Lafia Journal of Scientific & Industrial Research (LJSIR), Vol. 3(1), 2025
p-ISSN: 3026 – 9288 e-ISSN: 3027 – 1800 pages: 40 – 46
https://lafiascijournals.org.ng/index.php/ljsir/index ⇒ Published by the Faculty of Science,
Federal University of Lafia, Nasarawa State, Nigeria

Phenotypic Diversity and Performance for some Agronomic Characters in Sesame (*Sesamum indicum* L.) Germplasm Collection from Nasarawa state, Nigeria

Usman Alhassan[1]*, Hauwa Kana[2] & Zainab Hassan[3]
[1]Department of Agronomy, Federal University of Lafia, Nasarawa State, Nigeria
[2]Department of Plant Science and Biotechnology, Federal University of Lafia, Nasarawa State, Nigeria
[3]College of Agriculture, Science and Technology

Abstract

Sesame is one of the most important oilseed crops in the tropical and subtropical regions of the world. Despite its importance, sesame yield in Nigeria is poor due to lack of improved and high yielding varieties. The aim of the work was to study genetic diversity in some agro-morphological traits of sesame germplasm. Germplasm exploration was carried out using systematic survey from October 2022 to September 2023 in different sites across Nasarawa State. One hundred and twenty (122) germplasm was collected and evaluated in an incomplete randomized block design with 3 replications at the Faculty of Agriculture, Federal University Lafia, during October 2023 under irrigation. Data was collected on plant height (cm), number of primary branches (NBR), number of Capsules per plant and seed yield per plant (g), Analysis of variance revealed significant ($p < 0.01$) variation among the 122 genotypes for all the traits studied. Partitioning the significant variations into variance components showed that genotypic variance range from 0.92 for SYP to 287.34 for PHT. The genotypic effects have significant contribution to the phenotypic variation in all traits. The magnitude of the genotypic variance component resulted in high heritability estimates for PHT and CAP. Biplot PCA on agro-morphological traits displayed three principal components that contributed for 71.38% variations. Cluster analysis grouped the collected germplasm into three main clusters. The phenotypic diversity observed in this study may be exploited in the selection of parental lines for hybridization when breeding sesame for high seed yield.

Keywords: *Sesamum indicum*, genetic diversity, phenotypic variation, principal components

Article History
Submitted
October 21, 2024
Revised
December 28, 2024
First Published Online
January 05, 2025

Corresponding author
U. Alhassan ✉
almuh2013@yahoo.com

doi.org/10.62050/ljsir2025.v3n1.380

Introduction

Sesame (*Sesamum indicum* L.; *2n = 2x = 26*) belongs to the family Pedaliaceae. It is a predominantly self-pollinating crop. Sesame seed oil and derived products serve the food, feed, and cosmetics industry globally. Sesame has higher seed oil content ranging from 40% to 60% when compared to soybean (~20%), rapeseed (~40%), sunflower (~45%), and groundnut (45–56%) [1]. Sesame oil comprises about 85% unsaturated and 15% saturated fatty acids [1]. The unsaturated fatty acids include linoleic acid (~46%) and oleic acid (~38%), while the saturated fatty acids are palmitic acid (~12%) and stearic acid (~4%) [2]. The higher quantity of unsaturated fatty acids present in sesame oil has human health benefits believed to minimize the risks of cardiovascular diseases, cancer, brain, and liver damage [3]. Sesame is widely traded in local, regional, and international markets [4]. A global total of 2.4 million tons of sesame grain was traded in 2020 with a monetary value of 3.2 trillion USD. Likewise, sesame consumption is steadily increasing due to high demands related to its unique nutritional values such as higher contents of vitamins (e.g., A and E), minerals, fiber, desirable fatty acids, carbohydrate (~13.5%), and protein (~24%) [4]. Furthermore, population pressure, urbanization, and the changing lifestyle have increased the global demand for sesame products [4].

About 70% of the world's sesame seed is processed to produce food oil, while the seedcake left after oil processing is used to prepare livestock meals [4]. The global annual human consumption of sesame is about 65% and 35% in the form of processed food oil and grain, respectively [5]. In 2020, world sesame grain production was 7.25 million tons [6]. Sudan is the largest sesame grain-producing country with 1.52 million tons per annum, followed by China (0.89 million tons), Myanmar (0.74 million tons), the United Republic of Tanzania (0.71 million tons), India (0.65 million tons), Nigeria (0.49 million tons), Burkina Faso (0.27 million tons), and Ethiopia (0.26 million tons) [6]. The actual mean seed yield of sesame in sub-Saharan Africa is <0.6 tons ha^{-1}), which is far below the attainable yield of the crop, reaching up to 4.00 tons ha^{-1}) [6]. Relatively higher sesame seed yield productivity is reported in Lebanon (3.29 tons ha^{-1}), Jordan (2.38 tons ha^{-1}) Israel (2.04 tons ha^{-1}), China (1.62 tons ha^{-1}), Tajikistan (1.59 tons ha^{-1}), and Uzbekistan (1.52 tons ha^{-1}) [6].

The low yield level in sub-Saharan Africa is attributable to the use of unimproved traditional varieties or landraces. Moreover, sesame yields are hindered by the indeterminate growth habit of some varieties, capsule shattering, and excessive seed loss pre- and post-harvest [7]. Nearly all the global sesame varieties are prone to capsule shattering, and they are not suitable for machine harvesting [4], a pre-harvest yield loss of 50% in some sesame varieties due to capsule shattering. Hence, manual sesame harvesting is the method of choice globally, which significantly increases the production and market costs of the produce [4, 8].

Genetic erosion has been very fast in recent years due to rapid modernization of the society and genetic diversity has been replaced by introduction of few high yielding varieties. Farmers are leaving their own traditional varieties and growing the improved cultures thereby many of the landraces have become extinct. The need for both in situ and ex situ conservation is now felt as the sesame cultivation in the country is largely affected by extreme natural calamities after rapid climate change, through an erratic monsoon. Earlier the biggest challenge was flood, but subsequently other factors like salinity after frequent, temperature rise and drought like situation in many parts of the country have put the challenge before sesame researchers to incorporate these genetic factors in the plant. Although many sesame germplasm are conserved in the world gene bank but information on germplasm is not complete. Germplasm without characterization and evaluation data cannot be utilized for crop improvement programme. Hence a systematic characterization, evaluation and documentation of important traits against each germplasm required to be done for its better utilization by the breeder.

One of the key objectives of the Faculty of Agriculture of is the acquisition of new germplasm and evaluation of existing germplasm collections for used in crop-improvement research and development. For any germplasm to be used, it must be shown to be useful. A component of this objective is to broaden the germplasm resources of plants to ensure maximum genetic diversity for improved productivity through collection, classification, evaluation, preservation, and distribution of plant germplasm and assess its potential for meeting agricultural needs. Significant progress on the evaluation, enhancement, and genetic analysis of the sesame germplasm collection will impact essentially all aspects of sesame research, development, and production. One approach to assembling a gene pool is to collect material from diverse geographic origins, with a concentration of accessions from the presumed centers of diversity in individual samples. Representative samples from the complete geographic range of the sesame can help to ensure conservation of co-adapted gene complexes. Identification of new diverse sources will help in better utilization of germplasm in the breeding programmes, aimed at producing agronomically superior cultivars with broad genetic base. The objective of the sesame germplasm collection mission was to capture maximum variability of sesame germplasm within the state and to meet the need of breeders trying to identify genotypes with high seed yield and quality to include in the breeding programmes to develop sesame varieties for use by farmers in the savannah agro-ecologies of Nigeria.

Materials and Methods

Germplasm exploration was carried out using a systematic survey (random sampling method) from October 2022 through to September 2023 in different sites across Nasarawa State. The team comprised of the Principal Investigator, 2 technical staff and a Driver who discussed with the local farmers and identify the most important sesame-growing region in the local government areas of the state. The team surveyed door-to-door, fields in collecting the sesame germplasm. Collection for each sample was tagged and packaged separately. The locations of the collection sites were identified using Global Positioning System (GPS). Each germplasm collected was properly dried cleaned and dispatched as voucher sample in medium term storage for future references. The sole objective of exploration/research was to document the morphological/genetic characterization and evaluation of collected accessions so as to identify the best available local sesame germplasm that can adapt to the moisture stress conditions as well as to standardize the suitable high yielding germplasm for sesame cultivation in the state.

Phenotyping of the collection

One hundred and twenty germplasm collected was collected and evaluated in two replicated trials at the Faculty of Agriculture, Federal University of Lafia, during October 2023 under irrigation. Experiment was laid out in an incomplete randomized block design. Healthy and bold seed of sesame were sown with a seed rate of 20-25 kg/ha and spacing of 20 cm ×25 cm. Recommended dose of fertilizer viz. 120-60-40 kg NPK ha^{-1} (100% RDF) were applied through DAP and MOP. Morpho-agronomic characters for both vegetative at harvest and reproductive stages were recorded over five randomly selected plants and subjected to the statistical analysis (ANOVA). Data was standardized for the traits to a mean of zero and a standard deviation of one for multivariate analysis. Principal Component Analysis was performed using the standardized data with a covariance matrix in SAS. The linear effect model for ANOVA for the traits with one location was as follows:

$$y_{ijk} = \mu + \alpha_i + \beta_j + e_{ijk} \qquad (1)$$

The means of significant different traits ($p < 0.05$) among the sesame germplasm was separated using the Fisher's protected least significance difference test.

Variability analysis

Variability parameters, including heritability, genotypic coefficient of variance (*GCV*), phenotypic coefficients of variation (*PCV*), genotypic and phenotypic variances, were calculated using formulas proposed by Singh and Chaudhary [9] as follows:

The genotypic variance was calculated as:

$$\sigma_g^2 = \frac{MSG - MSE}{r} \quad (2)$$

where σ_g^2 stands for genotypic variance, *MSG* refers to the mean squares for genotypes, *MSE* stands for the mean sum of squares for error, and *r* refers to the number of replications.

The phenotypic variance was calculated as:

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2 \quad (3)$$

Where σ_p^2 stands for phenotypic variance and σ_e^2 for environmental variance, which is equal to the mean squared error

Genotypic and phenotypic coefficients of variance were calculated as:

$$GCV = \frac{\sqrt{\sigma_g^2}}{\overline{X}} \text{ and } PCV = \frac{\sqrt{\sigma_p^2}}{\overline{X}} x100 \quad (4)$$

In the above equations, *GCV* stands for genotypic coefficient of variance, *PCV* stands for phenotypic coefficient of variance, σ_p^2 stands for phenotypic variance, σ_g^2 stands for genotypic variance, and $\overline{X}$ is the mean of the population.

Broad-sense heritability for all the traits was measured as:

$$Hb = \frac{\sigma_g^2}{\sigma_p^2} x100 \quad (5)$$

In the above equation, *Hb* is broad-sense heritability, σ_g^2 is genotypic variance, and σ_p^2 is phenotypic variance. Heritability was calculated by adjusting the scale to below 30% as low, 30–60% as moderate, and greater than 60% as high, as aligning with Kehie *et al.* [10].

Rank summation index

The rank summation index (RSI) a selection index that ranks genetic materials for traits by adding the ranks of each trait's genetic materials was used in selecting 25 best germplasm. The formula for the RSI as presented by Mulamba and Mock [11] is as follows:

$$I = \sum_{i=1}^{n} rank(X_i) \quad (6)$$

Principal component analysis

Contribution of each trait to the total variability was determined through principal component analysis (PCA) based on a correlation matrix of all variables, and principal components with Eigen values > 1.0 was selected. To assess extent of relatedness among the okra accessions, a cluster analysis using Ward's minimum variance method by accession was conducted to generate a dendrogram using PROC CLUSTER and PROC TREE [12].

Results and Discussion

Analysis of variance of agronomic traits

The estimated components of variance and their effects on phenotypic variation are shown in Table 1. The analysis of variance revealed significant ($p < 0.01$) variation among the 122 genotypes for all the traits studied. Portioning the significant variation into variance components showed that genotypic variance (σ_g^2) range from 0.92 for SYP to 287.34 for PHT. The genotypic effect has a significant contribution to the phenotypic variation in all traits. The magnitude of the variance component σ_g^2 resulted in high heritability *Hb* estimates for PHT and CAP, which were greater than 60%. The phenotypic variance σ_p^2 and phenotypic coefficient of variability (*PCV*) were slightly higher than genetic variance (σ_g^2) and genotypic coefficient of variance (GCV) for all traits, confirming the influence of environment on the expression of these characters. The difference between PCV and GCV was relatively high for the traits NBR, CAP and SYD, suggesting that the environment substantially influences these traits. Smaller differences between PCV and GCV were noted for PHT and DFF, showing that these traits were less influenced by environment, so that phenotypic selection can be reliably and effectively practiced for improving these traits. In the present study, GCV, PCV and *Hb*, showed a considerable amount of variation, indicating that there is enough scope for the selection of the desired germplasm based on agronomic traits (Table 2). The best 25 germplasm were identified using Rank Summation Index (RSI) based on all the morphological traits used in this study (Table 3).

Table 1: Mean square analysis for some morphological traits of sesame germplasm collection evaluated in Nasarawa state evaluated in 2023

Sources of variation	Df	Mean squares				
		PHT (cm)	NBR	CAP	DFF	SYP (g)
Replication	2	4829.10	91.31	6572.3	0.865	0.089
Genotype	121	1665.90**	12.38**	947.6**	16.39**	3.808**
Error	242	287.30	4.58	248.0	0.417	0.095
CV (%)		15.07	22.41	28.82	1.87	0.94
Maximum		211.00	20.00	157.00	42.00	34.67
Minimum		50.00	0.00	0.00	23.00	18.76
Mean		112.51	3.43	22.88	34.58	112.51
SEm		112.50	3.43	22.88	34.58	5.77
CD (5%)		9.79	1.24	9.73	1.10	1.60
CD (1%)		27.26	3.44	27.11	3.07	4.56

Table 2: Estimates of variance components, phenotypic, genotypic coefficient of variation and heritability of 122 germplasm collection evaluated in Nasarawa state evaluated in 2023

Traits	Variance components			PCV (%)	GCV (%)	ECV (%)	Hb (%)
	σ_e^2	σ_g^2	σ_{ph}^2				
PHT (cm)	35.93	287.34	459.53	24.29	19.05	15.07	61.53
NBR	4.58	2.60	7.18	78.16	47.05	62.40	36.25
CAP	284.01	221.20	505.22	98.23	65.00	73.65	43.78
DFF	3.65	13.16	16.1	11.85	10.49	5.52	78.28
SYP (g)	0.61	0.31	0.92	2.40	1.40		33.72

Table 3: Performances using Rank Summation Index for selection the best 25 genotypes based on five important traits of sesame grown in Lafia, 2023/24 dry seasons

Genotype	Rank Summation Index					Rank
	PHT (cm)	NBR	CAP	DFF	SYP (g)	
CHI001	3	3	18	1	11	1
T70	2	4	2	22	1	2
T114	13	34	5	9	14	3
T46	26	27	8	29	18	4
T40	8	5	13	71	9	5
T51	1	96	1	2	15	6
T58	4	51	9	36	12	7
T25	31	18	6	54	19ß	8
T19	25	9	20	61	25	9
T120	7	1	10	111	33	10
T59	5	25	30	70	65	11
T62	9	61	53	7	20	12
T17	35	10	34	52	47	13
T77	12	33	12	79	17	14
T50	27	84	16	12	67	15
T105	40	2	3	100	45	16
T43	30	43	51	23	28	17
T21	38	39	22	50	57	18
T39	18	17	7	107	78	19
T32	47	28	43	32	24	20
T72	33	38	63	17	61	21
T37	44	13	85	16	13	22
T65	20	35	19	87	67	23
T102	23	36	66	40	56	24
T44	24	7	45	89	16	25

Table 4: Rotated component matrix for different traits of sesame genotypes grown in Lafia, 2023/24 dry seasons

Parameter	PC axis			
	PC1	PC2	PC3	PC4
SD	1.3496	1.0168	0.8433	0.6584
PV	0.4553	0.2585	0.1778	0.1084
CP	0.4553	0.7138	0.8916	1.0000
	Eigenvectors			
PHT (cm)	-0.6020018	0.2038833	0.072616	0.67615289
NO BRCH	0.49390317	-0.25086175	-0.8274553	0.09190087
NO CAP	-0.62535822	-0.47846681	0.268579	-0.72844723
D50F	-0.05079961	0.94304981	0.3230175	0.06112396
SYP (g)	0.55066133	-0.4374555	-0.0937031	-0.07059953

SD = Standard deviation; **PV** = Proportion of variance; **CP** = Cumulative Proportion

Results for PCA (Table 4) revealed that the first principal component (PC1) was mostly related with yield traits such as seed yield, number of primary branches per plant and number of capsules per plant. The second principal component (PC2) was dominated by traits such as plant height and number of days to 50% flowering while PC3 was associated with days to 50% flowering. On the basis of PCA, most of the important yield attributing and quality traits were present in PC1, PC2 and PC3. Baraki *et al.* evaluated 13 sesame genotypes and reported that out of eight, first three PCs accounted for 88.49% of the total variance and these three PCs were considered as significant [13]. PCA-biplot based on agro morphological traits displayed three principal components that contributed for 71.38% to the overall phenotypic variability among the sesame collections (Fig 2). In particular, the PC1 explained 45.53% of total variation, where NBR and DFF appeared those mainly involved. The PC2 accounted for 25.80% of total variation and the traits involved were PLH and CAP (Table 4). The first two PCs were able to distinguish the sesame collection according to their major contributing traits. Genetic dissimilarity was calculated from agro-morphologic data by cluster analysis based on Euclidean distance and Ward's method. Cluster analysis grouped the 122 sesame germplasm into three main clusters with distinguished genetic profiles (Fig. 1). The first enclosed the 3 early maturing (DFF), tall (PHT) and highest yielding genotypes (T70, T51and T120). The second cluster grouped 18 landraces with higher SYD and high NBR. The third and last cluster was mainly composed of high SYD, NBR and CAP with 100 sesame genotypes.

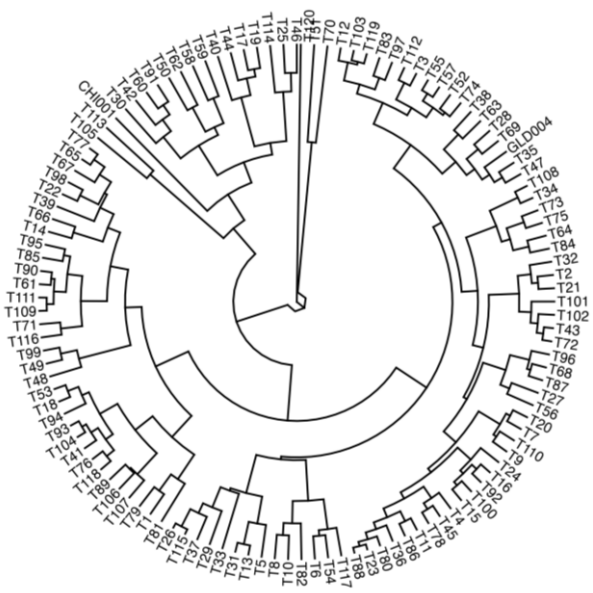

Figure 1: Phylogenetic relationship of the Sesame Germplasms

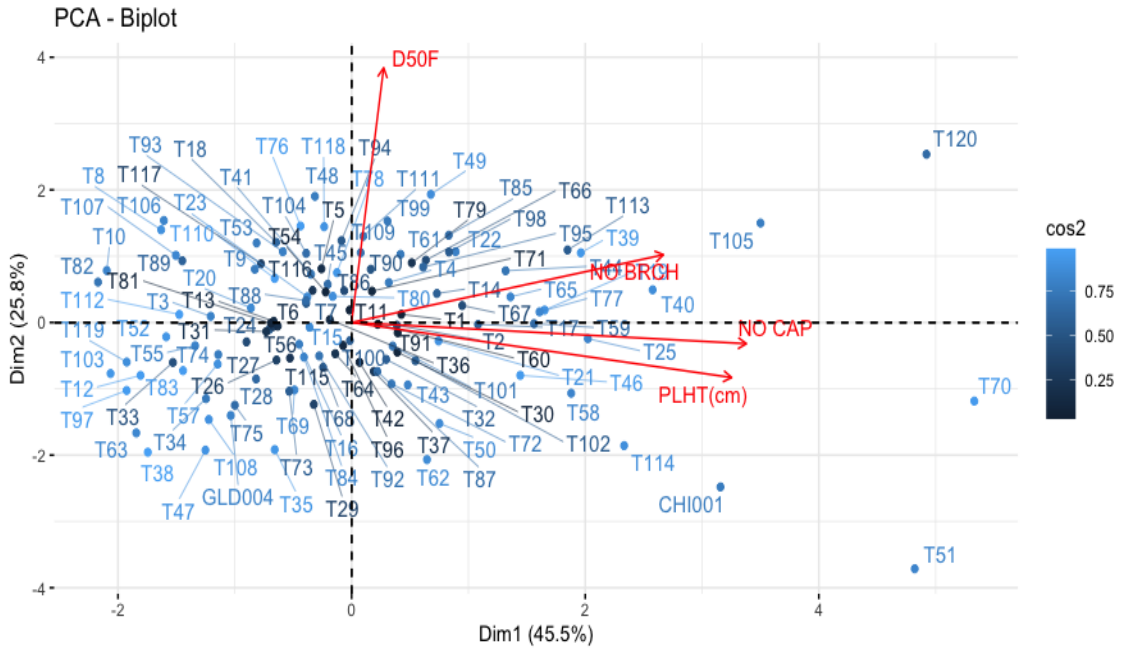

Figure 2: Principal component analysis of sesame genotypes and their traits (the codes for genotypes and traits are as described in Table 4)

As the magnitude of diversity and availability of plant resources are vital for crop improvement [14], estimation of genetic diversity and relationships between crop germplasm is the key step [15] and the loss of genetic diversity is a major danger for the survival and breeding of crop species [16]. The primary breeding objectives for sesame, which are tightly linked to human needs, are increasing the seed yield, improving the morphological architecture of the plants, tolerance to biotic and abiotic stresses, indehiscent capsules, and improving oil quality.

Conventional breeding approaches mainly involve the existence of wild relatives, elite cultivars, and landraces to enable the assortment of superior lines for quality enhancement. Genetic differences examined using morphological markers are also an essential tool among sesame genotypes. A few investigations dependent on morphological markers have shown the presence of high genetic diversity in sesame populations [17]. As part of broadening the genetic base of sesame (*Sesamum indicum* L.) in Nigeria through germplasm enhancement, a selection was made of 25 of the most diverse and unadapted parental lines, including one accession of the wild species *S. mulayanum*, and these will be intercrossed in various combinations to maximize genetic diversity and to develop locally adapted pools of genetic resources.

A perusal of the results revealed that for all the characters phenotypic coefficient of variation (PCV) were significantly higher than the genotypic coefficient of variation (GCV) and there were narrow differences in their values. This implies that expression of character is mainly governed by the genotypes itself along with a meager effect of environment. High heritability estimates coupled with high genetic advance was observed for seed yield per plant and plant height, indicating greater role of additive gene effects on the expression of these traits which could be easy targets for phenotypic selection and consequently, may be improved genetically via simple plant selection methods.

Variability measures in terms of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) help us to evaluate the contribution of genetic and environmental factors. The phenotypic character, days to 50% flowering showed a moderate GCV and PCV as also reported by some workers [18, 19]. However, the same trait recorded highest heritability and similar observations were also made by Kiruthika *et al.* [20]. In contrast, number of capsules recorded low GCV and high PCV with low heritability as that of many workers [21, 22]. Plant height exhibited moderate GCV and PCV with high heritability in this study as observed by earlier studies [23].

Morphological traits were subjected to the environment influence as well as natural and human selection [24]. The high variability among days to 50% and seed yield, which are related to sesame adaptation to the environment, suggested that the collections were adapted to a large range of environments supported also by alternative agronomic practices in different growing regions. Thus, our results are in agreement with a previous report on Algerian maize landraces, which pointed out that even though the landraces originated from subtropical regions, they showed adaptation to both sub-humid and dry continental environments [25]. Significant correlations among agro-morphological traits were identified, representing a useful tool for directing breeding programs (data not shown). However, environment plays also a pivotal role, affecting concurrently the traits in the same or opposite direction.

The principal component analysis (PCA) was performed to cluster the 122 germplasm based on discriminant morphological traits. According to Clifford and Stephenson, the first three principal components included the overall phenotypic variation, taken into account discriminant traits able to distinguish germplasm [26]. Among them, days to flowering, number of branches and yield per capsule well as were highly significant for clustering sesame germplasm. Our results are also in agreement with Rahul *et al.* [27], which reported days to 50% flowering number of primary branches and seed yield as the most important traits for grouping sesame germplasm. Cluster as well as PCA analyses were not able to distinguish germplasm from the same geographic origin being dispersed in different clusters. Similar results were already reported by some researchers, which observed a lack of relationship between clustering and landraces geographic origin [28, 29]. Finally, it is noteworthy that landraces from dry, of poor soil and highly radiated environments origin showed adaptation traits as shortness and early flowering, considered important sources of gene diversity for developing drought tolerant genotypes [30].

Conclusion

The present study provides initial results from the 122 sesame germplasm collections and clears a path to develop improved varieties of sesame. The variation within germplasm provides a breeding resource pool for use in controlled crossing to develop ideotype varieties with desirable phenotypic traits. Genetic evaluation of crop germplasm is vital for the identification of potential parents and important traits of interest to be use in crop breeding. This study using quantitative traits revealed important genetic variability among the 122 germplasm.Genotype grouping and principal component analysis confirmed this important genetic variability. These indigenous sesame germplasm should be properly conserved; they should considered sesame improvement for adaptation, increased seed yield with improved oil quality.

Conflict of interest: The authors declare that there is no conflict of interest.

Acknowledgements: We would like to sincerely acknowledge funding from theTertiary Education Trust Fund (TETFund) through Federal University of Lafia (FULAIA). Also, we thank Mr James from Department of Plant Science, Ahmadu Bello University Zaria that handled the statistical analysis.

References

[1] Dossa, K., Wei, X., Niang, M., Liu, P., Zhang, Y., Wang, L., Liao, B., Cissé, N., Zhang, X. & Diouf, D (2018). Near-infrared reflectance spectroscopy reveals wide variation in major components of sesame seeds from Africa and Asia. *Crop Journal*, 6, 202–206. https://doi.org/10.1016/j.cj.2017.10.003

[2] Were, B. A., Onkware, A. O., Gudu, S., Welander, M. & Carlsson, A. S. (2006). Seed oil content and fatty acid composition in East African sesame (*S. indicum* L.) accessions evaluated over 3 years. *Field Crops Res.*, 97, 254–260. http://dx.doi.org/10.1016/j.fcr.2005.10.009

[3] Yol, E., Toker, R., Golukcu, M. & Uzun, B (2015). Oil content and fatty acid characteristics in Mediterranean sesame core collection. *Crop Science*, 55, 2177–2185. https://doi.org/10.2135/cropsci2014.11.0771

[4] Myint, D., Gilani, S. A., Kawase, M. & Watanabe, K. N. (2020). Sustainable sesame (*Sesamum indicum* L.) Production through Improved Technology: An overview of production, challenges, and opportunities in Myanmar. *Sustainability*, 12, 3515. https://doi.org/10.3390/su12093515

[5] Morris, J. B. (2002). Food, industrial, nutraceutical, and pharmaceutical uses of sesame genetic resources. In *Trends in News Crops and New Uses*; Janick, J., Whipkey, A., Eds.; ASHS Press: Alexandria, Egypt, pp. 153–156.

[6] FAOSTAT (2020). The Food and Agriculture Organization Corporate Statistical Database (FAOSTAT), Rome, Italy. Available online: http://www.fao.org/faostat/en/#data/QC

[7] Teklu, D. H., Shimelis, H., Tesfaye, A. & Abady, S (2021). Appraisal of the sesame production opportunities and constraints, and farmer-preferred varieties and traits, in Eastern and Southwestern Ethiopia. *Sustainability*, 13, 11202. https://doi.org/10.3390/su132011202

[8] Langham, D. R. & Wiemers, T (2002). Progress in mechanizing sesame in the US through breeding. In *Trends in New Crops and New Uses*; Janick, J., Whipkey, A., Eds.; ASHS Press: Alexandria, Egypt, pp. 157–173.

[9] Singh, R. K. & Chaudhary, B. D. (1985). *Biometrical Methods in Quantitative Genetics Analysis*. New Delhi-Ludhiana.

[10] Kehie, T., Shah, P., Chaturvedi, H. P. & Singh, A. P. (2020). Variability, correlation and path analysis studies in sesame (*Sesamum indicum L.*) genotypes under foothill condition of Nagaland. *Int. J. of Current Microbio. and Applied Sci.*, 9(5): 2917 – 2926. doi:10.20546/ijcmas.2020.905.335

[11] Mulamba, N. N. & Mock, J. J. (1978). Improvement of yield potential of the Eto Blanco maize (*Zea mays* L.) population by breeding for plant traits. *Egyptian Journal of Genetics and Cytology*, 7: 40-51.

[12] SAS Institute Inc. (2010). *Statistical Analysis Software Release 9.3*. User's Guide. SAS Inst., Cary, NC.

[13] Baraki, F., Tsehaye, Y. & Abay, F. (2015). Grain yield based cluster analysis and correlation of agronomic traits of sesame (*S. indicum* L.) genotypes in Ethiopia. *J. Nat. Sci. Res.*, 5(9), 11-17.

[14] Govindaraj, M., Vetriventhan, M. & Srinivasan, M. (2015). Importance of genetic diversity assessment in crop plants and its recent advances: An overview of its analytical perspectives. *Genetics Res. Int.*, ID 431487, 14p. https://doi.org/10.1155/2015/431487

[15] Rafalski, J. A. (2011): Genomic tools for the analysis of genetic diversity. *Plant Genetic Resources*, 9: 159–162. https://doi.org/10.1017/S1479262111000104

[16] Olivera, P. D. & Steffenson, B. J. (2009): *Aegilops sharonensis*: Origin, genetics, diversity, and potential for wheat improvement. *Botany*, 87: 740–756. https://doi.org/10.1139/B09-040

[17] Akbar, F., Rabbani, M. A., Shinwari, Z. K. & Khan, S. J. (2011). Genetic divergence in sesame (*Sesamum indicum* L.) landraces based on qualitative and quantitative traits. *Pakistan. Journal of Botany*, 43(6): 2737-2744.

[18] Iqbal, A., Pati, P. K., Akhtar, R., Begum, T. & Dasgupta, T. (2018). Diversity in sesame accessions. *Int. J. of Agric., Env. and Biotech.*, 11(5): 725-73. 10.30954/0974-1712.10.2018.3

[19] Samadhi, P. & Muralidharan, V. (2011). Analysis of genetic variability, association and path analysis in the hybrids of sesame (*Sesamum indicum* L). *Tropical Agricultural Research and Extension*; 22:13(3) doi: http://dx.doi.org/10.4038/tare.v13i3.3140

[20] Kiruthika, S., Narayanan, S. L., Parameswari, C., Mini, M. L. & Arunachalam, P. (2018). Genetic variability studies for yield and yield components in sesame (*Sesamum indicum* L.). *Electronic J. of Plant Breeding*, 9(4): 1529-37. doi: 10.5958/0975-928X.2018.00189.8

[21] Hika, G., Geleta, N. & Jaleta, Z. (2015). Genetic variability, heritability and genetic advance for the phenotypic traits in sesame (*Sesamum indicum* L.) populations from Ethiopia. *Sci., Techn. and Arts Res. Journal*, 4(1): 20-26. http://dx.doi.org/110.4314/star.v4i1.3

[22] Patil, A. S., Sigal, P., Yael, L., Ye, C., Josh, C., Peggy, O-Akins & Ran, H. (2018). Genetic insight and mapping of the pod constriction trait in Virginia-type peanut. ˆ*BMC Genetics* 19: 93. https://doi.org/10.1186/s12863-018-0674-z

[23] Muthulakshmi, C., Selvi, S. & Manonmani, S. (2020). Genetic potential and possible improvement of *Sesamum indicum* L. doi: http://dx.doi.org/10.5772/intechopen.94885

[24] Asfaw, Z. (1989). Relationship between spike morphology, hordeins and altitude within Ethiopian barley, *Hordeum vulgare* L. (Poaceae). *Hereditas*, 110: 203–209.

[25] Djemel, A., Revilla, P., Hanifi-Mekliche, L., Malvar, R. A., Alvarez, A. & Khelifi, L. (2011). Maize (*Zea mays* L.) from the Saharan oasis: Adaptation to temperate areas and agronomic performance. *Genetic Resources and Crop Evolution*, 59: 1493–1504.

[26] Clifford, H. T. & Stephenson, W. (1975). *An Introduction to Numerical Classification*. New York: Academic Press.

[27] Rahul, S., Rajani, B. & Pallavi, S. (2023). Assessment of exotic sesame (*Sesamum indicum*) accessions through principal component analysis. *International Journal of Environment and Climate Change* doi: 10.9734/IJECC/2023/v13i113170

[28] Hartings, H., Berardo, N., Mazzinelli, G. F., Valoti, P., Verderio, A. & Motto, M. (2008). Assessment of genetic diversity and relationship among maize (*Zea mays* L.) Italian landraces by morphological traits and AFLP profiling. *Theoretical and Applied Genetics*, 117: 831–842.

[29] Sharma, L., Prasanna, B. M. & Ramesh, B. (2010). Analysis of phenotypic and microsatellite-based diversity of maize landraces in India, especially from the north east Himalayan region. *Genetica*, 138: 619–631. doi: 10.1007/s10709-010-9436-1

[30] Iqbal, J., Shinwari, Z. K. & Rabbani, M. A. (2015). Maize (*Zea mays* L.) germplasm agro morphological characterization based on descriptive, cluster and principal component analysis. *Pakistan J. of Botany*; 47:255–264.

Citing this Article

Alhassan, U., Kana, H. & Hassan, Z. (2025). Phenotypic diversity and performance for some agronomic characters in sesame (*Sesamum indicum* L.) germplasm collection from Nasarawa State, Nigeria. *Lafia Journal of Scientific and Industrial Research*, *3*(1), 40 – 46. https://doi.org/10.62050/ljsir2025.v3n1.380