



**GENETIC VARIABILITY STUDIES OF BENNISEED (*Sesamum indicum* Linnaeus)  
ACCESSIONS IN NIGER**

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**ABSTRACT**

The study evaluated genetic variability among sixteen (16) benniseed accessions in Nigeria with the aim of identifying superior genotypes for yield and shattering resistance. Field trials were conducted at Badeggi and Mokwa using a randomized complete block design (RCBD) with three (3) replications. Data were collected on agronomic, phenological, yield, and shattering traits. The results revealed a significant ( $P \leq 0.05$ ) genetic variability among the accessions for all traits studied, indicating good potential for selection and improvement. Genotype NGB02756 consistently exhibited superior performance in terms of yield (826.61g) across both locations, while NGB04125 (2) and NGB03209 shows high resistance to shattering (0.52% and 0.57% respectively). High heritability estimates were observed for key yield-related traits which ranges from 17% to 96%, Principal component analysis which extracted the first five (5) components explaining 84% of total variation further revealed that a few major traits contributed most to the total variation among the genotypes. Cluster analysis grouped accessions into three distinct clusters, with Cluster II containing the high-yielding genotypes. NGB02756 is recommended for variety release, while NGB04125 (2) and NGB03209 are valuable sources of shattering resistance. The study highlights the potential of these genotypes for use in breeding programmes aimed at improving yield and reducing harvest losses in benniseed production in Nigeria.

**Keywords:** Genotypes, Heritability, Phenotypic, Multivariate, Superiority and Variability

**INTRODUCTION**

Benniseed (*Sesamum indicum* L.) is a major oilseed crop in sub-Saharan Africa, valued for its high-quality oil (40–60%), protein (20–25%), and lignan antioxidants (Dossa *et al.*, 2023; Mili *et al.*, 2021). Nigeria is the largest producer in West Africa and the third largest globally, yet average yields remain low (0.25–0.35 t/ha) compared to the global average of 1.5–2 t/ha (FAO, 2022). The major constraints include limited access to improved varieties, high seed shattering at harvest, and insufficient understanding of the genetic structure of local germplasm (Yusuf *et al.*, 2020; Ndagurwa *et al.*, 2023). Genetic variability is the foundation of crop improvement (Shakyawal *et al.*, 2024). Several studies have reported significant variation in agronomic and yield traits among sesame accessions (Patel *et al.*, 2024; Ghasil *et al.*, 2024; Tadesse *et al.*, 2024). However, many of these studies have been conducted outside Nigeria or have used limited germplasm. Multivariate techniques such as principal component analysis (PCA) and cluster analysis are powerful tools to dissect the structure of genetic diversity and identify the most discriminating traits (Bekele *et al.*, 2025; Sanni *et al.*, 2025). Despite its economic importance, benniseed production in Nigeria faces challenges such as low yields, limited access to improved varieties, and inadequate agronomic practices. Benniseed productivity in Nigeria is very low, about 250 to 350kg/ha compared to the global yield level of 1.5 to 2 tons/ha (FAO 2022), due to environmental stress factors like inconsistent rainfall and soil fertility differences affect benniseed yield, yet studies quantifying these effects in specific location like Niger is scarce. According to Oluwatosin *et al.* (2022) emphasizes the importance of phenotypic and molecular characterization of benniseed accessions to enhance breeding for improved yield and quality, using germplasm as a valuable resource for this purpose. Research published by Yusuf *et al.* (2020) highlighted the significant genetic diversity among Nigerian benniseed landraces, suggesting that this diversity can be harnessed to breed varieties with resistance to a variety of stresses.



Ahmad *et al.* (2021) discussed the global need for drought-tolerant benniseed varieties and link this goal directly to the exploration and utilization of genetic variability present in diverse germplasm collections. By characterizing the genetic diversity of benniseed accessions in Nigeria, this study is to assess the yield and yield components of the benniseed accessions and determine the most suitable benniseed accessions for the agro-ecology.

## MATERIALS AND METHODS

The field experiments were conducted at the National Cereals Research Institute (NCRI), Badeggi and the Mokwa Outstation, both in the Southern Guinea Savanna of Nigeria. Sixteen benniseed accessions (NGB04126, NGB04140, NGB02222, NGB02760, NGB04125(2), NGB03209, NGB04128, NGB07823, NGB02334, NGB02756, NGB04149, NGB04122, NGB04119, NGB04124, NGB02325, and NGB04116) were obtained from the National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan. The treatments were arranged in a randomized complete block design (RCBD) with three replications for both locations. Each plot measured 3 m × 1.5 m (4.5 m<sup>2</sup>) with inter-row spacing of 0.5 m and intra-row spacing of 0.05 m. Sowing was done in mid-August using a drilling method with seeds rate of 4 kg ha<sup>-1</sup>. NPK 15:15:15 was applied at 50 kg ha<sup>-1</sup> by side dressing. Weeding was with pre-emergence herbicide (glyphosate + butachlor) supplemented by manual hoe weeding at 4 weeks after planting. Data were recorded on Seed yield (SY, g plot<sup>-1</sup>): total seed weight after threshing and drying; Unshattered seed weight (USHSW, g plot<sup>-1</sup>): Seed weight obtained by manual threshing from the five tagged plants; Shattered seed weight (SHW, g plot<sup>-1</sup>): Seeds that fell onto the drying tarpaulin before threshing; Fodder yield (FY, g plot<sup>-1</sup>): Dry weight of stems, branches, pod walls and petioles after seed removal; Plant height (PH, cm) at 9 weeks after planting (9WAP) and at maturity (PH@M); Number of branches per plant (NBR); Number of seeds per capsule (NSPC) and 1000-seed weight (1000SW, g).

### Statistical Analysis

Analysis of variance (ANOVA) was performed using a combined model across locations with genotype as fixed effect and location as random effect (Breeding Management System v.1.9). Means were separated by Fisher's LSD at  $p \leq 0.05$ . Principal component analysis (PCA) was conducted on the correlation matrix of 14 quantitative traits using the factoextra package in R. Eigenvalues >1 was retained, and variables with absolute loadings  $\geq 0.30$  were considered to contribute significantly to a component.

Cluster analysis (dendrogram): Euclidean distance matrix was calculated, and hierarchical clustering was performed using Ward's linkage method. The dendrogram was visualised to identify distinct groups.

## RESULTS

### Variation in Seed Yield and Yield Components

ANOVA (Table 1) showed highly significant ( $p \leq 0.01$ ) genotypic effects for all yield-related traits across the two locations, indicating substantial genetic variability. Location effects were also significant for most traits, reflecting differences in environmental conditions between Badeggi and Mokwa.

**Table 1.** Combined Mean Square Analysis of Variance for Yield and Yield Component Traits

Source	Df	SY(g)	USHSW(g)	SHS (%)	FY(g)	NSPC	1000SW(g)
Location	1	578636.95**	574424.31**	47.74*	1807862.53**	198.38**	0.17**
Rep (Loc)	4	0.22ns	0.20ns	0.00ns	0.22ns	0.08ns	0.00ns
Genotype	15	116118.65**	115919.66**	30.88**	487416.98**	119.26**	0.53**
Error	60	0.16	0.16	0.01	0.36	0.17	0.00

\*\* = significant at  $p \leq 0.01$ ; \* =  $p \leq 0.05$ ; ns = not significant.

SY = seed yield; USHSW = unshattered seed weight; SHS = shattering %; FY = fodder yield; NSPC = seeds per capsule; 1000SW = 1000-seed weight.

### Seed Yield and other Associated Traits across the Locations

Table 2. shows the Mean performance of seed yield and associated traits across the two locations (Badeggi and Mokwa). The result further showed that in both locations, genotype NGB02756 consistently produced the highest seed yield: 862.6 g per plot in Badeggi and 330.9 g in Mokwa, significantly ( $p < 0.05$ ) superior to all other accessions (Table 2). The lowest yields were recorded for NGB04119 (42.0 g and 37.1 g, respectively). Unshattered seed weight followed a similar pattern, with NGB02756 yielding 857.5 g (Badeggi) and 320.6 g (Mokwa). Shattering percentage ranged from 0.52% (NGB04125(2)) to 9.10% (NGB04119) in Badeggi, and from 0.37% (NGB03209) to 10.00% (NGB04119) in Mokwa. Notably, NGB02756 had low shattering (0.61–1.31%) despite its high yield.

**Table 2.** Mean Performance of Seed Yield and Associated Traits across the Two Locations (Badeggi and Mokwa)

Genotype	SY(g)		USHSW (g)	SHS (%)		NSPC	1000SW(g)
	Badeggi	Mokwa		Badeggi	Mokwa		
NGB04126	66.68n	67.06m	62.94n	3.84c	3.74d	53.67	4.31a
NGB04140	297.86g	140.65f	289.70h	2.06de	1.94g	57.33	3.45f
NGB02756	862.61a	330.92a	857.52a	0.61j	1.31h	57.33	3.46ef
NGB04125(2)	393.61c	38.85o	381.88c	0.52j	4.61c	57.00	4.25b
NGB03209	559.93b	203.65d	556.73b	0.57j	0.37j	57.67	3.50de
NGB04119	42.01o	37.10p	37.21o	9.10a	10.00a	42.00	3.40g
SE ±	4.61	2.86	4.59	0.06	0.09	0.32	0.01

Means in a column followed by the same letter are not significantly different ( $p \leq 0.05$ ).

Table 3 presents the correlation matrix which reveals the interrelationships among all some measured traits. The correlation matrix confirmed that SY was strongly and positively correlated with USHSW ( $r=1.00$ ), FY ( $r=0.99$ ), NSPC ( $r=0.68$ ) and PH@M ( $r=0.56$ ), and negatively correlated with SHS ( $r=-0.63$ ), indicating that shattering reduction directly improves harvestable yield.

**Table 3:** Estimation of Phenotypic Correlation Coefficients for Yield and Yield Component Traits of Benniseed Accessions across the Locations

	PH@M	SHW	USHSW	SY	SHS%	NSPC	1000SW	FY
PH@M	1.0000							
SHW	0.18*	1.0000						
USHSW	0.56**	0.29*	1.0000					
SY	0.56**	0.29*	1.00**	1.0000				
SHS%	-0.55**	0.12*	-0.63**	-0.63**	1.0000			
NSPC	0.45**	0.18*	0.68**	0.68**	-0.75**	1.0000		
1000SW	0.23*	-0.38**	-0.04*	-0.04*	-0.09*	0.06*	1.0000	
FY	0.49**	0.31**	0.99**	0.99**	-0.56**	0.62**	-0.06*	1.0000

PH@M: Plant height at Maturity (cm), SHW: Shattering Weight(g), USHSW: Unshattered Seed Weight, SY: Seed Yield, SHS: Shattering Score (%), NSPC: Number of Seed per Capsule, 1000SW: 1000 Seed Weight, FY: Fodder Yield

\*= significant

\*\*= highly significant

### Principal Component Analysis (PCA)

PCA was performed on 14 quantitative traits. The first five principal components (PC1 to PC5) had eigenvalues  $> 1.0$  and cumulatively explained 84% of the total phenotypic variation among the 16 accessions (Table 3).

PC1 explained 42% of the variation and was highly positively loaded by SY (0.35), FY (0.33), plant height at 9WAP (0.33), PH@M (0.28), NSPC (0.27) and NBR (0.23). Shattering percentage (-0.27) had a strong negative loading on PC1. Thus, PC1 clearly represents a yield-productivity axis where high yield is associated with tall plants, many branches, many seeds per capsule and low

shattering. PC2 (17% variation) was dominated by days to 50% flowering (-0.45), days to maturity (-0.37) and leaf area (0.37), reflecting a phenology-growth dimension. PC3 (11% variation) was mainly influenced by 1000-seed weight (-0.68), shattering weight (0.42) and capsule width (0.42). PC4 (9% variation) and PC5 (5% variation) captured additional minor trait differences.

**Table 4:** Eigenvalues, Proportion of Variance and Trait Loadings for the First Five Principal Components

Trait	PC1	PC2	PC3	PC4	PC5
9WAP (cm)	0.33	0.21	-0.04	0.10	-0.24
PH@M(cm)	0.28	0.04	-0.30	0.13	0.00
Leaf area (cm <sup>2</sup> )	0.20	0.37	-0.10	0.14	0.33
NBR	0.23	0.05	-0.10	0.42	0.39
Days to 50% Flowering	-0.13	-0.45	0.03	0.13	0.47
Days to Maturity	-0.24	-0.37	-0.16	0.13	0.24
Capsule length	0.17	-0.37	0.10	0.32	-0.02
Capsule width	0.21	-0.27	0.42	0.06	-0.23
SHW(g)	0.18	0.25	0.42	0.07	0.24
USHSW(g)	0.35	-0.09	-0.02	-0.30	0.17
SY(g)	0.35	-0.09	-0.02	-0.30	0.17
SHS(%)	-0.27	-0.28	0.20	0.00	0.35
NSPC	0.27	-0.32	-0.05	-0.12	-0.11
1000SW(g)	-0.03	0.02	-0.68	-0.05	-0.02
FY(g)	0.33	-0.07	0.00	-0.34	0.28
Eigenvalue	6.65	2.71	1.74	1.43	0.83
% Variance	42	17	11	9	5
Cumulative %	42	56	70	78	84

The PCA biplot placed NGB02756, NGB04149, NGB04122 and NGB04116 in the high-yield region of PC1, while NGB04119 and NGB04126 occupied the opposite, low-yield side. The separation of genotypes along PC1 and PC2 confirmed that seed yield and shattering resistance are the primary drivers of genetic divergence.

#### Cluster Analysis (dendrogram)

The dendrogram generated using Euclidean distance and Ward's linkage is presented in Figure 1. At a rescaled distance of approximately 10–15, the 16 accessions were grouped into three main clusters.

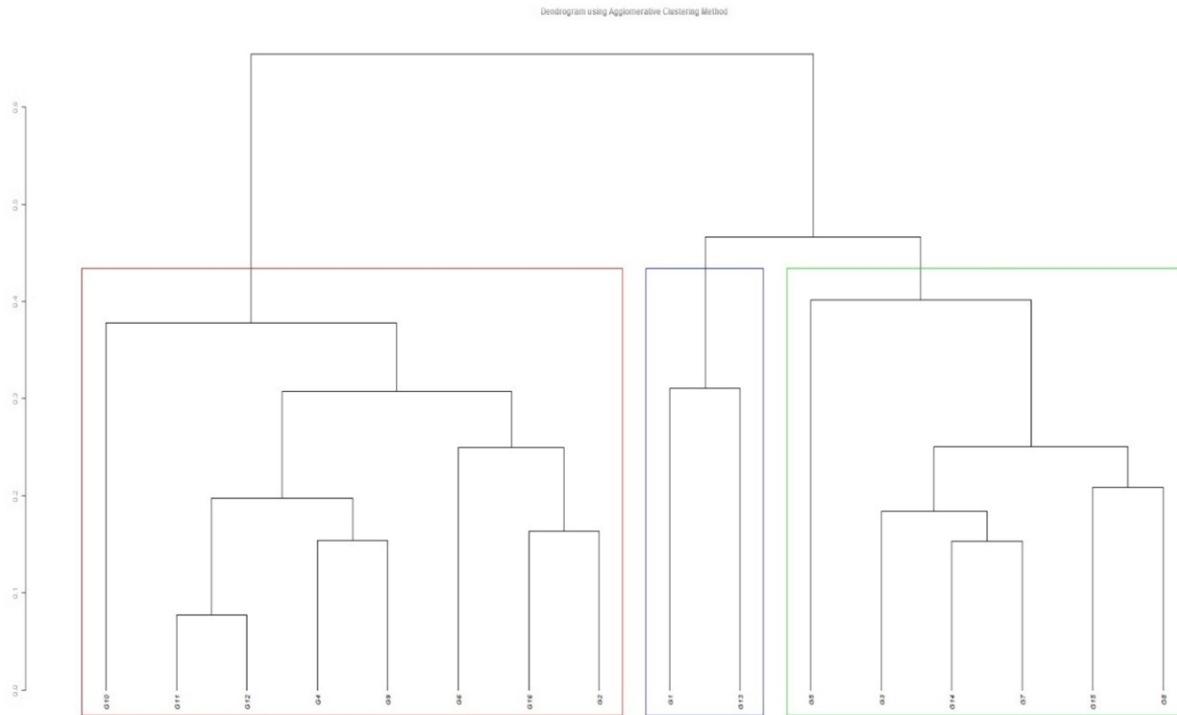
Cluster I comprised two genotypes: NGB04126 and NGB04119. These were the most genetically distant from all others, characterised by very low seed yield, high shattering percentage and late maturity. Cluster II was the largest, containing eight genotypes: NGB02756, NGB04149, NGB04122, NGB04116, NGB04140, NGB02760, NGB03209 and NGB02334. This cluster included all high-yielding accessions, the genotypes with the lowest shattering percentages (NGB03209, NGB04125(2) was placed elsewhere) and the best overall agronomic performance. Cluster III consisted of six genotypes: NGB04124, NGB02325, NGB02222, NGB04125(2), NGB04128 and NGB07823. These were intermediate in yield and shattering, with a mix of early and medium maturity.

**Table 5:** Cluster Composition of 16 Genotypes (including checks) of Benniseed

Cluster	Number of Genotypes	Genotypes
I	2	NGB04126, NGB04119
II	8	NGB02756, NGB04149, NGB04122, NGB04116, NGB04140, NGB02760, NGB03209, NGB02334
III	6	NGB04124, NGB02325, NGB02222, NGB04125(2), NGB04128, NGB07823

The dendrogram clearly showed that, NGB02756 and NGB04116 are closely related (short branch length within Cluster II), suggesting similar trait profiles. The long-distance separating Cluster

I from Clusters II/III indicates that crossing genotypes from Cluster I with those from Cluster II could produce heterotic F<sub>1</sub> progenies.



**Figure 1:** Dendrogram of 16 Bennisseed Accessions Based on 14 Quantitative Traits using Ward's Linkage and Euclidean Distance.

## DISCUSSION

The highly significant genotypic variance for seed yield, unshattered seed weight, shattering percentage and other yield-related traits confirms the presence of broad genetic variability among the Nigerian bennisseed accessions studied. This agrees with recent reports by Patel *et al.* (2024), Ghasil *et al.* (2024) and Tadesse *et al.* (2024), who also found large variation for seed yield in bennisseed germplasm. The wide range of seed yield (42 g to 862 g per plot) demonstrates that selection and hybridisation can lead to substantial gains. The consistent superiority of genotype NGB02756 across two contrasting locations (Badeggi and Mokwa) indicates broad adaptation and high yield stability, a key attribute for variety release (Bekele *et al.*, 2025).

The negative correlation between shattering percentage and seed yield ( $r = -0.63$ ) underlines the economic importance of shattering resistance. Genotypes such as NGB03209 and NGB04125(2) exhibited very low shattering (<0.6%), making them valuable donors for breeding non-shattering or semi-shattering varieties. Similar findings have been reported by Ndagurwa *et al.* (2023) and Sanni *et al.* (2025), who identified shattering as a prime target for mechanical harvesting.

Principal component analysis is a powerful tool to reduce the dimensionality of multivariate data and identify the most discriminating traits (Shakyawal *et al.*, 2024). In this study, the first five (5) PCs explained 84% of the total variation, which is comparable to the 75–90% ranges reported by Bekele *et al.* (2025) and Sanni *et al.* (2025) for sesame diversity panels. The high loading of seed yield, fodder yield, plant height and seeds per capsule on PC1 confirms that yield potential is the dominant source of genetic divergence. The negative loading of shattering percentage on PC1 further supports the idea that yield improvement is tightly linked to reduce seed loss. PC2 distinguished genotypes based on phenology (days to flowering and maturity), which is important for adaptation to growing season length.



The hierarchical clustering (dendrogram) grouped the 16 accessions into three distinct clusters, a pattern often observed in benniseed germplasm from West Africa (Durodola *et al.*, 2023; Alege *et al.*, 2024). The concentration of all high-yielding genotypes in Cluster II suggests that these accessions share a common genetic background for superior yield. This cluster can be considered a core collection for breeding programmes aiming at yield improvement. Conversely, Cluster I (NGB04126 and NGB04119) represent genetically distant, low-yielding types that might carry unique alleles for stress tolerance or other adaptive traits, and thus should be conserved (Li *et al.*, 2024). The moderate genetic distance between Cluster II and Cluster III indicates that crosses between these groups may still generate useful recombinants, but the greatest heterosis is expected from crosses between Cluster I and Cluster II.

Overall, the combined use of PCA and cluster analysis has effectively captured the genetic structure of the Nigerian benniseed germplasm. The results provide breeders with clear selection criteria (emphasising PC1 traits) and a rational basis for choosing parents (e.g., NGB02756 from Cluster II crossed with NGB04119 from Cluster I). This approach has been successfully applied in other oilseed crops and is now validated for sesame in Nigeria.

## CONCLUSION AND RECOMMENDATION

This study evaluated genetic variability for seed yield and related traits in 16 benniseed accessions grown in two Nigerian locations. Significant genotypic differences were observed for all traits. Genotype NGB02756 emerged as the highest and most stable yielder, while NGB03209 and NGB04125(2) showed excellent shattering resistance. Principal component analysis revealed that yield-related traits (PC1) are the primary sources of variation, explaining 42% of total diversity. Cluster analysis grouped the accessions into three distinct classes, with Cluster II containing all superior genotypes. We recommend NGB02756 for direct variety release and as a parent for yield improvement, and NGB03209 as a donor for shattering resistance. The genetic diversity identified here provides a solid foundation for future benniseed breeding programmes in Nigeria and West Africa.

Based on the findings of this study, Genotype NGB02756 should be subjected to further multi-location and multi-year trials to confirm its stability and suitability for possible variety release in Niger. Accessions NGB04125 (2) and NGB03289, which exhibited strong shattering resistance, should be utilized as parental materials in benniseed breeding programmes aimed at developing varieties with reduced seed loss.

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## CONFLICT OF INTEREST

The authors declare no conflict of interest.

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