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Agro-Morphological Trait Characterization of Selected Soybean [Glycine *Max (L.)* Merr.] Accessions at Dabus in Assosa

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***Abstract:** As study Soybean is the most important and widely grown legume crop worldwide with its multipurpose use and grows in the tropical, subtropical and temperate climates. In Ethiopia, soybean is becoming a high potential promising crop for the development of agricultural sectors. Targeting variety selection in its growing environments is the prime interest of any plant breeding program with respect to important parameters of morphological traits. Twenty soybean accessions were obtained from three geographic areas of Assosa and laid out in a randomized complete block design with three replications. Higher phenotypic and genotypic variance was observed for grain yield. Branches per plant, pods per plant, seeds per pod and grain yield had higher PCV while plant height exhibited moderate PCV. Genotypic coefficient variance was high for pods per plant and grain yield whereas plant height and seeds per pod showed moderate GCV. Days to flowering and maturity, plant height, pods per plant and seeds per pod had high heritability whereas relatively moderate H^2 was recorded for HSW and grain yield. Significant genetic variability in mean performance of all the traits under studied material indicated that genotypes have considerable amounts of genetic variation that could be used for further breeding programs in variety development. Finally, characterization of soya bean accession with genotype of GDM7 had highest 2478kg/ha grain yield and this accession is recommended for better adaptation and yield for cultivation of farmers' in Assosa zone and similar agro ecology in Ethiopia.*

***Keywords:** Crop; Family; Genotype; Heritability; Seed; Yield.*

Abbreviation

PCV: Phenotypic Coefficient of Variation
GCV: Genotypic Coefficient of Variation
GA: Genetic Advance
ANOVA: Analysis of Variance
RCBD: Randomized Complete Block Design
GLM: General Linear Model
LSD: Least Significant Differences
GH: Growth Habit
LS: Leaf Shape
SS: Seed Size
TC: Testa Color
PC: Pod Color
HC: Hair Color
DM: Days Maturity
PH: Plant Height
BPP: Branches Per Plant
HSW: Hundred Seed Weight
SPP: Seeds Per Pod
GY: Grain Yield

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I. INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a small erect and branching annual leguminous plant classified under the family *Fabacae* and subfamily *Paplionodeae* [30]. Soybean is an important global legume crop that grows in the tropical, subtropical and temperate climates [28]. It is one of the most important and widely grown legume crops worldwide due to its multipurpose use particularly in the animal feed industries and human nutrition [25]. Its high quality protein and balanced amino acid profile in ration formulation and human diets are the driving forces of soybean production [26]. Soybean seed is referred to as the "protein hope" of the future, because of its high nutritive value, containing about 42–45% protein [36]. As a legume plant, it has great agro technical significance in crop rotation [9], because along with Brady rhizobium japonicum bacteria on its root, it enriches the land with nitrogen [1]. Bacteria convert inorganic nitrogen N_2 from the atmosphere into a form appropriate for the plant NH_2 [39].

Black soybean is one of the largest sources of edible oil and accounts for roughly 50% of the total oilseed production of the world [40]. Oil crops in general and soybean in particular play an indispensible role to ensure national food security, increase smallholder farmers' income and increase export earnings particularly for developing countries including Ethiopia [41]. Despite its high production potential and economic importance, the level of adoption of improved soybean varieties and dissemination are constrained by many factors. Anthocyanins are groups of reddish or purple flavonoids which have been reported to reduce the risk of coronary heart disease. Anthocyanins are also known to have anti-cancer, hypoglycemic, and anti-inflammatory effects, which have been used in the treatment of various circulatory disorders [42].

Furthermore, these functions provide synergic effects with various nutrients in vivo, so their nutritional values are of great interest. Recently, consumption of black soybeans is rapidly growing due to their nutritional value and potential to develop as healthy functional food ingredients in different countries, especially in the east. In recent times, besides the use as a raw material of food and also it can be used as a biofuel alternative [12]. In Ethiopia, soybean is becoming a high potential promising crop identified in the framework of the strategy for the development of agricultural sectors. It is becoming a high potential crop in the country with increasing production to meet the required quantities be achieved through an increase in yield per unit area by cultivation of high-yielding improved varieties Generally Soybean is an economically important leguminous crop for feed and food products due to its relatively high seed protein (40%) and oil (20%) contents. The crop is ranked number one in the world production in the international trade markets among the major oil legume crops [31]. Targeting variety selection into its growing environments is the prime interest of any plant breeding program. To realize this, breeding programs usually undertake a rigorous genotypes performance evaluation across locations and years mostly at the final stage of the variety development process. On the other hand, the information as well as assessment of genetic variability in the existing genotype of a particular crop is sought as a prerequisite Furthermore, heritability of a plant trait is very important in determining the response to selection because it implies the extent of transmissibility of traits into next generations. Hence, the present study was carried out to evaluate and performance soybean genotypes on the basis of different qualitative traits and quantitative to analyze the variability that exists among the genotypes.

II. MATERIALS AND METHODS

A. Description of the Study Area

The experiment was conducted during 2023/2024 rain cropping (May to February) season at Dabus testing of Benishangul-Gumuz National Regional State, in Assosa Zone. The woreda's administrative town is known as Assosa. It is also the Zonal and Regional administrative town. The town is 668 km away from Addis Ababa through the Nekemte road in western direction. Assosa woreda is bordered in the North-western direction by Kurmuk and Komosha woreda, North-eastern direction bordered by Mange woreda, southern direction by Mao-Komo, Western direction by Sudan and in the Eastern direction bordered by Bambasi woredas of Benishangul-Gumuz Region.The average temperature of the woreda is 27 °C. The rainfall pattern is mono-modal rainfall distribution. The rainy season starts in May and extends to October; and the dry season starts in November and extends to the end of April. The dry seasons have a wider temperature difference mainly on the onset; it is too cold in the morning and at the night; and too hot in the midday. It has an altitude range of 1552 to 1580 m.a.s.l and lies in a geographic coordinate of 10° 02′57" N latitude and 34° 33 '26"E longitudes. It is characterized by hot humid agro-ecology having mean annual rainfall of 1316 mm per annum. The predominant soil type is Niti sols with the soil pH ranges from 5.0 to 6.0.(As [7] Assosa woredas has a total of 231,700 hectare of land. Out of the total land, 60,983 hectares of land are used for annual crop production and 13,300 hectares of land are used for perennial crops mainly fruits such as Mango, Lemon and Orange. The commonly produced field crops are maize, sorghum, soybean, finger millet and sesame [2].

B. Treatments and Experimental Design

Treatments consisted in twenty soybean accessions (GDM1, GDM2, GDM3.GDM4, GDM5, GDM6, GDM7, GDM8, GDM9, GD10, GDM11, GDM12, GDM13, GDM14, GDM15, GDM16, GDM17, GDM18, GDM19, GDM20) were collected from three geographic areas of Assosa zone using passport data. The treatments were laid out in a randomized complete block design with three replications. Plot size was 4 m wide and 3.6 m long with a total gross area of 14.4 m^2. Before planting, the experimental field was plowed, pulverized and leveled in order to have a smooth seedbed for planting. Seeds were hand planted by placing two seeds per hill at row spacing of 40 cm and plant spacing of 10 cm with seed rate of 70 kg/ha. All recommended agronomic practices such as cultivation, weeding etc., were employed during crop growing period.

Table-I: Soybean Accessions (Glycine Max (L.) Merr) and Their Area of Collection

	Accessions	Region	Woreda	District site	Latitude	Longitude
1	MPG1	Beneshagul	Abrahamo	Mengele	9º45.25’’ N	34º 48. 50’’E
2	MPD2	Beneshagul	Abrahamo	Amba 26	9º42.27’’ N	34º 45. 60’’E
3	MPG3	Beneshagul	Homesha	Ashula	10º33.25’’ N	34º 23. 50’’E
4	MPG4	Beneshagul	Homesha	Alemetema	10º33.15’’N	34º 23. 50’’E
5	MPG5	Beneshagul	Homesha	Dungaheromela	10º30.28’’N	34º 22.43’’E
6	MPG6	Beneshagul	Homesha	Shula	10º34.55’’ N	34º 28. 59’’E
7	MPG77	Beneshagul	Homesha	Molomengele	10º35.25’’ N	34º 27. 50’’E
8	MPG8	Beneshagul	Menge	kashafi	10º38.55’’ N	34º 20. 45’’E
9	MPG9	Beneshagul	Assosa	Amba6	10º5.66’’ N	34º 33. 55’’E
10	MPG10	Beneshagul	Assosa	Amba7	10º5.59’’ N	34º 33. 48’’E
11	MPG11	Beneshagul	Assosa	Amba 2	10º39. 59’’ N	34º 19. 48’’E
12	MPG12	Beneshagul	Assosa	Amba 4	10º38. 57’’ N	34º 18.41’’E
13	MPG13	Beneshagul	Assosa	Mengele 29	10º5. 76’’ N	34º 33. 32’’E
14	MPG14	Beneshagul	Assosa	Amba 12	10º4. 56’’ N	34º 23. 38’’E
15	MPG15	Beneshagul	Assosa	Amba5	10º5. 43’’ N	34º 35.44’’E
17	MPG17	Beneshagul	Assosa	Amba4	10º5. 44’’ N	34º 36. 48’’E
18	MPG18	Beneshagul	Assosa	Amba14	10º4. 56’’ N	34°42.22″ E
19	MPG19	Beneshagul	Bambasi	Sonka	9°45.42″ N	34°47.32″ E
20	MPG20	Beneshagul	Bambasi	Sonka	9°45.44″ N	34°47.23″ E
21	MPG21	Beneshangul	Ura	Amba 24	10º 3. 77’’ N	34°43.20″E
22	MPG22	Benshangul	Ura	Amba8	10º3. 67’’ N	34°42.27″ E

C. Data Collection

All quantitative data were measured by taking the mean value of five plants, which were tagged randomly before the time of data collection. Descriptors for Soya bean (*Glycine max* (L) Merr.)

developed each accession both for quantitative and qualitative characters.

Table-II: Qualitative Traits of Soya Bean (Glycine Max (L.) Merr.) Accessions with Respective Code and Character Code

Character	Code	Character code
Growth habit	Gh	Erect (1) Semi Erect (2) Semi spreading (3)
Leaf shape	LLS	Rounded ovate (1) pointed ovate (2) Lanceloate (3) Traingular (4)
Seed size	SS	Large (1), Samll (2), Medium (3)
Testa color	TC	Yellow green (1), Yellow (2), Green (3), Black (4)
flower color	BFC	Yellow (1), Light Yellow (2), Orange Yellow (3)
Pod color	PC	Medium green (1), Light Green (2), Dark Green (3)
Seed shape	SSH	Spherical flattened (1), Spherical (2), Elongated Flattened (3)
Hair color	HC	Dense down (1), Sparse (2), Light (3), Hairless (4)
Presence of Pubesence	PB	Present (1), Absent (2)

Table III: Quantitative Morphological Characters of Soya Bean (Glycine max (L.) Merr.) Accessions with Respective Code and Description

Traits	Code	Description
Days to 50% flowering(count)	DF	Number of days from emergence to when50% of plants have started flowering in a plot
Days to maturity	DM	Number of the day from emergence to maturity showing color changes from green to lemony color
Plant height (cm)	PH	It was measured for five randomly selected plants per plot at physiological maturity from the ground level to tip of a plant.
Branches per plant	BPP	Counting total number of primary branches per main stem In randomly selected 5 plants in each plot
Pod per plant	FPP	Number of Pod per plant Mean from five representative plants in each plot
Hundred seed weight (g)	HSW	Weight of 100seed counts at 12%moisture content
Seeds per pod	SPP	Number of Seed per Pod Mean from five representative plants in each plot
Grain yield	GY	Grain yield was harvested from net plot area and measured in kilograms per hectare after adjusting moisture content 10%a

- *Morphological Traits:* Plant growth habit, leaf shape, flower color, testa color, hair color, hairless, pubescence, leaf color, seed size, pod color and seed shape.
- *Phenological and Growth Parameters:* Phenological and growth parameters recorded were days to flowering, days to maturity of Pods, plant height and branches per plant.
- *Yield Components and Yield:* Parameters recorded for these traits were pods plant, seeds per pod, hundred seed weight (HSW) and grain yield. Similarly morphological traits recorded were plant growth habit, leaf shape, Hair color, seed size, seed shape and pod color.

III. STATISTICAL ANALYSIS

Data were subjected to analysis of variance (ANOVA) appropriate to factorial experiment in RCBD according to the General Linear Model (GLM) of GenStat15th edition [14] and interpretations were made following the procedure described by [16]. Whenever the effects of the treatments were found to be significant, the means were compared using the Least Significant Differences (LSD) test at 5% probability level.

The estimation of genetic parameters was done to identify and ascertain the genetic variability among the accessions and determine the extents of environmental effect on various characters. Variance components due to phenotype (σ^2p), genotype(σ^{2g}) and the environment ($\sigma^2 e$) were calculated by adopting the following formula suggested by name of author [11].

Genotypic Variance (2g) = MSg-MSer
Phenotypic Variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2$ e
Environmental Variance 2e =Error mean square
Where,
Msg = Mean squares due to genotypes
Mse = mean squares due to error
r = number of replications

The phenotypic and genotypic coefficients of variances were expressed as [32].

PCV=Phenotypic variance Population mean for traitor
PCV = 2PXx 100
Where PCV = phenotypic coefficient of variation
GCV = Genotypic variance
Population mean for traitor GCV = 2gx x 100
Where GCV = Genotypic coefficient of variation
X = the grand mean of a character

Heritability in a broad sense was calculated for each trait by using the formula [5].

H^2 (%) =2g2p x100
Where,
H = Heritability in broad sense
σ^2g = genotypic variance
σ^2_p = Phenotypic variance

Genetic advance (GA) under selection, assuming the selection intensity of 5% was calculated according to [20]:

$$GA = K.^2{}_p.^2g\ ^2{}_p = K.H{*}^2{}_p$$

Where, GA = Expected genetic advance
K = the selection differential (K= 2.06 at 5% selection intensity)

Genetic advance as a percent of the mean was calculated to compare the extent of predicted advances of different traits under selection using the formula [13].

GAM = GAxX 100
GAM = Genetic advance as percent of mean
GA = Genetic advance under selection
X = Mean value

IV. RESULTS

A. Qualitative Traits

i.Growth Habit and Leaf Shape

The morphological descriptors used to characterize the soybean accessions were growth habit, leaf shape, flower color, testa color, hair color, hairless, presence of pubescence, leaf color, seed size, pod color and seed shape and are depicted in Table IV. The accessions exhibited distinct growth habits of erect, semi erect and semi spreading where erect types dominated accounting 52% and followed semi erect ones amounted to 46%. The remaining 2% were characterized with a semi spreading growth habit. The leaf shape variability was observed among accessions to be rounded ovate (56%), pointed ovate (28%), lanceolate (8%) and triangular (8%).

ii.Flower Color, Testa, Hair Color and Hairless

The flower color of soybean accessories showed noticeable variation from white to purple green where 85% of accessories had white flower color while 15% retained purple green flower color. With respect to testa color, about 70% of the accessions exhibited yellow green, 25% yellow, 4% green and 1% black testa color. Information recorded on hair color for accessions showed that 65% dense down, 15% sparse, 10% light and 10% were hairless. With respect to hairless, 95% of accessions had hair and the remaining 5% were hairless (Table IV).

iii.Pubescence, Leaf Color and Seed Size

Soybean genotypes with pubescence dominated being accounted to be 90% and the remaining 10% accessions were without pubescence. Regarding the leaf color, 52% genotypes had dark, 47% medium and 1% exhibited light color. With respect to seed size, about 55% of accessions were large sized seed, 34% were small size and 11% were observed to be medium sized (Table IV).

iv.Pod Color and Seed Shape

Occurrence of pod color varies across the soybean agermplasm with 50% of accessions were with medium green, 30% light green and 20% of accessions were dark green pod color. Variability of seed shape among accessions was observed where 58% were spherical flattened, 32% spherical and 10% were elongated flattened (Table IV). For 20 accessions of soybean considered, the qualitative traits dominated were growth habit erect type (52%), rounded leaf shape (56%), white flower color (85%), yellow green testa color (70%), dense down hair color (65%), presence of hair (95%), presence of pubescence (90%), dark leaf color (52%), large sized seed (55%), medium green pod color (50%) and spherical flattened seed shape (58%) (Table IV). Morphological characterization results depicted the presence of sufficient morphological traits variability among the genotypes. Reported that there were considerable variations among soybean genotypes for morphological characters that directly or indirectly lead to yield gain [6].

Table-IV: Frequency of Distribution Qualitative Traits in 20 Accessions of Soybean at Dabus During 2023/2024 Cropping Season

Trait	Variable	Frequency (%)
Growth habit	Erect	52
	Semi-erect	46
	Semi-spreading	2
Leaf shape	Rounded ovate	56
	Pointed ovate	28
	Lanceolate	8
	Triangular	8
Flower color	White	85
	Purple green	15
Testa color	Yellow green	70
	Yellow	25
	Green	4
	Black	1
Hair color	Dense down	65
	Sparse	15
	Light	10
	Hairless	10
Hairless	Present	95
	Absent	5
Presence of Pubescence	Present	90
	Absent	10
Leaf Color	Dark	52
	Medium	47
	Light	1
Seed Size	Large	55
	Small	34
	Medium	11
Pod Color	Medium green	50
	Light green	30
	Dark green	20
Seed Shape	Spherical flattened	58
	Spherical	32
	Elongated flattened	10

B. Analysis of Variance

The results of the analysis of variance for agronomic traits of soybean accessions are shown in (Table V). Analysis results revealed that mean squares due to soybean accessions for agronomic traits were significant with exception of branches per plant and number of seeds per pod. This evidence shows the presence of considerable level of variations among accessions for most of the traits observed and hence this disparity might be attributed to their inherent differences. The results of the study indicated the presence of substantial amounts of genetic variation in the current population for yield and yield related traits, which could be exploited in soybean improvement programs.

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Table-V: Mean Squares from Analysis of Variance for Agronomic Traits of Soybean Accessions Grown at Dabus During 2023/2024 Cropping Season

Trait	Rep (DF=2)	Accession (DF=19)	Error (DF=38)	CV (%)	Grand Mean
Days to flowering	19.07	19.87*	2.19	2,42	61.24
Days to maturity	15.82	86.94*	3.85	1.46	134.03
Plant height	101.83	164.54*	25,21	10.42	48.19
Branches per plant	0.28	0.32^{NS}	0.17	20.61	2.74
Pods per plant	90.15	262.30*	17.75	10.91	38.6
Seeds per pod	0.15	0.87^{NS}	0,05	8.18	2.73
HSW	0.07	0.06*	0.22	3.66	12.92
Grain yield	150995	1023096.00*	312542	13.27	1737.9

C. Quantitative Traits

i. Days to Flowering and Maturity

Analysis of variance showed that significant differences were detected for soybean accessions with respect to days to flowering and maturity (Table VI). Generally, days to flowering varied from 55.to 67 and days to maturity from 120 to 140. Ascension GDM10 took the longest days to flowering (67) and maturity (140). The shortest days to flowering (55) and maturity (120) were recorded for accession GDM17. This probably evidences that all the accessions (genotypes) were characterized by relatively homogeneity in phenological traits. Based on these results, the accessions could possibly be categorized as relatively similar maturity groups. This homogeneity among the accessions observed implies narrowness in their genetic distance for the traits under consideration. This result agreed with the report finding that days to maturity were significantly affected by soybean varieties [37]. Moreover, [34] reported that soybean genotypes had significant differences on days to flowering and maturity.

ii. Plant Height and Branches Per Plant

Analysis of variance indicated that soybean accessions were significantly different for plant height (Table VI). Plant height for accessions ranged from 37.00 to 60.00 cm. The tallest plant height (60.00 cm) was recorded for accession GDM5 followed by accession GDM8 with mean plant height of 55.33 cm. The shortest plant height (37.00 cm) was recorded for accession GDM9. The variation in plant height among the soybean accessions probably contributed to genotypic variations. This result agrees with the reporter that soybean genotypes exhibited significant differences with respect to plant height attributing to their inherent difference [34]. Moreover, Reported that height of the crop plants is mainly controlled by the genetic makeup of a genotype and it can also be affected by the environmental factors [27]. In contrast, soybean accession did not show significant differences on number of branches per plant (Table VI)

Table-VI: Mean Performance of Soybean Accessions for Phenological and Growth Traits Grown at Dabus During 2023/2024 Cropping Season

Accession	Days to Flowering	Days to Maturity	Plant Height (cm)	Branches
GDM1	59.50g-i	138.33ab	47.67d-i	2.87
GDM2	59.43g-i	134.67cd	52.00a-g	2.67
GDM3	61.67c-g	138.67a	54.33a-e	2.38
GDM4	61.33d-h	134.33cd	50.00c-h	2.86
GDM5	59.67f-i	127.00ef	60.00a	2.86
GDM6	64.33ab	139.00a	36.00k	2.67
GDM7	64.00bc	138.00ab	39.00jk	3.15
GDM8	63.33b-d	133.67cd	55.33a-d	2.88
GDM9	60.00e-i	132.67cd	37.00k	2.97
GDM10	66.67a	140.33a	45.67f-j	2.62
GDM11	62.00b-f	138.33ab	38.67jk	2.60
GDM12	6217b-e	138.67a	41.00i-k	2.44
GDM13	60.33e-h	132.33cd	42.67h-k	2.73
GDM14	59.10hi	128.33e	53.67a-f	2.97
GDM15	61.00d-h	132.00d	46.67e-j	2.80
GDM16	61.33d-h	135.33bc	54.00a-e	2.99
GDM17	55.33j	120.33g	58.33ab	2.85
GDM18	61.67c-g	139.33a	56.00a-c	2.18
GDM19	64.33ab	134.33cd	44.17g-k	2.49
GDM20	57.67ij	125.00f	51.67b-g	2.88
LSD	2.44	3.24	8.30	NS
CV (%)	2.42	1.46	10.42	4.62

Means labeled by different superscript letters in the columns are significantly different according to Turkey's Student Range Test ($p<0.05$)

D. Pods Per Plant, Seeds Per Pod and Hundred Seed Weight

Analysis of variance showed that accessions of soybean were significantly different for the number of pods per plant and HSW (Table VII). Number of pods per plant varied from 26.00 to 55.33. The greatest number of pods per plant (55.33) was observed for accession GDM17 followed by accession GDM14 with mean number of pods per plant of 54.67. The lowest number of pods per plant (26.00) was seen for accession GDM10. The differences among accessions for the parameter might be attributed to their inherent variations in the growing environment. Such wide variations indicated the scope of improving for this trait. Similarly, HSW for soybean accessions varied from 110.1 to 17.00 g with maximum HSW (17.00 g) achieved from accession GDM17 followed by accession GDM5 with mean HSW of 15.00 g. The lowest HSW (11.01 g) was obtained from accession GDM6. Conversely, soybean accessions did not show significant differences on the number of seeds per pod (Table VII).

E. Grain yield

Grain yield was significantly varied for soybean accessions and it varied from 537 to 2478 kg/ha (Table VII). Soybean accessions with relatively low yielders (< 1500 kg/ha) were GDM3, GDM6, GDM10, GDM11, GDM12, GDM15 and GDM18. Likewise, accessions with relatively intermediate yielder (1500- 2000 kg/ha) encompass GDM2 and GDM19. Accessions GDM1, GDM4, GDM5, GDM7, GDM8, GDM9, GDM13, GDM14, GDM16, GDM17 and GDM20 gave relatively higher yield (> 2000 kg/ha) over others. With respect to the overall effect, the highest grain yield (2478 kg/ha) was recorded for accession GDM7 followed by accession GDM16 with mean grain yield of 2312kg/ha [3]. The lowest grain yield (537 kg/ha) was achieved from accession GDM10 [23]. This finding clearly indicated that there were significant differences among the accessions for grain yield indicating the existence of considerable genetic variation in the experimental materials [37]. reported a wide range of variation of soybean genotypes for number grain yield.

Table-VII: Mean Performance of Soybean Accessions for Phenological and Growth Traits Grown at Dabus During 2023/24 Cropping Season

Accession	Pods per Plant	Seeds Per Pod	HSW (g)	Grain Yield (kg/ha)
GDM1	28.67gh	2.42	11.96ij	2080a-d
GDM2	35.33e-g	2.48	12.39e-i	1989a-d
GDM3	28.67gh	2.10	11.35jk	874e
GDM4	34.00e-g	2.48	12.14g-i	2078a-d
GDM5	52.67ab	3.53	15.00b	2196a-c
GDM6	26.33h	2.40	11.01k	1198de
GDM7	33.33e-g	2.27	12.05h-j	2478a
GDM8	43.00cd	2.73	13.09de	2063a-d
GDM9	38.33de	2.69	12.97d-f	2125a-c
GDM10	26.00h	1.86	11.12k	537e
GDM11	36.00ef	2.62	13.65cd	943e
GDM12	30.67f-h	2.57	12.23f-i	843e
GDM13	38.00de	2.73	12.28f-i	2022a-d
GDM14	54.67a	3.42	13.95c	2064a-d
GDM15	46.67bc	3.10	14.25bc	1297c-e
GDM16	37.00d-f	2.54	12.89d-g	2312a
GDM17	55.33a	4.00	17.00a	2078a-d
GDM18	38.00de	2.40	12.80e-h	1374b-e
GDM19	36.67d-f	2.68	12.39e-i	1977a-d
GDM20	52.67ab	3.62	13.88c	2228ab
LSD	6.96	NS	0.78	924
CV (%)	10.91	8.18	3.66	13.27

Means labeled by different superscript letters in the columns are significantly different according to Turkey's Student Range Test ($p<0.05$) letter HSW indicate = hundred seed weight

F. Variance Components

i. Phenotypic and Genotypic Variations

Estimates of phenotypic variances (σ^2p), genotypic variance (σ^2g), phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) are presented in Table VIII. In this assessment, the estimation of phenotypic variance was higher than that of genotypic variance. Phenotypic variance (б^{2}g) of soybean accessions varied from 0.11 for HSW to 549393.13 for grain yield. Higher phenotypic variance (≥ 100) was observed for grain yield only whereas relatively medium phenotypic variance (50-100) was observed for traits days to flowering, days to maturity, plant height and pods per plant. On the other hand, lower phenotypic variance (< 50) was recorded for branches per plant, seeds per pod and HSW. Generally, genotypic variance (σ^2g) ranged from 0.05 for branches per plant and HSW to 236851.33 for grain yield which was the highest one. Only pods per plant had moderate genotypic variance (σ^2g) while days to flowering, days to maturity, plant height, branches per plant, seeds per pos and HSW were traits observed to be lower genotypic variance (Table VIII).

In general, phenotypic coefficient of variation (PCV) varied from 2.57 for HSW to 42.65% for grain yield (Table VIII). Categorized PCV as high if PCV > 20%, moderate if PCV is 10-20% and low if PCV is below 10% [33]. Based on this categorizing, traits branches per plant, pods per plant, seeds per pod and grain yield had higher PCV. Conversely, only a trait plant height exhibited moderate PCV whereas traits days to flowering, days to maturity and HSW showed lower PCV with PCV value below 10%. This could be evidenced as the prominent influence of environment for the expression of these traits. In line with this, genotypic coefficient variance (GCV) varied from 1.73 to 28.01% where traits pods per plant and grain yield had high and plant height and seeds per pod showed moderate GCV value. In contrast, traits days to flowering, days to maturity, branches per plant and HSW were observed to be with low GCV values (Table VIII). In this study the value of phenotypic variance was higher than a genotypic variance for all the traits studied, but the difference is not that much high. The relative narrow gap between the phenotypic variance and genotypic variance values indicated the smaller contribution of the environmental effects to the phenotypic variance in the studied traits.

ii.Broad Sense Heritability and Genetic Advance

The concept of heritability enables us to know whether phenotypic variations noticed among various genotypes are the cause of genetic changes or environment [20]. Generally, heritability in broad sense (H^2) ranged from 13.51% for branches per plant which was the lowest to 87.79% for days to maturity which was the highest value (Table VIII). Grouped heritability estimates as low if < 30%, moderate if 30-60% and high if > 60% [35]. Based on this grouping, traits days to flowering, days to maturity, plant height, pods per plant and seeds per pod had high heritability values [4]. Thus, high heritability indicates that expression of the characters is least influenced by the environment [8]. recorded high H^2 for these traits in soybean. Relatively moderate H^2 was recorded for traits HSW and grain yield which may have occurred due to influence of the environment on the polygenic nature of these traits [29]. It was observed that heritability (H^2) was low for a trait branch per plant and hence the low heritability that recorded for this trait limits the possibility of including the trait in selection of desirable genotypes in breeding programs. This may be due to higher environmental impact of the environment for the expression of phenotypic variation than genotypic variation.

Genetic advance as a percent mean was ranged from 2.39% for HSW to 43.65% for pod per plant (Table VIII). This result indicated that selecting the top 5% of the accessions could result in an advance of 2.39 to 43.65% over the respective population mean. Classified genetic advance as percent of mean as low if < 10%, moderate if 10-20% and high if > 20% [33]. Based on this classification, plant height, pods per plant, seeds per pod and grain yield exhibited high genetic advance. On the other hand, traits days to flowering, days to maturity, branches per plant and HSW had low genetic advance (Table VIII). According to [20] high heritability estimates with high genetic advance is usually more helpful in predicting increase under selection than heritability estimates alone. Regarding this suggestion, combined high GCV, high heritability and high GAM was recorded for pods per plant (GCV=23.39%, H^2= 82.12% and GA= 43.65%) which means this trait is controlled more of by additive genes [24], Hence, this trait could be improved through direct selection more easily than that of other traits. Generally, the observed variability of agronomic traits is dependent on genetic factors, environmental variables and the interaction factor.

Table-VIII: Phenotypic and Genotypic Coefficient of Variability, Heritability and Genetic Advance for Soybean Accessions Grown at Dabus During 2023/2024 Cropping Season

Trait	σ^2p	σ^2g	σ^2e	PCV (%)	GCV (%)	H^2(%)	GA (%)
Days to flowering	8.08	5.89	2.19	4.64	3.96	72.90	6.97
Days to maturity	31.54	27.69	3.85	4.19	3.93	87.79	7.58
Plant height	71.65	46.44	25.21	17.57	14.14	64.82	23.45
Branches	0.37	0.05	0.32	22.20	8.16	13.51	6.20
Pods per plant	99.27	81.52	17.75	25.81	23.39	82.12	43.65
Seeds per pod	0.32	0.27	0.05	20.72	19.03	84.38	35.89
HSW	0.11	0.05	0.06	2.57	1.73	45.45	2.39
Grain yield	549393.33	236851.33	312542.00	42.65	28.01	43.11	37.89

iii.Correlation of Agronomic Traits

The data for correlation coefficients of agronomic traits for soybean accessions are presented in Table IX. In general, the correlation coefficient (r value) varied from -0.94 to 0.91. Agronomic traits branches per plant, pods per plant and seeds per pod were significantly positively correlated with grain yield whereas days to maturity was significantly negatively associated with grain yield.

This is evidence that the traits branches per plant, pods per plant and seeds per pod are important to be used as criteria for direct selection in breeding for improving grain yield in soybean. [17] reported the presence of positive and relatively strong correlations between grain yield and other traits and hence the improvement in grain yield could be achieved by direct or indirect selection for yield determining traits. Likewise, sShowed that in bamboo groundnut higher correlation values were observed for plant height, pods per plant, seed per pod, and HSW indicating that these traits are very important to be used in selection for the crop improvement [22]. On the other hand, the association of days to flowering, plant height and HSW with grain yield was not significant. Thus, morphological characterization has provided more accurate estimation of genetic diversity of the raw material of plant breeding.

Table-IX: Correlation of Agronomic Traits of Soybean Accessions Grown at Dabus During 2023/2024 Cropping Season

Trait	DF	DM	PH	Br	PPP	SPP	HSW	GY
Days to flowering (DF)	-	0.20^{NS}	-0.23^{NS}	-0.30^{NS}	-0.20^{NS}	-0.07^{NS}	-0.11^{NS}	-0.36^{NS}
Days to maturity (DM)		-	-0.48*	-0.44*	-0.91*	-0.94*	-0.85*	-0.55*
Plant height (PH)			-	-0.02^{NS}	0.55*	0.44*	0.50*	0.27^{NS}
Branches (Br)				-	0.37^{NS}	0.35^{NS}	0.29^{NS}	0.71*
Pods per plant (PPP)					-	0.94*	0.89*	0.49*
Seeds per pod (SPP)						-	0.91*	0.45*
Hundred seed weight (HSW)							-	0.35^{NS}
Grain yield (GY)								-

V. DISCUSSION

Morphological characterization results depicted the presence of sufficient morphological traits variability among the genotypes [18]. These characteristics can assist breeders in genotype selection dependent on phenotype in the genetic improvement in breeding scheme [10]. Based on these morphological traits, it could be possible to identify elite genotypes for grain yield purposes within the genotype population [15]. Reported that there were considerable variations among soybean genotypes for morphological characters that directly or indirectly lead to yield gain. Moreover, it indicated that there was prominent morphological variability in soybean genotypes that could possibly be exploited in the breeding scheme [21]. Phenologically, the accessions exhibited homogeneity in days to flowering and maturity implies the ease of making harvesting easy and practically feasible for mechanization in commercial production [37]. This homogeneity among the accessions observed implies narrowness in their genetic distance for the traits under consideration [38]. This result agreed with the report that days to maturity were significantly affected by soybean varieties [19]. Moreover, it reported that soybean genotypes had significant differences on days to flowering and maturity [34]. The accessions significantly differed in plant height since plant height at flowering and seed setting are of particular interest for the breeding program because the presence of plants with tall and thin stems will increase the rate of lodging near harvesting and this could lead to loss of dry matter with subsequent decline in grain yield. Consequently, selection of accessions with short stature is necessary in further breeding programs. The accessions exhibited a significant difference in the number of pods per plant, seeds per pod and HSW which clearly indicated the presence of a wide spectrum of variability among the genotypes of soybean [19]. Phenotypic variance was higher than genotypic variance for all the traits studied, but the difference is not that much high. The relative narrow gap between the phenotypic variance and genotypic variance values indicated the smaller contribution of the environmental effects to the phenotypic variance in the studied traits. The findings of the research revealed a high prevalence of relative genetic heterogeneity among genotypes, both genotypic and phenotypic variation. For morphological and agronomical traits with broad genetic base having high GCV and PCV that could be useful in genotype selection in subsequent generations of soybean breeding. Additive gene action provides a basis for high heritability estimates and genetic advance over percent mean of traits, and hence selection will be more effective in improvement of the crop.

VI. CONCLUSION

Significant genetic variability in mean performance of almost all the traits under studied material indicated that genotypes have considerable amounts of genetic variation which may be used for further breeding programs in variety development of soybean desirable type. Indeed, morphological characterization results depicted the presence of sufficient morphological traits variability among the genotypes. Analysis results revealed that soybean accessions for agronomic traits were significant with exception of branches per plant and number of seeds per pod. Phenotypic, genotypic, heritability and genetic advance were observed to vary at different degrees with sufficient amounts in order to carry out selection at different growth stages of soybean for improvement. Agronomic and morphological evaluations have provided more accurate estimation of genetic diversity and the raw material for plant breeding. In general, this study enabled us to determine how the influential traits direct to improve soybean genotypes.

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DECLARATION STATEMENT

After aggregating input from all authors, I must verify the accuracy of the following information as the article's author.

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