Original Article

# Characterisation of sunflower (*Helianthus annuus* L.) Seeds from selected States in Northern Nigeria

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## ABSTRACT

This study assessed the morphological characteristics of sunflower seeds (*Helianthus annuus* L.) collected from selected cultivating states in Northern Nigeria, with the aim of strengthening the baseline knowledge for crop improvement. A field survey across Kaduna, Gombe, and Plateau states yielded eleven (11) distinct seed accessions: two (2) from Kaduna, six (6) from Gombe, and three (3) from Plateau. Standard Sunflower descriptor was used for the characterisation. The characterisation revealed considerable morphological diversity among the germplasm collected, underscoring the genetic richness of local germplasm. Black seeds were predominant (70%), followed by brown (20%) and grey (10%). Seed shapes were mostly oval wide (55%), rounded (30.3%) and oval elongated (15.2%) types were also observed. Medium seed thickness dominated across the accessions, except for one thick accession (ZAR 002, Kaduna). Cotyledon morphology varied, with oval types (45.5%) being the most frequent, followed by extended (30.3%) and rounded (24.2%) forms. Cotyledon size was mainly medium (90%), with a small proportion of small cotyledons (10%) recorded. These findings represent one of the few systematic attempts to characterise sunflower seed accessions in Nigeria, providing novel baseline data for germplasm conservation and utilisation. The observed variability highlights the potential for selecting adaptive and high-yielding genotypes, which is critical for breeding programs aimed at enhancing oilseed productivity, resilience, and food security in the region. Future research should integrate molecular tools with morphological characterisation to classify accessions into robust genetic groups, thereby accelerating their use in breeding pipelines and sustainable agricultural development.

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## INTRODUCTION

Sunflower (*Helianthus annuus* L.) is a globally important oilseed crop, ranking fourth after soybean, palm, and rapeseed [1]. It provides high-quality edible oil rich in unsaturated fatty acids, and its adaptability to diverse agro-ecological zones has made it an attractive option for smallholder farmers [2,3].

Despite its agronomic potential, sunflower production in Nigeria remains limited and inconsistent. Farmers in Northern Nigeria regard the crop as versatile and easy to manage, yet yields are constrained by low-yielding varieties, poor cultural practices, and dependence on imported seed [4,5]. Although the northern region has been identified as suitable for sunflower expansion [6], systematic characterisation of locally available germplasm is still scarce.

The success of breeding and improvement programs relies heavily on the variability present in the germplasm pool [5]. However, most sunflower studies in Nigeria have focused on agronomic performance trials, with limited emphasis on morphological characterisation of seed traits, which is critical for germplasm conservation and selection of promising parental lines. This study therefore set out to collect and characterise sunflower seed accessions from major cultivating states in Northern Nigeria. By providing baseline data on phenotypic variation, the research contributes to the conservation of local germplasm and supports future breeding programs aimed at improving oilseed productivity and strengthening food security.

## MATHERIALS AND METHODS

### Germplasm Collection of Sunflower Accessions

A purposive sampling strategy was adopted **because sunflower cultivation in Nigeria is localized to specific regions rather than being evenly distributed**. Hence, targeting the major producing states—Kaduna, Gombe, and Plateau—ensured that representative accessions were obtained (Ref). Within these states, key Local Government Areas (LGAs) were selected based on production

intensity: Zaria (Kaduna); Barkin Ladi, Bokkos, and Bassa (Plateau); and Deba, Billiri, and Balanga (Gombe). Seed samples of *Helianthus annuus* L. were collected either directly from farms at harvest or from farmers' stores to ensure authenticity and reduce admixture. Extension officers and local cooperatives facilitated farmer contacts, while questionnaires (with interpreters where needed) captured basic information on demographics, cultivation practices, purpose of production, and challenges. Accessions were assigned codes by state of origin (e.g., GMB = Gombe, JOS = Plateau, ZAR = Kaduna), packaged under dry aerated conditions to preserve viability, and documented with local variety names and collection-site details. Samples were then transported to the Department of Plant Biology, Federal University of Technology, Minna, for cataloguing and further characterization.

### Determination of Phenotypic Characteristics of the Sunflower Accessions
### Qualitative Traits

The morphological characterisation of seed traits was carried out using the Descriptors for Sunflower developed by the International Board for Plant Genetic Resources [7]. The qualitative characters evaluated were seed colour, seed shape, presence or absence of stripes, cotyledon size, cotyledon shape, and seed thickness. Visual assessments were made by trained evaluators under standardized laboratory conditions to minimize observer bias. Standard colour charts and reference descriptors [8] were used to ensure uniform scoring across all accessions.

### Quantitative Traits: Weight of 100 Seeds

Quantitative evaluation involved the determination of 100-seed weight for

each accession. For each sample, 100 seeds were manually counted and weighed using a digital precision balance (Model: Scout Pro SPU123, Ohaus Corporation, USA). The procedure was repeated in three replicates per accession. The mean weight per accession was calculated as:

$Mean\ 100 - seed\ weight\ (g) = Sum\ of\ rep$ (1)

Measurements were recorded in grams (g), providing an estimate of seed size variation across accessions.

## Data Analysis

Data obtained from both qualitative and quantitative traits were subjected to descriptive statistical analysis. For qualitative traits, frequency distributions and percentages were computed to summarize diversity patterns among accessions. For quantitative traits, means, standard deviations, and ranges were calculated to assess intra- and inter-accession variability. In addition, one-way Analysis of Variance (ANOVA) was performed on 100-seed weight data to test for significant differences among accessions, with means separated using the Least Significant Difference (LSD) test at 5%

probability level ($p < 0.05$). All analyses were carried out using IBM SPSS Statistics version 25.0.

## RESULTS
### Sources and description of sunflower germplasm

A total of eleven (11) sunflower (*Helianthus annuus* L.) accessions were collected across Kaduna, Gombe, and Plateau States, Nigeria, which are among the leading sunflower cultivating areas in Northern Nigeria. The sources and descriptions of sunflower germplasm collected from cultivating states in Northern Nigeria are summarised in Table 1. Gombe State contributed the largest share of accessions (57%), followed by Plateau (27%) and Kaduna (18%). For instance, in Gombe, accessions such as "Talase" (GMB 001, Balanga), "Lano" (GMB 002, Deba), and "Karr" (GMB 003, Billiri) highlight adaptation to specific agro-ecological zones. Plateau State accessions included "Mai" (JOS 001, Barikin Ladi) and "Binmai" (JOS 002, Bokkos), while Zaria in Kaduna State contributed "Mai mai" (ZAR 001) and "Mara mai" (ZAR 002). The proportional representation of accessions across states is presented in Figure 1.

Table 1. Sources and description of Sunflower germplasm From Cultivating States in Northern Nigeria

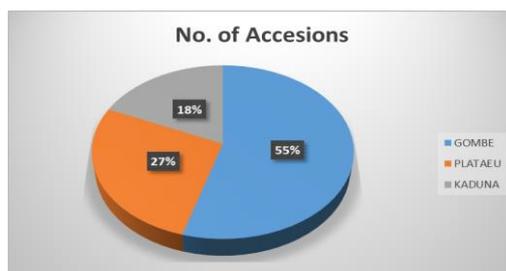| Accession Number | Local name | Local Government |
|---|---|---|
| GMB 001 | Talase | Balanga |
| GMB 002 | Lano | Deba |
| GMB 003 | Karr | Billiri |
| GMB 004 | Kuri | Deba |
| GMB 005 | Pral | Deba |
| GMB 006 | Kwadom | Deba |
| JOS 001 | Mai | Barikin ladi |
| JOS 002 | Binmai | Bokkos |
| JOS 003 | Kato | Bokkos |
| ZAR 001 | Mai mai | Zaria |
| ZAR 002 | Mara mai | Zaria |

Figure 1: Percentage number of Accessions Collected from the States

## Phenotypic characteristics (qualitative) of sunflower evaluated

Considerable morphological diversity was observed among the accessions. Seed shape ranged from ovoid elongated (OE) and ovoid wide (OW) to rounded forms (Table 2; Plate I). Seed thickness was predominantly medium, except in ZAR 002, which exhibited a distinctly thick seed coat. Cotyledon shape varied across accessions, with oval cotyledons being most common, while a smaller proportion displayed extended or rounded forms. Cotyledon size was generally medium (90% of accessions), although a few smaller variants were identified (Table 2; Plate II).

In terms of seed coat colour, 70% of accessions were black, 20% brown, and 10% grey. Most accessions lacked striping, though two (JOS 002 and JOS .

003) exhibited lateral and marginal stripe patterns, respectively (Table 2; Plate III–IV). The weight of 100 seeds exhibited significant variation (p < 0.05) among the sunflower accessions, ranging from 16.94 g in GMB 005 to 34.68 g in GMB 004 (Table 2). The heaviest seed lots were recorded in accessions GMB 004, GMB 006, JOS 002, and JOS 003, all of which exceeded 31 g, and were statistically similar (p > 0.05) to each other. In contrast, the lightest seed weights were observed in GMB 005, GMB 002, JOS 001, and ZAR 002, with values below 20 g, and these did not differ significantly (p > 0.05) within their group. Accessions such as GMB 001 and ZAR 001 showed intermediate seed weights (~26 g) and were statistically distinct (p < 0.05) from both the heaviest and lightest groups. This variation reflects underlying genetic and environmental influences on seed development

Table 2. Phenotypic Characteristics (qualitative) of Sunflower Accessions Evaluated

| Accessions | Seed Colour | Seed Shape | Thickness of Seed | Shape of Cotyledon | Size of Cotyledon | Weight of 100 Seeds (g) | Position of stripe |
|---|---|---|---|---|---|---|---|
| GMB 001 | Black | Ovoid E | Medium | Extended | Medium | $26.29 \pm 0.24^b$ | Absent |
| GMB 002 | Black | Rounded | Medium | Oval | Medium | $19.10 \pm 1.18^c$ | Absent |
| GMB 003 | Black | Rounded | Medium | Oval | Small | $21.46 \pm 1.46^c$ | Absent |
| GMB 004 | Black | Ovoid E | Medium | Oval | Medium | $34.68 \pm 2.20^a$ | Absent |
| GMB 005 | Black | Ovoid W | Medium | Oval | Medium | $16.94 \pm 1.51^c$ | Absent |
| GMB 006 | Grey | Ovoid W | Medium | Oval | Medium | $33.83 \pm 0.46^a$ | Absent |
| JOS 001 | Brown | Rounded | Medium | Extended | Small | $19.10 \pm 1.18^c$ | Absent |
| JOS 002 | Black | Ovoid W | Medium | Rounded | Medium | $32.26 \pm 2.50^a$ | Lateral and |
| JOS 003 | Brown | Ovoid E | Medium | Rounded | Large | $31.10 \pm 0.48^a$ | Marginal |
| ZAR 001 | Black | Rounded | Medium | Extended | Medium | $26.29 \pm 0.24^b$ | Absent |
| ZAR 002 | Brown | Ovoid W | Thick | Oval | Medium | $19.10 \pm 1.18^c$ | Absent |

OW= ovoid Wide, OE= ovoid elongated



1 Elongated    2 Ovoid elongated    3 Ovoid wide    4 Rounded

Plate I: Seed Shape



1 Elliptical    2 Oval    3 Extended    4 Rounded

Plate II: Shape of Cotyledon



Plate III: Seed Sample of GMB 001



Plate IV: Seed Sample of GMB 002

Plate V: Seed Sample of GMB 003



Plate VI: Seed Sample of GMB 004



Plate VII: Seed Sample of GMB 005



Plate VIII: Seed Sample of GMB 006



Plate IX: Seed Sample of JOS 001



Plate X: Seed Sample of JOS 002



Plate XI: Seed Sample of JOS 003



Plate XII: Seed Sample of ZAR 001

Plate XIII: Seed Sample of ZAR 002

## DISCUSSION

This study revealed considerable morphological diversity among sunflower accessions collected from Kaduna, Gombe, and Plateau States, underscoring the genetic richness of sunflower germplasm in Northern Nigeria. The observed variation in traits such as seed colour, seed shape, cotyledon morphology, and seed weight highlights the potential value of these accessions for breeding and crop improvement. Morphological descriptors remain important first steps in germplasm characterisation, as they provide practical indicators of variability that can guide targeted selection and subsequent molecular evaluation [9,10].

The variability recorded across qualitative and quantitative traits indicates the presence of diverse genetic resources within the studied accessions. For instance, the wide range of 100-seed weights (2.10–12.30 g) suggests variation in seed size and density, traits that are highly relevant to both yield and oil productivity. Larger-seeded accessions such as JOS 003 could be prioritized in breeding programs focused on improving seed yield, while accessions with distinct traits, such as stripe patterns (JOS 002, JOS 003), may serve niche breeding objectives. Such phenotypic variability aligns with previous reports that emphasize the role of morphological differences in guiding breeding strategies [11,12].

The distribution of morphological traits across the surveyed states reflects adaptation to different agro-ecological zones. For example, accessions from Gombe State, which constituted the largest share of the collection (57%), displayed notable variation in seed shape and weight. These differences are consistent with the role of local environments in shaping morphological diversity [13]. The predominance of black seeds (70%) across regions may also suggest adaptive responses, as seed coat colour has been linked to stress tolerance and ecological fitness in related crops [10]. Such evidence supports the conclusion that regional conditions contribute significantly to the observed diversity, without implying unverified historical origins.

The documented diversity provides a valuable foundation for conservation and sustainable use of sunflower germplasm. Effective conservation ensures the long-term availability of genetic resources for breeding programs, particularly in the face of climate variability and biotic stresses. As emphasized by [12], maintaining broad genetic diversity is critical for sustaining agricultural biodiversity and developing resilient crop varieties. In this context, the accessions characterized in the present study represent important resources for Nigeria's sunflower improvement efforts. Conservation through both ex situ collections and on-farm management should be prioritized to safeguard this diversity. While the

present study provides baseline morphological characterization, integrating molecular tools will be essential for more precise evaluation of genetic relationships among accessions. Such complementary approaches would strengthen breeding pipelines and further clarify the adaptive traits observed. Overall, the findings highlight that Northern Nigeria harbours a diverse sunflower germplasm pool with significant potential for breeding, adaptation, and conservation, thereby contributing to national food and oil security strategies.

## CONCLUSION

This study demonstrated that sunflower germplasm collected from Northern Nigeria possesses significant morphological variability in traits such as seed colour, seed shape, cotyledon morphology, and seed weight. These differences reflect not only the adaptability of sunflower to diverse agro-ecological conditions but also the presence of valuable genetic resources that can be harnessed for crop improvement. The predominance of accessions from Gombe State further highlights its role as a major cultivation hub, offering a concentrated pool of diversity for breeding initiatives. The dataset generated from this study provides a foundation for breeding programs aimed at improving seed yield, oil content, and stress tolerance. By identifying accessions with desirable traits, plant breeders can develop improved varieties tailored to both local conditions and market needs. Furthermore, the results underscore the importance of strengthening conservation strategies, both ex situ and in situ, to safeguard this diversity for future agricultural use. Policy support will be critical in facilitating germplasm conservation and integrating local landraces into breeding pipelines. Finally, the documented diversity has practical implications for farmer adoption, as access to improved varieties derived from these local resources can enhance productivity, resilience, and food security in Nigeria.

## Declarations Section

### Authors Contribution

*YZM: conceptualized the study, conducted field and laboratory work, analysed and interpreted data, drafted manuscript. DOAY: conceptualized the study, interpreted data, supervised, reviewed, GAA: supervised and reviewed AA and BIM reviewed the manuscript, OII: participated in the laboratory work All authors contributed to the development of final manuscript approval and submission*

### Disclosure of Conflict of Interest

*None*

### Ethics Approval and Informed Consent.

*This study did not use human or animal subjects. Therefore, ethical consideration was not applicable.*

### Disclosure of Funding

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