and environmental variability in soybeans. Agron. J., 47: 314-318.
16. Lush, J.L., 1949. Heritability of quantitative characters in farm animals. Hereditas, 35: 356-375.
17. Lee, C.F., J. Lee, J.R. Chang and T. Tai, 2016. Essentials of Excel, Excel VBA, SAS and Minitab for Statistical and Financial Analyses. 1st Edn., Springer, Cham, Switzerland, ISBN: 978-3-319-38867-0, Pages: 1041.
18. Sokal, R.R., 1979. Testing statistical significance of geographic variation patterns. Syst. Biol., 28: 227-232.
19. Amogne, A., M. Atnaf and M. Bantayehu, 2020. Association of traits in soybean (*Glycine max* (L.) Merrill) genotypes in Northwestern Ethiopia. Int. J. Sci. Eng. Sci., 4: 8-14.
20. Osekita, O.S. and O. Olorunfemi, 2014. Quantitative genetic variation, heritability and genetic advance in the segregating F3 populations in soybean (*Glycine max* (L.) Merril. Int. J. Adv. Res., 2: 82-89.
21. Tesfaye, A., M. Githiri, J. Derera and T. Debele, 2017. Genetic variability in soybean (*Glycine max* L.) for low soil phosphorus tolerance. Ethiopian J. Agric. Sci., 27: 1-15.
22. Neelima, G., S.P. Mehtre and G.W. Narkhede, 2018. Genetic variability, heritability and genetic advance in soybean. Int. J. Pure Appl. Biosci., 6: 1011-1017.
23. Getnet, B.E., 2019. Genetic variability, heritability and expected genetic advance as indices for selection in soybean [*Glycine max* (L.) Merrill] varieties. Am. J. Life Sci., 6: 52-56.
24. Guleria, H., P. Kumar, B. Jyoti, A. Kumar, A. Paliwal and A. Paliwal, 2019. Genetic variability and correlation analysis in soybean (*Glycine max* (L.) Merrill) genotypes. Int. J. Chem. Stud., 7: 1928-1932.
25. Robinson, H.F., R.E. Comstock and P.H. Harvey, 1955. Genetic variances in open pollinated varieties of corn. Genetics, 40: 45-60.
26. Malek, M.A., M.Y. Rafii, M.S.S. Afroz, U.K. Nath and M.M.A. Mondal, 2014. Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. Sci. World J., Vol. 2014. 10.1155/2014/968796
27. Ali, A., S.A. Khan, N. Ali and I. Hussain, 2016. Estimation of genetic parameters in soybean for yield and morphological characters. Pak. J. Agric. Agric. Eng. Vet. Sci., 32: 162-168.
28. Yirga, M., Y. Sileshi and M. Hailemariam, 2021. Genetic variability of soybean (*Glycine max* (L) Merrill) genotypes under moisture stress areas of Ethiopia. J. Plant Sci., 9: 316-322.
29. Debela, C., T. Tana and L. Wogi, 2021. Effect of rhizobium inoculation, NPS fertilizer and vermicompost on nodulation and yield of soybean (*Glycine max* (L). Merrill) at Bako, Western Ethiopia. J. Chem. Environ. Biol. Eng., 5: 49-61.
30. Larik, A.S. and L.S. Rajput, 2000. Estimation of selection indices in *Brassica juncea* L. and *Brassica napus* L. Pak. J. Bot., 32: 323-330.

31. Kumar, S., V. Kumari and V. Kumar, 2018. Genetic variability and character association studies for seed yield and component characters in soybean [*Glycine max* (L.) Merrill] under North-Western Himalayas. Legume Res., 43: 507-511.
32. Malik, M.F.A., M. Ashraf, A.S. Qureshi and M.R. Khan, 2011. Investigation and comparison of some morphological traits of the soybean populations using cluster analysis. Pak. J. Bot., 43: 1249-1255.