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Morphological Characteristics of Sesame (*Sesamum indicum* L.) Genotypes Via Genetic Diversity and Characters Association in Amibara, Ethiopia

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Abstract: Ethiopia's sesame productivity is low and below the world average. This low productivity is influenced by different yield limiting factors, the most important one is a lack of high-yielding improved varieties. It is basic to be understand the genetic variation and characters association. As a result, the objectives of this research was to determined the extent of genetic variation and its relationship to yield and 19 yield components. From 2017 to 2018, 100 genotypes were tested at Amibara in a 10 x 10 triple lattice design over two consequetive cropping seasons. Combined analysis of variance over the two years, the genotypes differed significantly for all of the characters considered. Plant height, number of capsules per plant, harvest index and seed yield had medium PCV and GCV values, whereas shattering resistance had high PCV and GCV values. Shattering resistance, plant height, capsule per plant, harvest index and seed yield all had high heritability values combined with moderate to high genetic progress as a percentage of mean (GAM). The length of capsule bearing zone and first capsule, capsule per main axis, number of capsules per plant, harvest index and oil content were all related to seed yield in a positive and significant association. Path coefficient analysis revealed that capsules per main axis, capsules per plant and harvest index all had a positive direct effect on seed yield. D^2 analysis, the 100 sesame genotypes were divided into seven groups. As a result, the genotypes become moderately divergent. Allowing to principal component analysis, seven principal components assessed for 78.67% of the total variation. Genotypes with more capsules per main axis, capsules per plant, and high harvest index, harmonizing to the findings should increase sesame seed yield. In this study, these characters were discovered to be important yield contributing characteristics, and selection based on these characters would be most effective. More research in multiple locations, is required to provide conclusive results. In this study, only morphological characteristics were used. As a result, future research should deliberate using molecular markers and high-throughput molecular data to evaluate sesame genetic resources for marker assisted breeding.

Keywords: Clustering, Diversity, Genetic Advance, Heritability, Principal Component, Sesame

1. Introduction

Ethiopia is one of the alternative origins of sesame (*Sesamum indicum* L.) a member of the sesamum genus in the Pedaliaceae family [1]. Sesame cultivated species is diploid, with chromosome number 2n=2x=26 [2]. Sesame is one of the chosen strategic and export commodity crops. Similarly, a source of hard currency, food and cash for those involved in the sector and others in specific; in general, for Ethiopians'. Sesame seed is used in a variety of foods, the majority of which are processed into cooking oil and meal. The seed is also used to make *wet*, porridge, appetizers, flavoring, sweets, and beverages. It is a good source of vegetable oil and is known as the "queen of oil seeds" because of its high oil content (44-58%) with 83-90 percent unsaturated fatty acids, proteins (18-25%) and carbohydrate content (11-13%). The oil cake contains calcium and is suitable for animal feed. It is also high in lignans such as sesamin, sesamol and sesamolin, which have a high oxidation resistance and thus a long shelf life [3].

It is grown all over the world, covering approximately 14 million hectares and producing approximately 6.8 million metric tons. Sudan, India, China's mainland, Myanmar, Sudan (former), Nigeria, the United Republic of Tanzania, South Sudan, Ethiopia and Uganda are among the countries involved. In Africa, the harvested area and production of sesame is 9.7 million hectares, with a production of approximately 4.3 million metric tons. As a result, Africans assessed for 69.3 percent of total harvest area in million hectares and 63.2 percent of total production in million metric tons of sesame [4].

Amhara (59.1%), Tigray (31.2%), Oromia (7.6%), Benshungul Gumze (1.9%), Afar (0.3%) and Southern regions (0.3%) are Ethiopia's major sesame growing regions, and 71.9 percent of cultivated Ethiopian sesame is primarily for export. Consequently, Amhara and Tigray are Ethiopia's main sesame-growing regions. However, sesame productivity in Ethiopia is very low (0.8 ton ha^{-1}) compared to the national average (2.0 ton ha^{-1}) [5]. Many factors, including indeterminate flowering, capsule shattering at maturity, insects, diseases and abiotic stresses, contribute to low productivity in Ethiopia [3].

Ethiopian sesame production has a promising future due to its economic value and export potential. Sesame yield is extremely low, despite the crop's enormous genetic potential as a center of diversity. Several researchers have investigated the genetic variability of sesame and its associated characteristics [3, 6-9].

Information on genetic diversity and the association between yield and yield-related characters is required before beginning appropriate crop improvement breeding procedures and developing genotypes with high productivity [10]. The amount of genetic diversity in the gene pool and its heritability determine the effectiveness of selection for genetic improvement in yield and yield-contributing characters. As a result, the objectives of this study were to estimate genetic diversity among sesame genotypes using phenotypic and genotypic variability, as well as characters association using morphological characters.

2. Materials and Methods

2.1. Description of the Experimental Site

Field experiment was carried out at Werer Agricultural Research Center in Amibara; it is located 90^0 27 N and 40^0 15 E in north eastern part of Ethiopia. One hundred sesame genotypes were accompanied in the experiment (Metrological data, soil physiochemical result analysis and experimental material in Tables A1, A2 and A3.

2.2. Experimental Design and Trial Management

The experiment was conducted from 2017 to 2018 in two consecutive cropping seasons. The experiment was laid out in 10 x 10 triple lattice design replicated three times. Each plot was 4 m long and 1.2 m wide, which consisted of 3 rows with a spacing of 40 cm between rows and 0.4m between plots. Sowing was done by hand drilling. Thinning was carried out after 21 days, and plant to plant distance was kept at 10 cm. Other cultural practices were applied as per the research recommendation.

Data collected on plot basis: days to flower initiation, days to 50% flowering, capsule filling period, days to maturity, 1000 seed weight (g), biomass yield per hectare (ton**),** harvest index, seed yield per hectare (kg ha^{-1}) and oil content (%): oil content was determined by wide line nuclear magnetic resonance (NMR).

Data collected on plant basis: data were collected from five randomly taken plants per plot of experimental unit; like plant height (cm), length of capsule bearing zone (cm), length of first capsule (cm), capsule length (cm), capsule width (cm), capsule thickness (cm), number of primary branches per plant, number of capsules per main axis and capsules per plant, number of seed per capsule. Estimating the level of Shattering resistance (%) $ISR = RW * 100/TSW$; RW= retained seed weigh and TSW= total seed weight [11].

2.3. Data Analysis

All data were subjected to analysis using R software.

2.3.1. Analysis of Variance (ANOVA)

Data were checked for the normality assumption and all of the data encounter the normality assumption except for number of capsule per plant, seed per capsule, number of capsule per main axis, date of capsule filling period, length of capsule bearing zone, primary branch per plant and harvest index. Square root and Arc-sin transformation methods were used as per the standard technique in order to normalize the distribution [12]. The analysis of variances for each year were generated. The ANOVA model for individual year was:

$$Pijk = \mu + gi + bk(j) + rj + eijk$$

Where, P_{ijk} = phenotypic value of i^{th} genotype under j^{th} replication and k^{th} incomplete block within replication j; μ =grand mean; gi= the effect of i^{th} genotype; $b_{k(j)}$ = the effect of incomplete block k within replication j; r_j=the effect of replication j; and e_{ijk}= the residual or effect of random error.

Homogeneity test for the error variance of two years were done separately (Table A4). For combined analysis of variance over years, the homogeneity of error variance was tested by using F-max test [13], which is based on the ratio of the larger mean square of error (MSE) to the smaller mean square of error from the separate analysis of variance given by the formula: $Fmax = (Largest\ MSE)/(Smallest\ MSE)$. Then test showed all the characters non-significant met the homogeneity assumption and data were combined.

Therefore, combined analysis was computed based on general leaner model (GLM) procedures using R statistical package. The combined analysis of variance over two years was carried out according to the following model:

$$Pijks = \mu + gi + bk(j)(s) + rj(s) + Ss + (gs) + eijks$$

Where, P_{ijks}= phenotypic value of i^{th} genotype under j^{th} replication at s^{th} season(Years) and k^{th} incomplete block

within replication j and season s; μ= grand mean; g_i = the effect of i^{th} genotype; $b_{k(j)(s)}$ = the effect of incomplete blocks within replication j and season s; $r_{j(s)}$ = the effect of replication j within season s; S_s= the effect of season; $(gs)_{is}$ = the interaction effects between genotype and season; and e_{ijks} = the residual error.

2.3.2. Estimation of Genetic Parameters

Phenotypic and genotypic variances and coefficients of variation

Estimates of variance components were computed using the formula [14].

1) Phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 gS/S + \sigma^2 e/SR = MSG/RS$

Where: $\sigma^2 p$ =Phenotypic variance, σ^2g=Genotypic variance, σ^2gs =genotype by season variance, $\sigma^2 e$ = Environmental variance, R=number of replication, S= number of season and MSG=mean square of genotype.

2) Genotype variance $(\sigma^2 g) = (MSG - MSGxS/RS)$

Where: σ^2g = genotypic variance, MSG = mean square of genotype, MSG x S = mean square genotype by season, R= number of replication and S= number of season.

3) Genotype x season interaction variance (σ^2gs) = $(MSGxS - MSE/R)$

Where: σ^2gs= genotype by environment interaction variance, MSGxS= genotype by environmental interaction, MSE=mean square of error and R=number of replication.

4) Environmental variance (mean square error) (σ^2e) = MSE

5) Phenotypic and genotypic coefficient of variations were estimated using the methods [15]

$$\text{Phenotypic coefficients of variation (PCV)} = \frac{\sqrt{\sigma^2 p}}{\bar{x}} x100$$

$$\text{Genotypic coefficients of variation (GCV)} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} x100$$

Where: σ^2p = Phenotypic variation; σ^2g = Genotypic variation and $\bar{x}$ = Grand mean of the trait under consideration. Sivasubramaniam and Menon (1973) classified PCV and GCV values greater than 20% as high, less than 10% as low, and values between 10% to 20% as moderate [16].

Broad Sense Heritability (h^2b)

Heritability in broad sense for all characteristics were calculated using the formula classified as low (below 30%), medium (30-60%) and high (above 60%):- $\text{Heritability}(h^2b) = \frac{\sigma^2 g}{\sigma^2 p} x\ 100$ [17, 18], Where: h^2b = heritability in broad sense, σ^2p = Phenotypic variance and σ^2g = Genotypic variance.

Estimation of genetic advance

Anticipated genetic advance for each character at 5% selection intensity was calculated using the procedure designated [19]: $GA = \frac{k * \sigma ph * h^2 b}{100}$, Where; GA= expected genetic advance, K= constant (selection differential where K=2.063 at 5% selection intensity), σph = phenotypic variance, h^2b = heritability in broad sense.

Genetic advance as percent of mean (GAM) was calculated and classified as low (<10%), moderate (10-20%) and high (>20%) [18]: $GAM \frac{GA}{\bar{x}} X100$, Where: GAM=genetic advance as percent of mean, GA=genetic advance under selection, $\bar{X}$= mean of the population in which selection is effective.

2.4. Association of Characteristics

2.4.1. Estimation of Correlation Coefficients

The correlation coefficients among all possible trait combinations at phenotypic (rp) and genotypic (rg) levels were estimated [20]:-

$$\text{Phenotypic covariance } (\sigma p_{xy}) = \sigma g_{xy} + \frac{\sigma_{e\,xy}}{r}$$

$$\text{Genotypic covariance } (\sigma g_{xy}) = \frac{MSPg - MSPe}{r}$$

Where, MSPe =mean square of cross product for error, MSPg= mean square of cross products for genotypes, σ^exy environmental covariance between x and y, and r=number of replications.

Phenotypic correlation (rp), the observable correlation between two variables, which includes both genotype and environmental components between two variables was be estimated using the formula [18, 21]:-

$$\text{Phenotypic correlation coefficient (rpxy)} = (pcovx.y)/(\sqrt{\sigma^2 px}.\sigma^2 py),$$

$$\text{Genotypic correlation coefficient (rgxy)} = (gcovx.y)/(\sqrt{\sigma^2 gx}.\sigma^2 gy)$$

Where: rp_{xy} and rg_{xy} are phenotypic and genotypic correlation coefficients, respectively; pcovx.y and gcovx.y are phenotypic and genotypic covariance between variables x and y, respectively; σ^2px and σ^2gx are phenotypic and genotypic variances for variable x; and σ^2py and σ^2gy are phenotypic and genotypic variances for the variable y.

Test of significance of correlation were tested by using "r" tabulated value at n-2 degree of freedom, at 5% and 1% probability level, where n is the number of observation [22].

2.4.2. Path Coefficients Analysis

Path coefficient analysis was directed as recommended [23, 24] run and using the phenotypic as well as genotypic correlation coefficients to governed the direct and indirect effects of yield components on seed yield based on the following relationship: $rij = Pij + \Sigma rikpkj$;

Where: rij=mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient, Pij=Component of the direct effects of the independent trait (i) on the dependent variable (j) as measured by the path coefficient, Σrikpkj=Summation of components of indirect effect of a given independent trait (i) on the given dependent trait (j) by all other independent characteristics (k).

Whereas the contribution of the remaining unknown

characters measured residual effect estimated as follows: Residual effect $=\sqrt{1-R^2}$; Where: - $R^2 = \Sigma p_{ij} r_{ij}$, Where, R^2 is the residual factor, P_{ij} is the direct effect of yield by i^{th} characters, and r_{ij} is the correlation of yield with the i^{th} characters.

2.5. Genetic Diversity Analysis

2.5.1. Cluster Analysis

Clustering of genotypes in different sets was carried out by average linkage clustering method. The proper numbers of clusters were determined by following approach looking into three statistics namely Pseudo F, Pseudo t^2 and cubic clustering criteria [25]. The points where local peaks of the CCC and pseudo F-statistic join with small values of the pseudo-t^2 statistic followed by a larger pseudo-t^2 for the next cluster fashion.

2.5.2. Genetic Divergence Analysis

A measure of distance based on multiple characteristics was given by Mahalanobis D^2 [26] for quantitative characters in matrix notation, the distance between any two groups was estimated from the following relationship: $D^2_{ij} = (X_i - X_j)\, S^{-1}\, (X_i - X_j)$:

Where: D^2_{ij} = the squared distance between case i and j; X_i and X_j = vectors of the values of cases i^{th} and j^{th} genotypes; S^{-1} = the inverse of pooled variance covariance matrix within groups.

Testing the significance of the squared distance values obtained for a pair of clusters was taken as the calculated value of χ^2 (chi-square) and tested against the tabulated χ^2 values at p-1 degree of freedom at 1% and 5% probability level,

Where P = number of characters used for clustering genotypes [15].

2.5.3. Principal Component Analysis

Principal components (PCs) with Eigen value greater than 1.0 had been used as criteria to determine the number of PCs [27]. The general formula to compute the scores on the first component extracted in a principal component analysis is:-

$$PC_1 = b_{11}(X_1) + b_{12} + \ldots b_{1p}\,(X_p)$$

Where: PC1 = the subject's score on principal component 1 (the first component extracted); b1p = the regression coefficient (or weight) for observed variable p, as used in creating principal component 1; Xp = the subject's score on observed variable p.

3. Results and Discussion

3.1. Analysis of Variance (ANOVA)

The mean squares of the 20 ANOVA characters are shown for each year (in Appendix Tables A5 and A6) and for the two years combined in Table 1. All of the characters in year one and two were significantly different ($p<0.01$) for all characteristics. Table 1 displays the results of a combined ANOVA across years for the various characters.

Table 1. *Combined analysis of variance for 20 characteristics of 100 sesame accession evaluated in 2017 and 2018 growing years in Amibara.*

Characteristics	MSG (Df =99)	MSG x season (Df =99)	MS. season (Df =1)	MS. error (Df =369)	CV (%)
DFI	20.10**	4.22**	337.5**	2.64	4.30
DF	51.06**	6.88**	4113.4**	2.71	3.83
$DCFP	25.16**	10.26**	165.4**	2.45	3.14
DM	309.91**	67.79**	20265.3**	26.1	4.86
PLH	1414.64**	486.55**	23826.6**	64.4	7.15
$LCBZ	58.41**	9.51**	3710.1**	3.10	3.61
LFC	0.09**	0.04**	0.002^{ns}	0.03	6.72
CL	0.12**	0.04**	0.002^{ns}	0.024	6.24
CW	0.01**	0.01^{ns}	0.402**	0.003	7.21
CTK	0.01**	0.01**	0.002^{ns}	0.001	6.93
#PBPP	0.07**	0.05**	0.954**	0.024	8.20
$CPMA	22.51**	3.83^{ns}	1117.9**	3.243	6.68
$CPP	121.98**	24.30**	2009.3**	5.83	5.62
$SPC	31.24**	11.61**	58.9**	6.522	5.19
ISR	26.74**	1.82**	29.8**	0.55	16.4
BY	2.27**	1.20**	11.9**	0.25	9.80
$HI	39.62**	4.24**	581.5**	2.25	6.65
TSW	0.54**	0.09**	0.17**	0.03	5.20
OL	19.07**	4.68**	9.63*	2.10	2.88
YLD	227063**	30711**	188219**	9244	9.86

Df=degree of freedom, ns=non-significant, MS = mean square, G = genotypes, CV = coefficient of variation, *= Significant at ($p< 0.05$),$**= significant\ at$ ($p < 0.01$), DFI = days to flower initation, DF= days to 50% flowering, DCFP = days to capsule filing period, DM = days to physiologically maturity, PLH = plant height (cm), LCBZ = length of capsule filing zone (cm), LFC = length of first capsule (cm), CL = capsule length (cm), CW = capsule width (cm), CTK = capsule thickness (cm), PBPP = primary branch per plant, CPMA = capsule per main axis, CPP = capsule per plant, SPC = seed per capsule, ISR = percent of inverted shattering resistance (%), BY = biomass yield per hectare (ton), HI = harvest index (%), TSW = 1000 seed weight (g), OL = oil content (%) and YLD = yield $kgha^{-1}$; $ = indicates characters based on arcsine transformed data and, # = indicates characters based on square root transformed data.

All characteristics revealed highly significant genotypes variation ($P<0.01$), indicating that genotypic variation existed among the genotypes tested. Significant differences in days to 50% flowering, days to maturity, capsule filling period,

plant height, number of capsules per plant and number of primary branches [6].

The mean squares due to genotype x year interaction effects were highly significant (P<0.01) for all characteristics except capsule width and number of capsules per main axis. It demonstrates how genotypes perform differently based on the years. There are significant variation in the interaction of genotype, environment and genotype by year, indicating that genotype responds differently depending on the testing environment [8]. Except for length of the first capsule, capsule length and thickness in Table 2, the mean square due to years showed a highly significant variation (P<0.01) for the majority of the characteristics. These findings indicated that the phenotypic expression of the characters differed depending on the years. Similarly, significant years effect for 13 sesame genotypes across three years [28].

3.2. Mean and Range of Yield and Major Yield Related Characteristics

The estimated range, mean and standard deviation of 20 characters are shown in Table 2. The mean performance of ten (10) top and least out of 100 sesame genotypes for 20 characters were shown in Table A7. Average sesame seed yields ranged from 507 to 1391 Kg ha^{-1}. More than half of the genotypes had mean seed yield higher than the grand mean (975 kg ha^{-1}) and 15% produced mean seed yields higher than the standard check Adi. The top three genotypes had, Acc-203-336-4 (1391 Kg ha^{-1}), Hirhir-baker-sel-1 (1389 Kg ha^{-1}) and Acc-111-524-1 (1382 Kg ha^{-1}) all yielded more than the standard check Adi (1236 Kg ha^{-1}), while Acc-No-044 (507Kg ha^{-1}) yielded less than the local check (1101 kg ha^{-1}). Genotypes had a wide mean range in terms of seed yield. This indicated that existing genotypes differed due to a variety of materials tested, each with a unique genetic makeup, as well as the influence of the environment. Similarly, sesame genotypes have a wide range of seed yield due to genetic and environmental factors [6].

The oil content of the sample ranged from 42 to 55 percent. In Table 3, 9 percent of the genotypes outperformed the standard check, while 70% outshone the grand mean. The highest oil content was found in SPS-SIK-#811 (55 percent), Acc-BG-003 (53 percent), Acc-203-612 (53 percent), Acc-211-015 (53 percent) and Adi (52 percent); while the lowest oil content was found in Acc-WW-001 (4) (42 percent), which was also lower than the local check (47 percent) in Table A7. Because of its high yielder and oil content, the SPS-SIK-#811 genotype could be one of the potential genotypes for future improvement programs.

According to Table 2, shattering resistance ranged from 1.39 to 11.88. Acc-00019 (12%), Bounja-filwuha sel-6 (10.8%), NN-0036-1 (10.4%), Acc-203-630 (10.1%), and HB-38-FAM-2 BAR (10.1%) had the highest pod shattering, while Acc-111-821 had the lowest (1.8 percent). Pod shattering resistance is classified as follows: supper shattering <10%, shattering 10 to 50%, non-shattering 50-80%, and direct combine >80%, with indehiscent accessions retaining all of the seed [11]. Giving to this ordering, 96 percent of the genotypes studied were supper shattering, while only 4 percent were shattering.

3.3. Estimates of Variance Components and Coefficients of Variation

3.3.1. Estimates of Genotypic and Phenotypic Coefficients of Variation

The phenotypic coefficient of variation for oil content was 3.54 percent, while the phenotypic coefficient of variation for shattering resistance was 46.87 percent. Similarly, in Table 2, the genotypic coefficients of variation ranged from 3.07 percent for oil content to 45.43 percent for shattering resistance. PCV and GCV values greater than 20% are considered high, values less than 10% are considered low, and values between 10% and 20% are considered moderate [16]. According to this delineation, plant height (13.67, 11.07 percent), harvest index (11.38, 10.8 percent), and seed yield per hectare (19.95, 18.56 percent) had reasonable PCV and GCV values, whereas shattering resistance had high PCV and GCV values (46.87, 45.4 percent). It implies that phenotypic expression of the characters is a good predictor of genetic potential and that the diverse genotypes can provide materials for a successful breeding program. The number of capsules per plant (10.50, 9.39 percent) and biomass yield (11.98, 8.22 percent) had medium PCV and low GCV, respectively; this indicating that these characteristics vary phenotypically due influenced by the environment.

3.3.2. Estimates of Broad Sense Heritability (h^2b)

The percentage of shattering resistance had a heritability of 93.18 percent, while the primary branch per plant had a heritability of 38.14 percent (Table 2). Classified h^2b into three categories: low (less than 30%), medium (30-60%), and high (more than 60%) [18]. Days to flower initiation (78.99%), days to 50% flowering (86.52%), maturity date (78.12%), plant height (65.77%), length of capsule bearing zone (83.71%), capsule length (64.42%), number of capsules per main axis (82.98%), number of capsules per plant (80.08%), number of seed per capsule (62.83%), percentage of shattering resistance (93.18%). This validates how genetic variation affects trait inheritance, and it enables sesame breeders to capitalize on their characteristics by selecting based on phenotypic performance. Due to the relatively minor contribution of the environment to the phenotype, the genotype and phenotype would have a close correspondence.

Date of capsule filling period (59.21%), length of first capsule (54.50%), capsule width (45.18%), capsule thickness (56.23%), biomass yield (47.10%), and primary branch per plant (47.10%) all had medium heritability (35.48 percent). Because these characters have a medium heritability, their expression is heavily influenced by their environments. Medium heritability for the length of the first capsule, capsule width and primary branch per plant [29].

3.3.3. Estimates of Genetic Advance

Estimates of genetic gain for seed yield at Amibara 347.05 kg ha^{-1} (Table 2) show that using the best 5% of high yielding

genotypes as parents can increase mean seed yield of progenies from 975 to 1322 kg ha^{-1} over the base population. Days to 50% flowering (12.10%), maturity date (11.02%), plant height (18.51%), length of capsule bearing zone (11.05%), number of capsules per main axis (12.30%), number of capsules per plant (17.35%), biomass yield (11.64%), and 1000 seed weight (15.2%) all had high GAM, followed by seed yield per hectare (35.60%) and harvest index (35.60 percent) (20.97%). This advocates that the environment has only a minor influence on the characters' expressions. Selection based on characteristics with a low frequency of occurrence.

High heritability estimates combined with high GAM are usually more helpful in predicting gain under selection than heritability estimates alone [18]. High heritability with high genetic advance as percent of mean was obtained for percent of shattering resistance, harvest index and seed yield; whereas high heritability with moderate GAM was obtained for days to 50% flowering, date of maturity, plant height, length of capsule bearing zone, number of capsule per main axis, number of capsule per plant and 1000 seed weight, indicating a greater role of additive gene action for the inheritance of these character.

Table 2. *Estimates of ranges, mean, standard deviation (SD), variance components, phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad sense heritability (h^2b), expected genetic advance (GA) and genetic advance as percent of the mean (GAM) for 20 characters combined over the two years.*

Characteristics	Range						PCV	GCV	h^2b	GA	GAM
	Min	Max	Mean ±SD	σ^2e	σ^2p	σ^2g	(%)	(%)	(%)		(%)
DFI	33.76	43.88	38±1.6	2.643	3.351	2.6467	4.8	4.3	79.0	3.0	7.9
DF	38.55	53.67	43±1.7	2.711	8.510	7.3628	6.8	6.3	86.5	5.2	12.1
DCFP	46 (52)	57 (69)	50 (58)±1.6	2.453	4.193	2.4827	4.1	3.2	59.2	2.5	5.01
DM	94.56	127.1	105±5.1	26.06	51.65	40.3531	6.8	6.0	78.1	11.6	11.03
PLH	84.10	152.1	112±8.0	64.44	235.8	154.6825	13.7	11.1	65.6	20.8	18.6
LCBZ	41 (43)	57 (68)	49 (56)±1.8	3.10	9.74	8.1496	6.40	5.9	83.7	5.4	11.1
LFC	2.10	2.73	2.4±0.2	0.027	0.015	0.0081	5.02	3.7	54.5	0.2	5.6
CL	2.18	2.90	2.5±0.2	0.024	0.019	0.0124	5.58	4.5	64.4	0.2	7.4
CW	0.68	0.85	0.8±0.1	0.003	0.0012	0.0005	4.48	3.0	45.9	0.03	4.2
CTK	0.45	0.61	0.51±0.1	0.001	0.0007	0.0004	5.24	3.9	56.2	0.03	6.1
PBPP	1.6 (2)	2.3 (5)	1.9 (4)±0.2	0.023	0.0124	0.0047	5.83	3.6	38.2	0.09	4.6
CPMA	22. (15)	33 (26)	27 (20)±1.8	3.24	3.751	3.1126	7.19	6.5	83.0	3.3	12.3
CPP	32.5 (28)	60.3 (74)	43 (46)±2.4	5.83	20.33	16.2796	10.5	9.4	80.1	7.5	17.4
SPC	43 (48)	54.3 (67)	49.2 (57)±2.6	6.52	5.206	3.2708	4.64	3.7	62.8	3.0	6.0
ISR	1.39	11.88	4.5±0.7	0.55	4.457	4.1531	46.9	45.2	93.2	4.1	90.1
BY	3.62	6.763	5.1±0.5	0.25	0.379	0.1783	12.0	8.2	47.1	0.6	11.6
HI	14.3 (6)	29.32 (24)	22.6 (15)±1.5	2.25	6.604	5.8975	11.4	10.8	89.3	4.7	21.0
TSW	2.56	4.077	3.4±0.2	0.03	0.091	0.0758	8.80	8.1	84.1	0.5	15.3
OL	42.2	55.40	50.±1.5	2.11	3.178	2.3992	3.54	3.1	75.5	2.8	5.5
YLD	507	1391	975±96	9244	37848	32725.4133	20.0	18.6	86.5	347.1	35.6

()=represents non transformed data, DFI=days to flower initiation, DF= days to 50% flowering, DCFP= days to capsule filling period, DM=days to physiologically mature, PLH=plant height (cm), LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CW=capsule width (cm), CTK=capsule thickness (cm), PBPP= primary branch per plant, CPMA=capsule per main axis, CPP=capsule per plant, SPC=seed per capsule, ISR=percent of inverted shattering resistance (%), BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil content (%) and YLD=yield $kgha^{-1}$.

Seed per capsule, days to flower initiation, capsule length, and oil content had high heritability, but its GAM was low [30]. This suggests that the environment had little influence, but there is a high prevalence of non-additive gene action, indicating that simple selection will be ineffective. This refers to the genetic expression of the genotype as well as the trait's transmissibility from parent to offspring. The heritability of seed per capsule, days to flower initiation, capsule length and oil content was high while the GAM was low [30]. This indicates that the environment has little influence, but the prevalence of non-additive gene action suggests that simple selection will be less effective. This implies that the genotype is expressed genetically and that the trait is transmissible from parent to offspring.

3.4. Genotypic Correlation Coefficient of Seed Yield with Other Characters

The genotypic (rg) correlation estimates between the various characters are shown in Table 3. According to Table 3, the genotypic correlation ranged from 0.03 for the number of seeds per capsule to 0.60 for the harvest index. The length of the capsule bearing zone (rg = 0.25*), the length of the first capsule (rg = 0.24**), capsule length (rg = 0.24*), number of capsules per main axis (rg = 0.51**), number of capsules per plant (rg = 0.50**), harvest index (rg = 0.6**) and oil content (rg = 0.22*) all had a positive and significant genotypic with seed yield. The positive relationship and significant association between seed yield and the aforementioned characteristics advocated that improving one trait would also improve the other, resulting in a similar outcome. The date of flower inception (rg = -0.24*), the date of 50% flowering (rg = -0.28**), the date of maturity (rg = -0.28**), and the percent of shattering resistance (rg = -0.24*) all had a negative and significant genotypic relationship with seed yield. This means that improving one character causes the other to decline, necessitating the pursuit of independent character improvement.

It had little in common with the other characters [31].

Genotypic correlation coefficient among yield related characteristics:- Estimates of genotypic (rg) correlations between various characters are shown in Table 3. Date of capsule filling period, maturity date, plant height, primary branch per plant, percentage of shattering resistance and biomass yield all had positive and significant correlations with date of flower inception and 50% flowering.

Table 3. *Genotypic correlation coefficient for studied quantitative characteristics.*

Character	DFI	DF	MD	LCBZ	LFC	CL	CPMA	CPP	ISR	BY	HI	TSW	OL	YLD
DFI	1	0.8**	0.6**	0.1	-0.2	-0.2	-0.2	-0.1	0.2**	0.35 **	-0.4**	-0.4**	-0.2	-0.3*
DF	0.9**	1	0.8**	0.1	-0.1	-0.1	-0.2**	-0.1	0.3**	0.49**	-0.6**	-0.4**	-0.1*	-0.3**
MD	0.8**	0.9**	1	0.2	-0.1	-0.1	-0.1	-0.1	0.3**	0.19	-0.3**	0.1	-0.1	-0.3**
LCBZ	0.1	0.1	0.2	1	0.3**	0.4*	0.6**	0.4**	-0.1	0.44**	-0.6**	-0.3**	-0.1	0.3**
LFC	-0.2	-0.2	-0.2	0.4**	1	0.8**	0.4**	0.3**	-0.2	0.53**	-0.4**	-0.2**	0.1	0.3*
CL	-0.2	-0.2	-0.2	0.4**	0.9**	1	0.4**	0.2	-0.2**	0.27*	0.1	0.1	0.4**	0.2*
CPMA	-0.2	-0.2	-0.1	0.6**	0.5**	0.5**	1	0.7**	-0.2**	0.01	0.1	-0.1	0.4**	0.5**
CPP	-0.1	-0.1	-0.1	0.4**	0.2*	0.2	0.8**	1	0.1	-0.01	0.1	0.1	0.4**	0.5**
ISR	0.3**	0.3**	0.3**	-0.1	-0.3*	-0.3*	-0.3**	-0.2*	1	0.01	0.1	0.2*	-0.1*	-0.2**
BY	0.5**	0.6**	0.5**	0.3**	0.1	-0.1	0.1	0.1	0.2	1	0.1	0.1	0.1	-0.2*
HI	-0.5**	-0.6**	-0.6**	0.1	0.1	0.1	0.3**	0.3**	-0.2*	-0.37**	1	0.1	-0.1	0.6**
TSW	-0.4**	-0.4**	-0.3**	-0.01	-0.1	0.1	-0.1	-0.1	0.1	-0.28**	0.6**	1	0.4**	0.2*
OL	-0.2	-0.1	-0.2	0.4**	0.4**	0.4**	0.4**	0.3*	-0.4**	0.13	0.2	-0.1	1	0.2*
YLD	-0.3*	-0.3**	-0.3**	0.3*	0.3**	0.3*	0.5**	0.5**	-0.3*	-0.18	0.6**	0.2	0.2*	1

*=Significant at p<0.05,**highly significant at p<0.01, DFI=days to flower initation, DF=days to 50% flowering, DM=days to physiologically mature, LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CPMA=capsule per main axis, CPP=capsule per plant, ISR=percent of shattering resistance (%), BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000seed weight (g), OL=oil content (%) and YLD=yield kgha-1.

Yield was positively correlated with harvest index, 1000 seed weight, and number of capsules per main axis and plant; and oil content at the genotypic level. This means that late flowering genotypes have a longer capsule filling period and maturity date; tallest plants have the most primary branches and produce the highest biomass yield; and early flowering, capsule filling and maturing genotypes have a shorter plant, a higher harvest index, and a higher seed weight, resulting in a high yielder. To recap, the tallest and most mature types have the longest capsule filling time [6].

Plant height, shattering resistance, biomass yield, primary branch per plant, and capsule thickness all had a positive and significant relationship with maturity date; however, harvest index and 1000 seed weight had a negative and significant association. This means that genotypes with later maturation dates have taller plants, more branches and higher biomass yield. Harvest index and oil content were related to capsules per main axis and capsules per plant in a positive and significant way. Number of seeds per capsule was associated with oil content in a positive and significant [9].

3.5. Genotypic Path Coefficient Analysis

Characteristics with a significant correlation with grain yield (kg ha^{-1}) were advanced to genotypic path coefficient analysis in this study. The genotypic path coefficient analysis of yield and yield-related characteristics is shown in Table 4. The harvest index had a 0.59 direct positive effect on seed yield, which was nearly equal to the correlation coefficient (0.60**). This indicates that the true relationship, as well as direct selection through this character, will be effective. The date of flowering had a direct negative impact. Other characteristics had negligible effects on the indirect effects. As a result, the genotypic correlation with seed yield was largely due to the direct effect.

Table 4. *Genotypic Path coefficient analysis indicating the direct (diagonal) and indirect (off diagonal) effect of the characters.*

YLD	DFI	DF	MD	LCBZ	LFC	CL	CPMA	CPP	ISR	HI	OL	rg
DFI	1	0.237	-0.016	-0.001	-0.029	0.004	-0.037	-0.018	-0.014	-0.289	0.009	-0.244*
DF	-0.078	1	-0.019	-0.003	-0.022	0.003	-0.033	-0.022	-0.018	-0.368	0.007	-0.281**
MD	-0.067	0.242	1	-0.006	-0.022	0.003	-0.019	-0.010	-0.018	-0.371	0.009	-0.281**
LCBZ	-0.003	0.024	-0.004	1	0.053	-0.008	0.138	0.068	0.006	0.027	-0.021	0.250*
LFC	0.018	-0.041	0.003	-0.011	1	-0.019	0.098	0.037	0.014	0.036	-0.024	0.259**
CL	0.018	-0.038	0.003	-0.011	0.130	1	0.095	0.025	0.013	0.047	-0.022	0.238*
CPMA	0.015	-0.041	0.002	-0.019	0.066	-0.009	1	0.125	0.015	0.163	-0.024	0.511**
CPP	0.010	-0.037	0.001	-0.012	0.034	-0.003	0.168	1	0.013	0.181	-0.014	0.503**
ISR	-0.024	0.089	-0.007	0.003	-0.037	0.005	-0.061	-0.038	1	-0.137	0.020	-0.242*
HI	0.044	-0.169	0.014	-0.001	0.009	-0.002	0.060	0.049	0.013	1	-0.010	0.600**
OL	0.014	-0.031	0.003	-0.011	0.061	-0.008	0.089	0.039	0.019	0.104	1	0.221*

Residual=0.688, *= significant at p≤0.05, ** highly significant at p≤0.01, DFI=days to flower initiation, DF= days to 50% flowering, DM=days to physiologically mature, LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CPMA=capsule per main axis, CPP=capsule per plant, ISR=percent of inverted shattering resistance (%), HI=harvest index (%), OL=oil content (%), YLD=yield $kgha^{-1}$ and rg = genotypic correlation value.

The number of capsules per main axis, number of capsules per plant and length of the first capsule all had a direct positive effect. They had statistically significant and positive genotypic correlations with seed yield. Their indirect effects on other variables were overwhelmingly positive and minor. As a result, the majority of their positive correlation with seed yield was evaluated for by their direct effect. Number of capsules per plant had the greatest positive direct effect on seed yield, followed by the harvest index [8]. The genotypic path coefficient analysis yielded a residual value of 0.69, indicating that the characters in the path analysis explained 31.2 percent of the variability in seed yield, with the remaining 69 percent explained by other characters not considered in the path analysis and environmental factors.

3.6. Genetic Diversity Analysis

3.6.1. Cluster Analysis

Using D^2 values based on the pooled mean of genotypes, the 100 sesame genotypes were divided into seven clusters (Table 5 and See Figure 1). As a result, tested sesame genotypes had moderately divergent. The majority of the clusters differed significantly. Cluster III had the most sesame genotypes (28 percent) followed by Cluster I (21 percent), Cluster V (15 percent), Cluster IV (13 percent), and Cluster II (12 percent). It also contains two checks (standard check Adi inter in to cluster IV and local check in cluster III). Clusters VI and VII, on the other hand, have the fewest genotypes, with 9 percent and 2 percent, respectively.

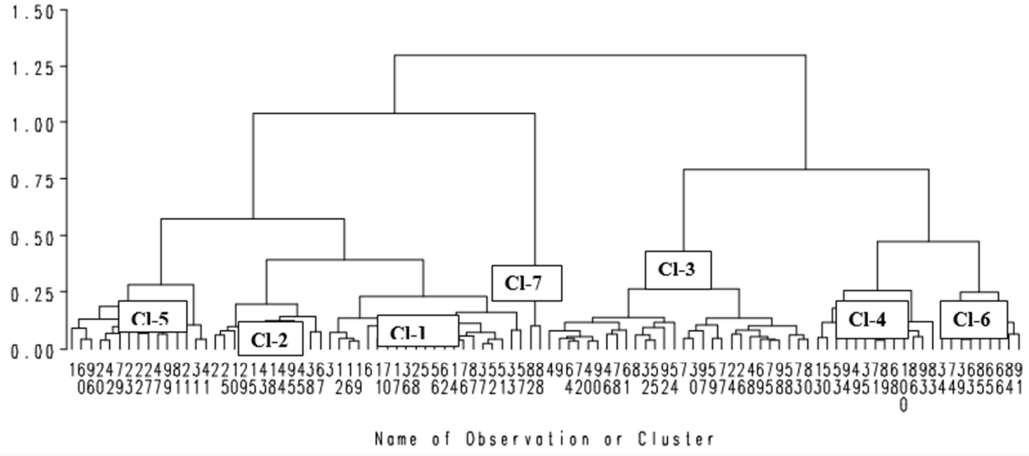

Figure 1. *Dendrogram showing the clusters of 100 sesame genotypes evaluated using 20 quantitative characteristics at Amibara.*

Table 51. *Distribution of the 100 sesame genotypes into different clusters at Amibara.*

Cluster	Number of Genotypes	Proportion	Name of genotypes
Cluster I	21	21%	Acc–00065, W–118, Acc-No 04 + 06 + 07, Ying White–2, Acc-No–05, Acc-EW–006, Acc-BG–001, NN–0054, AW–001, EW-017 (1), Acc-WW-001 (6), Acc-024-sel–1, Acc–044, Acc-No–049, BACKO-MW–42, China FAO (ACC- 68-542), Acc-203-336–2, HB-49 FAM-2–2, Acc-20–630, Acc-210-991–4 and EW-17 (5) x NS-001 # 48,
Cluster II	12	12%	Acc-211–015, Acc-EW-012 (7), Acc-210-986–1, Acc-205–344, NN–0021, HB-38 FAM-2 BAR Grey, Acc-WW-003 (4), Acc-BG–003, Tejareb-2 Late gindwuha, Acc-No–024, HB-22-FAM (-4); Acc-No-045
Cluster III	28	28%	Local check, NN-0068-2, Acc-BG–009, Acc-111-848–1, Acc-EW-017 (6), Unknown Nguara sel-9, Acc-EW-025 (1), BAR–002, NN-0029 (2), Unknown-sel–3, Acc-205–180, Acc-202-374–2, BCS-033, NN-0036–1, NN–0052, Bering bowng, NN-0108–2, EW-020 (1), Hirhir Adi Gosh sel-4, Acc–00019, USR-82 # 171 NS, Hirhir Humera sel-6, Venzula–1, Acc-203–187, M-80 # 402–2, Acc-BG-001 (3), Acc-024 sel–3 and K-74 X C_{22} (71-2)-3
Cluster IV	13	13%	Adi, Banja Gobate sel–4, Bounja-filwuha sel–8, BCS-001 (1), Acc-203–612, Acc # 033, Acc-205-374–2, Tejahir-2 Late ginwuha-sel-1, Hirhir Kebebew early sel-1, Acc-EW-009 (5), Acc-203–623, Bounja-fiyel kolet sel–4 and Unkown Kaja sel- 4
Cluster V	15	15%	G-03–1, Bounja-filwuha sel–2, Bounja-filwuha sel–6, Win black (Tall)–2, SSBS- (9 -2)-3, BA–0004, Acc-111-821, AW–007, Acc-GA-005 (1), Clusu-Acc–2, Acc-202–363, NN-0129-2, JAPAN-651, Acc-NS-007 (2) and Acc-WW-001 (4)
Cluster VI	9	9%	NN-088–2, Acc-EW-011 (1), SPS-SIK- # 811, NN-0183–3, Tmax, Acc-203-336-4, X-30/40 # 403, Acc-111-524–1 and Hirhir Baker sel–1
Cluster VII	2	2%	Acc-205-374–1 and Acc-No–044

Ethiopian genotypes were found in all clusters, with the majority found in clusters I and III. Moreover, the Ethiopian genotypes were distributed in seven different clusters, indicating that the Ethiopian genotypes were more diverse. FAO genotypes were found in clusters other than VII, indicating that there was less variation among genotypes. The lack of differentiation between the FAO and Ethiopia genotypes, which is most likely due to gene flow, could

describe the overlapping genotypic cluster patterns [32]. In general, Ethiopian genotypes revealed a more variable clustering pattern than FAO genotypes (Table 5). As Ethiopia is the center of origin for sesame, future sesame genotype exploitation exertions should pay special consideration to the major sesame producing regions [33].

3.6.2. Cluster Mean Performance

The mean value of the 20 characters for each cluster group is shown in Table 6. Cluster I was described as being of moderate extent. Cluster II had the highest mean cluster values for thick capsule (0.53 cm), number of seeds per capsule (50.18) and biomass yield (5.44 ton). Cluster III was also of a reasonable magnitude. Cluster IV had the shortest plant height (104.65cm), the smallest number of primary branches (1.85), the lowest biomass yield (4.76 tons) and the highest oil content (51.18). Cluster V's capsules were the shortest (2.38 cm) and widest (0.77 cm), with the remaining characteristics being moderate.

Table 6. *Cluster means value of 20 characters of 100 sesame genotypes.*

Characteristics	cluster-I	cluster-II	cluster-III	cluster-IV	cluster-V	cluster-VI	cluster-VII
DFI	37.87	38.13	37.64	37.39	38.23	36.59*	42.27**
DF	42.90	43.87	42.61	42.15	44.01	41.40*	51.19**
DCFP	50.09	50.03	50.01	49.48	50.05	49.22*	53.12**
MD	105.10	106.59	104.73	102.79	106.77	101.08*	124.46**
PLH	112.58	118.46	110.10	104.65*	116.20	111.34	128.00**
LCBZ	48.50	49.91	48.56	49.18	48.35	50.37**	41.52*
LFC	2.42	2.46	2.41	2.45	2.38*	2.51**	2.385
CL	2.48	2.51	2.47	2.54	2.46	2.56**	2.35*
CW	0.76	0.76	0.75	0.76	0.77**	0.74	0.72*
CTK	0.51	0.53**	0.52	0.51	0.52	0.50	0.48*
PBPP	1.90	1.89	1.93	1.85*	1.88	1.95	2.09*
CPMA	26.47	27.56	26.95	28.20	25.66	28.76**	21.97*
CPP	42.06	43.23	43.67	44.86	39.35	47.14**	35.48*
SPC	49.56	50.18**	49.09	49.29	48.55	48.88	46.62*
ISR	4.91	4.52	4.69	3.86	4.86	2.74*	6.97**
BY	5.15	5.44**	5.11	4.76*	5.24	5.10	5.36
HI	21.62	22.05	23.65	24.09	20.34	25.08**	16.48*
TSW	3.36	3.35	3.48	3.46	3.37	3.50**	2.91*
OL	50.19	51.09	50.26	51.18**	49.65	50.84	49.27*
YLD	821.80	927.31	1052.42	1218.94	707.70	1348.14**	520.13*

**= highest value, *= lowest value, DFI=days to flower initation, DF= days to 50% flowering, DCF= days to capsule filing period, DM=days to physiologically mature, PLH=plant height (cm), LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CW=capsule width (cm), CTK=capsule thickness (cm), PBPP= primary branch per plant, CPMA=capsule per main axis, CPP=capsule per plant, SPC=seed per capsule, ISR=percent of inverted shattering resistance (%), BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil content (%) and YLD=yield kgha^{-1}.

Cluster VI had the earliest flower initiation (36.59 days) and flowering date (41.40 days), the earliest maturity genotypes (101.08 days), the longest capsule bearing zone (50.37 cm) and capsule length (2.56 cm), the weightiest harvest index (25.08 percent) and 1000 seed weight (3.50g), the highest number of capsule per main axis (28.76), capsule per plant (47.14), the highest seed weight (1348.14kg). Cluster VII had the earliest flower initiation (42.27 days), the longest 50% flowering date (51.19 days), the shortest capsule bearing zone (41.52 cm), the earliest maturing type (124.00 days), the tallest plant (128.00 cm), and the shortest capsule bearing zone (41.52 cm); the narrowest capsule (0.48cm), most branched (2.09), the smallest number of capsule per main stem (35.48) and capsule per plant (46.62).

3.6.3. Genetic Divergence Analysis

Generalized divergence, as measured by Mahalanobis D^2 statistics, revealed the genetic distance and significant variation ($p<0.01$ and $p<0.05$) among the seven clusters (Table 7). According to the findings, the genotypes used in this study are moderately divergent. The chi-square test revealed highly significant differences between clusters except for clusters I and II, cluster II and III, cluster I and V; cluster IV and VI. The inter cluster distances were always greater than the intra cluster distances, signifying that the genotypes of different groups were more varied. Cluster VI and VII (D^2 = 1012) had the greatest squared inter-cluster distance, followed by IV and VII (D^2 = 764.8), V and VI (D^2 = 507), and III and VII (D^2 = 474). Clusters II and III have the shortest squared distances (D^2 = 21). These genotypes were not genetically diverse, and there was little genetic diversity between them, as indicated by the minimum inter cluster distance. Crossing genotypes from these four clusters may not result in a high heterotic value in F_1 and a limited range of variation in the separating F_2 population.

The parents chosen from divergent clusters are likely to have the highest level of genetic recombination. Crosses involving parents from clusters 6 and 7 are anticipated to have the most recombination and progenies separation, followed by clusters 4 and 7, 5 and 6, and 3 and 7. Cluster VII (7.8) had the greatest intera cluster distance, while Cluster II (7.9) had the smallest (2.5). This means that genotypes in Cluster VII were more variable than genotypes in any other cluster. Selection of parents should consider the

distinct benefits of each cluster and genotype within a cluster, as well as the specific purposes of hybridization [34].

Table 7. *Inter and Intra (bolded along diagonal) generalized distance (D^2) among clusters.*

Cluster	I	II	III	IV	V	VI	VII
I	3.1	21.5^{ns}	69.0**	205.7**	21.2^{ns}	343.3**	207.6**
II		4.2	21.0^{ns}	109.4**	70.5**	213.3**	328.4**
III			2.5	42.8**	152.2**	111.9**	474.0**
IV				4.1	335.9**	25.9^{ns}	764.8**
V					3.8	507.4**	121.4**
VI						4.8	1012.0**
VII							7.8

** = significant, X^2 = 30.14 at 5% & 36.19 at 1% probability level, respectively, ns= non-significant and bold number represent intra-cluster distance.

3.6.4. Principal Component Analysis

The first seven principal components with eigenvalues greater than one assessed for 78.67% of the variance (Table 8). The first principal component (PC_1), which evaluated for 26.00 percent of the diversity, was the date of flower inception, date of 50% flowering, date of capsule filling period, maturity date, capsule length, capsule width, capsule per main axis, seed per capsule, shattering resistance, biomass yield per hectare and oil content. In the second principal component analysis, maturity date, plant height, length of capsule bearing zone, length of first capsule, capsule width, primary branch per plant, capsule per main axis, shattering resistance and 1000 seed weight all assessed for 17.84 percent of total variability among genotypes. Discriminatory characteristics such as capsule length, capsule width, and capsule per plant, as well as shattering resistance, harvest index, and seed yield, were all attributed to the third principal component (PC_3), which evaluated for 10.73 percent of total genotype variability.

Table 8. *Eigen vector and Eigen value of the first seven principal components (PCs) for characters.*

Character	PCA1	PCA2	PCA3	PCA4	PCA5	PCA6	PCA7
Date of flower initiation	0.881	0.044	-0.268	-0.022	0.091	-0.075	-0.168
Date of 50% flowering	0.553	0.073	0.589	0.211	-0.252	-0.113	0.098
Date of capsule filing period	0.940	0.038	0.102	0.109	-0.073	-0.098	-0.056
Maturity date	0.817	0.348	0.018	0.120	-0.098	-0.007	-0.174
Plant height (cm)	0.272	0.751	0.299	0.041	-0.116	0.043	-0.202
Length of capsule b/ng zone (cm)	-0.278	0.785	-0.008	-0.018	-0.326	0.081	0.106
Length of 1st capsule (cm)	-0.206	0.789	0.068	-0.148	-0.272	0.006	0.216
Capsule length (cm)	0.418	-0.035	0.599	0.202	0.310	0.073	0.288
Capsule width (cm)	0.341	0.430	0.554	0.036	0.412	0.019	-0.054
Capsule thickness (cm)	-0.032	-0.164	-0.232	0.672	-0.040	0.368	-0.314
Primary branch per plant	-0.211	0.773	-0.112	0.312	0.101	-0.268	0.021
Capsule per main axis	-0.348	0.455	-0.275	0.606	0.150	-0.152	0.020
Capsule per plant	0.032	0.271	-0.339	-0.037	-0.021	0.630	0.461
Number of seed per capsule	0.428	-0.254	0.047	0.218	-0.563	0.170	0.178
% of Inverted Shattering resistance	0.529	0.370	-0.318	0.037	0.100	0.354	-0.152
Biomass yield per hectare (ton)	-0.819	-0.083	0.128	0.253	0.198	0.125	-0.143
Harvest index (%)	-0.285	-0.298	0.604	0.294	0.034	0.408	-0.064
100 seed weight (g)	-0.162	0.593	0.063	-0.423	0.375	0.262	-0.103
Oil content (%)	-0.591	0.268	-0.034	0.185	-0.238	-0.141	-0.229
Yield ($kgha^{-1}$)	0.258	-0.036	-0.332	0.401	0.313	-0.226	0.530
Eigen value:-	5.460	3.746	2.252	1.629	1.262	1.153	1.019
% of total variance	26.000	17.840	10.730	7.760	6.010	5.490	4.850
% of Cumulative variance	26.000	43.840	54.560	62.320	68.330	73.820	78.670

The fourth principal component (PC_4) estimated for 7.76% of total variation, with capsule thickness, primary branch and capsule per main axis, 1000 seed weight, and seed yield being the most important contributing characters. The fifth principal component (PC_5), which explained 6.01 percent of the variation among genotypes, was the length of the capsule bearing zone, capsule length, capsule width, seed per capsule, 1000 seed weight and seed yield; the sixth principal component (PC_6) explained 5.49 percent of the total variability, with capsule thickness, capsule per plant, percentage of shattering resistance and harvest index being the main contributors to PC_6.

Similarly, capsule thickness, capsule number per plant and seed yield estimated for 4.85 percent of the 7th principal component (PC_7). Out of the 19 quantitative characteristics evaluated, capsule width, percent of shattering resistance, and yield; all contributed to variations in four of the seven principal components (Table 8). In over-all, the principal component analysis revealed that the genotypes under investigation vary. This suggests opportunities for genetic improvement through direct selection of genotypes from accessions and/or the selection of diverse parents for a hybridization, as well as

genotype conservation for future use. Four principal components (PCs) explained approximately 63.63 percent of total variation among 105 sesame accessions, which is consistent with the current findings [35].

4. Summary and Conclusion

Crop improvement is determined by the material used, the level of variability present, and knowledge of quantitative characteristics associated with grain yield and among themselves. The current study included 100 sesame genotypes that were evaluated over two successive years at Amibara in order to determine genetic diversity and character associations. Combined analysis of variance, genotypes differed significantly for all of the characters studied. Plant height, harvest index, and seed yield all had high PCV and GCV values, whereas shattering resistance had medium PCV and GCV values. High heritability estimates were combined with high genetic advance as a percentage of mean for percent of shattering resistances, harvest index and seed yield (GAM). Date of 50% flowering, maturity, plant height, length of capsule bearing zone, number of capsules per main axis, capsule per plant and 1000 seed weight had a moderate GAM in combination with high heritability estimations.

The length of the capsule bearing zone and first capsule, capsule length, and the number of capsules per main axis, number of capsules per plant, harvest index, and oil content were all associated with seed yield in a positive and significant genotypic manner. By selecting for these characteristics, it is possible to increase sesame seed yield. According to path coefficient analysis, the harvest index had the greatest positive direct effect on seed yield. Furthermore, seed yield was related to the number of capsules per plant and the number of capsules per main axis. Based on D^2 analysis of the pooled mean of genotypes; 100 genotypes were divided into seven clusters, indicating that they are moderately divergent. According to principal component analysis; the first seven principal components (PC1 to PC7) with Eigen values greater than one evaluated for 78.67% of the total variation in the characters. Harvest index, capsule per plant and capsule per main axis all had medium genotypic coefficients of variation, medium to high heritability, higher genetic advance as percent of mean, and a positive correlation coefficient, as well as a direct effect on seed yield. These characteristics will be useful for indirect selection in order to increase sesame seed yield. In this study, only morphological characteristics were used. As a result, future research should consider using molecular markers and high-throughput molecular data to assess sesame genetic resources for marker assisted breeding.

Data Availability Statement

If there is a data set associated with the paper included in appendix table.

Acknowledgements

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Appendix

Table A1. *Metrological data for test season of experiment sit (monthly maximum, minimum and average temperature; and average rain fall.*

Year	Temperature (°C)				Rain Fall (RF)
	Month	Min	Max	average	
2017	July	24.3	37.4	30.8	213.8
2017	August	23.4	35.9	29.6	193.2
2017	September	21.3	36.2	28.7	97.0
2017	October	21.6	35.4	27.6	0.0
2017	November	16.4	35.2	25.8	0.0
2017	December	12.1	31.3	21.7	0.0
2018	January	14.3	30.8	22.6	0.0
2018	February	18.1	33.0	23.1	6.0
2018	March	19.8	33.6	26.7	25.6
2018	April	22.6	35.2	27.9	262.0
2018	May	23.3	37.1	30.2	18.9
2018	Jun	24.3	37.7	30.0	47.6

Table A2. *Soil Physicochemical characteristics of the experimental site.*

Year	Sample. No	ID	pH	EC (ds/m)	Percentage of							
					OOC	TOC	OM	TN	(Clay+Silt)	Clay	silt	Sand
2017	1R1	M-2017	7.60	1.12	0.80	1.06	1.85	0.09	87.20	55.20	32.00	12.80
2017	2R1	M-2017	8.36	1.13	0.92	1.22	2.12	0.11	87.20	53.20	34.00	12.80
2017	3R2	M-2017	8.44	1.11	0.92	1.22	2.12	0.11	87.20	57.20	30.00	12.80
2017	4R2	M-2017	7.87	1.01	0.78	1.04	1.81	0.09	89.20	53.20	36.00	10.80
2017	5R3	M-2017	7.91	1.63	0.74	0.99	1.72	0.09	89.20	53.20	36.00	10.80
2017	6R3	M-2017	8.32	1.17	1.11	1.48	2.57	0.13	89.20	57.20	32.00	10.80
2018	1R1	M-2018	7.82	1.37	0.57	0.76	1.31	0.07	78.00	26.00	52.00	22.00

Year	Sample. No	ID	pH	EC (ds/m)	Percentage of							
					OOC	TOC	OM	TN	(Clay+Silt)	Clay	silt	Sand
2018	2R1	M-2018	8.01	1.52	0.57	0.76	1.31	0.07	74.00	24.00	50.00	26.00
2018	3R2	M-2018	8.14	2.43	0.54	0.72	1.24	0.06	80.00	30.00	50.00	20.00
2018	4R2	M-2018	8.23	1.24	0.51	0.68	1.17	0.06	82.00	30.00	52.00	18.00
2018	5R3	M-2018	8.18	1.01	0.42	0.56	0.97	0.05	84.00	34.00	50.00	16.00
2018	6R3	M-2018	8.01	3.36	0.45	0.60	1.03	0.05	80.00	34.00	46.00	20.00

EC=Electrical conductivity, OOC=Oxidizable organic carbon, TOC=Total organic carbon, OM=organic carbon, TN= total nitrogen.

Table A3. *Description of genetic materials.*

No	Name of genotypes	Origin	No	Name of genotypes	Origin
1	Acc- 00019	ET	51	EW - 020 (1)-sel-2	ET
2	Acc- 00065	ET	52	G - 03 – 1	ET
3	Acc - 024 - sel- 1	ET	53	Hihir Baker sel- 1	ET
4	Acc - 024 sel- 3	ET	54	Hirhir Adi Gosh sel-4	ET
5	Acc- 044-sel-1	ET	55	Hirhir humera sel- 6	ET
6	Acc - 111 - 848 – 1	ET	56	Hirhir Kebebew early sel-1	ET
7	Acc - 202 – 363	ET	57	K-74 X C22 (71-2)-3	ET
8	Acc - 202 - 374 – 2	ET	58	M - 80 # 402 – 2	ET
9	Acc - 203 – 187	ET	59	NN – 0021	ET
10	Acc - 205 – 180	ET	60	NN - 0029 (2)	ET
11	Acc - 205 – 344	ET	61	NN - 0036 – 1	ET
12	Acc - 205 - 374 – 1	ET	62	NN – 0052	ET
13	Acc - 205 - 374 – 2	ET	63	NN – 0054	ET
14	Acc - 211 – 015	ET	64	NN - 0068 - 2	ET
15	Acc - BG – 001	ET	65	NN - 0108 – 2	ET
16	Acc - BG – 001 (3)	ET	66	NN - 0129-2	ET
17	Acc - BG – 003	ET	67	NN - 0183 – 3	ET
18	Acc - BG – 009	ET	68	NN - 088 – 2	ET
19	Acc - EW – 006	ET	69	Tejahir-2Late ginwuha-sel-1	ET
20	Acc - EW – 009 (5)	ET	70	Tejareb-2 Late gindwuha	ET
21	Acc - EW – 011 (1)	ET	71	W – 118	ET
22	Acc - EW - 012 (7)	ET	72	Acc - 203 - 336 – 2	FAO
23	Acc - EW – 017 (6)	ET	73	Acc - 203 - 336 - 4	FAO
24	Acc - EW – 025 (1)	ET	74	Acc - 203 – 612	FAO

Table A3. *Continued.*

No	Name of genotypes	Origin	No	Name of genotypes	Origin
25	Acc - GA – 005 (1)	ET	75	Acc - 203 - 623-sel-1	FAO
26	Acc - No – 024	ET	76	Acc - 203 – 630	FAO
27	Acc - No – 044	ET	77	Acc - 210 - 986 – 1	FAO
28	Acc - No – 045	ET	78	Acc - 210 - 991 – 4	FAO
29	Acc - No – 049	ET	79	BAR – 0004	FAO
30	Acc - No – 05	ET	80	BAR – 002	FAO
31	Acc - No 04+06+07	ET	81	Bering bowng	FAO
32	Acc - NS – 007 (2)	ET	82	China FAO (ACC-68-542)	FAO
33	Acc - WW - 001 (4)	ET	83	Clusu - Acc- 2	FAO
34	Acc - WW – 001 (6)	ET	84	HB - 22 - FAM (1- 4)	FAO
35	Acc - WW – 003 (4)	ET	85	HB - 38 FAM - 2 BAR Grey	FAO
36	Acc # 033	ET	86	HB - 49 FAM - 2 – 2	FAO
37	Acc -111- 524 – 1	ET	87	JAPAN-651	FAO
38	Acc -111- 821	ET	88	SPS - SIK - # 811	FAO
39	AW – 001	ET	89	SSBS - (9 - 2) -3	FAO
40	AW – 007	ET	90	Tmax	FAO
41	BACKO-MW-42	ET	91	Unknown - sel- 3	FAO
42	Banja Gobate sel- 4	ET	92	Unknown Nguara sel-9	FAO
43	BCS - 001 (1)	ET	93	Unkown Kaja sel- 4	FAO
44	BCS – 033	ET	94	USR - 82 # 171 NS	FAO
45	Bounja – filwuha sel- 2	ET	95	Venezuela – 1	FAO
46	Bounja – filwuha sel- 6	ET	96	Win black (Tall) – 2	FAO
47	Bounja – filwuha sel- 8	ET	97	X - 30/40 # 403	FAO
48	Bounja - fiyel kolet sel- 4	ET	98	Ying White – 2	FAO
49	EW – 017 (1)	ET	99	Local check	Check
50	EW-017 (5) x NS-001 # 48	ET	100	Adi	Check

WARC=Amibara Agricultural Research center, ET=Ethiopia collection; FAO=Food and Agricultural Organization.

Table A4. *Homogeneity test according to Hartley (1950), ratio of largest to smallest mean squares of error.*

Character	Mean square of error season 1	Mean square of error season 2	Ratio max to min Test
DFI	1.361	3.728	2.738
DF	1.327	3.900	2.939
DCFP	2.413	2.547	1.055
DM	17.229	33.019	1.916
PLH	30.495	83.060	2.724
LCBZ	2.135	3.648	1.709
LFC	0.022	0.025	1.134
CL	0.020	0.024	1.169
CW	0.003	0.003	0.945
CTK	0.001	0.001	0.601
PBPP	0.019	0.028	1.469
CPMA	2.006	4.231	2.110
CPP	4.245	6.384	1.504
SPC	4.825	8.396	1.740
ISR	0.569	0.536	0.942
BY	0.210	0.287	1.366
HI	1.925	2.541	1.320
TSW	0.025	0.036	1.409
OL	1.949	1.708	0.877
YLD	7021.14	11340.77	1.615

DFI=days to flower initation, DF=days to 50% flowering, DCFP=days to capsule filing period, DM=days to physiologically mature, PLH=plant height (cm), LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CW=capsule width (cm), CTK=capsule thickness (cm), PBPP=primary branch per plant, CPMA=capsule per main axis, CPP=capsule per plant, SPC=seed per capsule, ISR=percent of inverted shattering resistance (%), BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil yield (%) and YLD=yield kgha^{-1}.

Table A5. *Analysis of variance (ANOVA) summary for yield and yield related characteristics at season one (2017).*

Character	Mean square of Error								Efficiency relative to
	Trt (unadj) df=99	Trt (adj) df =99	Block (Rep) (adj)df =27	Rep df =2	Intra df =171	RCBD df =99	R^2 (%)	CV (%)	RCBD (%)
DFI	9.417	8.682**	3.156	4.990	1.361	1.767	0.815	3.149	126
DF	26.043	23.580**	2.455	9.723	1.327	1.629	0.922	2.850	121
$DCFP	24.495	22.723**	2.254	6.583	2.413	2.631	0.858	3.142	114
DM	282.522	262.078*	16.143	284.653	17.229	18.789	0.908	4.179	114
PLH	879.872	725.750**	55.889	113.470	30.495	37.354	0.945	5.210	121
$LCBZ	39.504	31.087**	3.326	4.263	2.135	2.527	0.917	3.156	118
LFC	0.064	0.056**	0.060	0.192	0.022	0.030	0.691	6.115	131
CL	0.097	0.083**	0.050	0.216	0.020	0.027	0.767	5.726	128
CW	0.006	0.005**	0.004	0.008	0.003	0.003	0.580	6.909	116
CTK	0.004	0.003**	0.002	0.005	0.001	0.002	0.659	7.441	119
#PBPP	0.047	0.046**	0.048	0.007	0.019	0.025	0.644	7.400	128
$CPMA	13.925	11.553**	2.042	4.960	2.006	2.212	0.808	5.534	114
$CPP	68.247	60.012**	7.908	7.963	4.245	5.219	0.906	5.013	121
$SPC	27.450	24.756**	7.297	13.623	4.825	5.678	0.781	4.493	117
ISR	14.205	12.027**	0.488	0.961	0.569	0.614	0.936	17.615	114
BY	2.226	1.941**	0.317	0.060	0.210	0.247	0.864	8.691	117
$HI	23.462	20.489**	1.796	2.771	1.925	2.098	0.878	6.425	114
TSW	0.329	0.307**	0.046	0.153	0.025	0.031	0.887	4.686	120
OL	16.561	14.587**	5.205	92.700	1.949	2.632	0.855	2.762	130
YLD	103067.440	83818.02**	7328.107	19121.570	7021.140	7769.302	0.897	8.442	114

df = degree of freedom, unadj=unadjusted, adj=adjusted,** highly significant at p≤0.01, df=degree of freedom, unadj=unadjusted, adj=adjusted DFI=days to flower initation, DF=days to 50% flowering, DCFP=days to capsule filing period, DM=days to physiologically mature, PLH=plant height (cm), LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CW=capsule width (cm), CTK=capsule thickness (cm), PBPP=primary branch per plant, CPMA=capsule per main axis, CPP=capsule per plant, SPC=seed per capsule, ISR=percent of inverted shattering resistance (%), BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil yield (%) and YLD=yield kgha^{-1}, #= square root transformed data, $= arc sin transformed.

Table A6. *Analysis of variance (ANOVA) summary for yield and yield related characteristics at season two (2018).*

Mean square					Error		Efficiency		
Characteristics	Trt (unadj) df=99	Trt (adj) df =99	Block (Rep) (adj)df =27	Rep df =2	Intra df =171	RCBD df =99	R^2 (%)	CV (%)	relative to RCBD (%)
NDFI	17.019	15.141**	5.584	20.520	3.728	4.379	0.746	5.009	117
DF	39.265	33.351**	5.568	33.723	3.900	4.540	0.860	4.326	117
$DCFP	12.817	11.774**	3.244	67.453	2.547	2.906	0.774	3.161	116

Mean square					Error		Efficiency		
Characteristics	**Trt (unadj) df=99**	**Trt (adj) df =99**	**Block (Rep) (adj)df =27**	**Rep df =2**	**Intra df =171**	**RCBD df =99**	**R^2 (%)**	**CV (%)**	**relative to RCBD (%)**
DM	124.379	111.893**	51.741	469.390	33.019	39.129	0.722	5.179	118
PLH	1212.247	1080.521**	201.738	2902.543	83.060	109.168	0.902	7.684	127
$LCBZ	42.741	35.855**	7.644	110.583	3.648	4.612	0.882	3.725	124
LFC	0.083	0.072**	0.039	0.604	0.025	0.030	0.712	6.506	118
CL	0.082	0.072**	0.028	0.572	0.024	0.027	0.712	6.199	115
CW	0.006	0.005*	0.003	0.052	0.003	0.003	0.615	7.192	115
CTK	0.003	0.003**	0.002	0.054	0.001	0.001	0.763	5.807	120
#PBPP	0.076	0.073**	0.037	0.222	0.028	0.032	0.652	8.603	116
$CPMA	17.582	14.300**	7.576	187.320	4.231	5.156	0.762	7.263	120
$CPP	100.527	85.956**	8.651	159.363	6.384	7.363	0.906	5.645	116
$SPC	18.764	17.684**	9.009	28.170	8.396	9.328	0.600	5.853	114
ISR	19.134	16.394**	0.294	0.752	0.536	0.553	0.954	15.486	119
BY	1.647	1.442**	0.310	0.216	0.287	0.319	0.778	10.732	115
$HI	25.940	22.871**	3.218	42.442	2.541	2.897	0.863	6.766	115
TSW	0.338	0.315**	0.051	1.838	0.036	0.041	0.863	5.508	117
OL	9.859	8.510**	2.366	2.083	1.708	1.978	0.781	2.600	116
YLD	195735.320	172221.57**	10291.030	510567.000	11340.770	12317.385	0.914	11.126	114

** highly significant at $p \leq 0.01$, df=degree of freedom, unadj=unadjusted, adj=adjusted DFI=days to flower initation, DF=days to 50% flowering, DCFP=days to capsule filing period, DM=days to physiologically mature, PLH=plant height (cm), LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CW=capsule width (cm), CTK=capsule thickness (cm), PBPP=primary branch per plant, CPMA=capsule per main axis, CPP=capsule per plant, SPC=seed per capsule, ISR=percent of inverted shattering resistance (%), BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil yield (%) and YLD=yield kgha^{-1} #= square root transformed data, $= arc sin transformed.

Table A7. *Mean performance of 10 top and ten least sesame genotypes for 20 yield and yield related traits tested at Amibara.*

No	Genotype	CPMA	CPP	SPC	ISR	BY	HI	TSW	OL	YLD
1	Acc-203-336-4	26.56 (19.47)	48.68 (55.83)	48.04 (56.22)	2.13	5.6	26.89 (21.00)	3.7	51.9	1391.0
2	Hirhir Baker sel-1	27.71 (23.17)	41.83 (44.67)	48.96 (56.52)	1.81	3.6	23.84 (16.17)	3.3	44.5	1388.5
3	Acc-111-524-1	30.04 (24.00)	49.20 (57.33)	47.90 (55.50)	2.19	5.7	22.66 (14.50)	3.4	51.5	1381.8
4	Tmax	32.29 (25.33)	54.84 (66.33)	45.48 (51.90)	5.80	4.9	24.97 (18.33)	3.4	51.9	1377.6
5	SPS-SIK-# 811	29.90 (23.50)	49.02 (57.67)	50.17 (59.65)	1.98	5.8	24.24 (17.17)	3.4	55.4	1344.7
6	NN-0183-3	26.71 (18.70)	41.99 (45.67)	45.57 (51.83)	2.13	4.9	28.33 (22.49)	3.6	50.7	1333.2
7	NN-088-2	30.25 (22.17)	51.99 (62.67)	52.09 (60.85)	2.54	4.9	26.24 (19.33)	3.7	50.2	1314.6
8	Acc-EW-011 (1)	26.45 (20.80)	43.86 (48.33)	52.14 (61.42)	2.04	5.2	26.34 (20.33)	3.3	51.4	1310.9
9	X-30/40 # 403	28.93 (25.17)	42.88 (45.67)	49.53 (56.33)	4.03	5.3	22.18 (14.50)	3.7	50.1	1290.8
10	BCS-001 (1)	27.01 (21.03)	46.86 (53.67)	51.09 (60.50)	3.68	4.1	29.32 (23.80)	4.0	50.1	1265.3
11	AW-007	26.70 (20.00)	41.81 (43.83)	48.72 (56.03)	3.96	6.1	16.92 (8.87)	3.3	50.1	714.8
12	G-03-1	21.95 (16.70)	32.61 (28.33)	49.84 (58.18)	3.20	5.2	21.03 (12.83)	3.6	49.8	710.3
13	Bounja-filwuha sel-2	25.14 (17.13)	38.29 (38.00)	49.35 (57.00)	4.50	5.4	20.19 (12.20)	3.2	50.1	709.1
14	Acc-WW-001 (4)	27.64 (19.00)	44.90 (50.17)	43.00 (47.52)	7.51	5.6	17.97 (9.55)	2.9	42.2	704.6
15	Acc-NS-007 (2)	27.70 (21.00)	41.72 (44.00)	51.39 (62.17)	2.82	5.2	20.73 (12.83)	3.1	50.6	691.9
16	BAR-0004	23.41 (18.50)	37.75 (36.67)	48.46 (54.88)	3.35	5.0	24.25 (16.33)	4.0	49.9	651.7
17	SSBS-(9-2)-3	24.82 (18.17)	37.91 (37.50)	50.71 (59.50)	5.47	4.2	20.46 (12.07)	3.6	50.9	646.5
18	Acc-111-821	25.34 (17.50)	35.13 (33.00)	48.05 (54.47)	1.80	5.7	19.12 (10.67)	3.3	50.1	642.9
19	Acc-205-374-1	21.98 (15.00)	36.87 (35.50)	43.82 (48.00)	6.60	6.2	18.69 (10.17)	3.0	50.4	533.3
20	Acc-No-044	21.96 (15.83)	34.08 (31.57)	49.41 (57.63)	7.33	4.5	14.27 (6.10)	2.9	48.1	506.9
	Mean	27.00 (20.38)	42.90 (46.45)	49.20 (57.23)	4.5	5.1	22.60 (14.96)	3.4	50.4	975
	CV %	6.68	5.62	5.19	16	9.8	6.65	5.2	2.88	9.86
	LSD at 5 %	2.03	2.72	2.92	0.8	0.6	1.71	0.2	1.64	109.5

Table A7. *Continued.*

No	Genotype	DFI	DF	CFP	MD	PLH	LCBZ	LFC	CL	CW	CTK	PBPP
1	Acc-203-336-4	37	41	47.16 (53)	96	116	48.04 (55.17)	2.6	2.6	0.7	0.5	2.26 (4.53)
2	Hirhir Baker sel-1	36	40	48.96 (57)	99	84	43.54 (46.53)	2.5	2.6	0.8	0.5	1.78 (2.65)
3	Acc-111-524-1	37	43	52.09 (61)	109	144	55.65 (68.17)	2.4	2.5	0.7	0.5	2.03 (3.57)
4	Tmax	37	43	48.65 (56)	102	112	53.63 (64.00)	2.3	2.4	0.7	0.5	1.95 (3.33)
5	SPS-SIK-# 811	38	43	49.52 (58)	105	119	50.99 (60.17)	2.6	2.6	0.7	0.5	1.92 (3.16)
6	NN-0183-3	37	42	49.16 (56)	101	110	51.63 (62.50)	2.4	2.4	0.8	0.6	1.92 (3.27)
7	NN-088-2	36	39	48.75 (57)	95	105	51.37 (61.00)	2.7	2.7	0.7	0.5	1.94 (3.27)
8	Acc-EW-011 (1)	35	40	47.55 (55)	97	100	45.07 (50.25)	2.5	2.6	0.7	0.5	1.91 (3.28)
9	X-30/40 # 403	37	42	51.12 (61)	105	111	53.45 (63.33)	2.6	2.6	0.8	0.5	1.85 (2.87)
10	BCS-001 (1)	37	40	49.61 (58)	100	105	49.09 (57.33)	2.4	2.5	0.8	0.5	2.05 (3.93)
11	AW-007	42	49	51.66 (62)	119	132	52.56 (62.10)	2.4	2.4	0.8	0.5	2.08 (4.00)
12	G-03-1	38	41	48.74 (56)	100	86	44.17 (47.67)	2.3	2.3	0.7	0.5	1.87 (3.03)

No	Genotype	DFI	DF	CFP	MD	PLH	LCBZ	LFC	CL	CW	CTK	PBPP
13	Bounja-filwuha sel-2	36	41	47.40 (54)	95	94	45.43 (49.83)	2.5	2.6	0.7	0.5	1.80 (2.60)
14	Acc-WW-001 (4)	40	49	54.66 (67)	124	147	49.70 (56.83)	2.4	2.4	0.8	0.5	2.02 (3.63)
15	Acc-NS-007 (2)	39	43	48.36 (56)	102	109	50.91 (59.83)	2.4	2.6	0.8	0.5	1.57 (2.07)
16	BAR-0004	39	43	48.95 (56)	105	92	41.78 (43.50)	2.2	2.2	0.8	0.5	1.95 (3.23)
17	SSBS-(9-2)-3	37	41	51.99 (62)	105	119	50.65 (61.00)	2.5	2.5	0.8	0.5	1.95 (3.10)
18	Acc-111-821	40	48	48.24 (55)	112	121	50.44 (59.50)	2.3	2.4	0.8	0.5	1.80 (2.77)
19	Acc-205-374-1	41	54	52.01 (62)	127	133	42.09 (44.47)	2.3	2.4	0.7	0.5	2.11 (3.93)
20	Acc-No-044	44	49	54.22 (66)	122	123	40.94 (42.50)	2.5	2.3	0.7	0.5	2.06 (3.42)
	Mean	38	43	50.00 (59)	105	112	48.80 (56.44)	2.4	2.5	0.8	0.5	1.91 (3.18)
	CV %	4.3	4	3.14	4.9	7.2	3.61	6.7	6.2	7.2	6.9	8.2
	LSD at 5 %	1.9	2	1.79	5.8	9.1	2	0.2	0.2	0.6	0.0	0.18

CV=coeffiecent of variation, LSD= least, CPMA=capsule per main axis, CPP=capsule per plant, ISR=percent of shattering resistance (%), BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil content (%) and YLD=yield kgha-1, DFI=days to flower initation, DF=days to 50% flowering, DM=days to physiologically mature, LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm).

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