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# GENETIC DIVERSITY FOR YIELD COMPONENTS IN SESAME (*Sesamum indicum* L.)

**Abdullahi Ibrahim Gadanya**

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# GENETIC DIVERSITY FOR YIELD COMPONENTS IN SESAME (*Sesamum indicum* L.)

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## DADOS CURRICULARES DO AUTOR

Abdullahi Ibrahim Gadanya was born on October 11, 1982 in Gadanya town, Bagwai Local Government Area of Kano State, Nigeria.

I had my Primary Education at Gadanya Central Primary School in 1994 and later attended Government Secondary School Bichi where I obtained Senior Secondary Certificate in 2000. I also proceeded to Federal College of Education (Technical) Bichi, where I obtained Nigeria Certificate in Education (NCE). I also moved to Bayero University Kano where I pursued my Bachelor of Science Degree in Agricultural Education in 2016.

I was admitted to the department of Agronomy (plant breeding and Genetics) for a Master's degree in 2021 and depended dissertation on 28/02/2024. Academic at Faculty of Agriculture and Veterinary Sciences – Unesp, Campus of Jaboticabal, in the Graduate Program on Agronomy (plant breeding and Genetics)

I am currently a lecturer III at Federal College of Education (Technical) Bichi, Kano State, Nigeria.

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Summary

**Genetic Diversity for Yield Components in Sesame (*Sesamum indicum* L.)**



## ABSTRACT

The study on genetic diversity for yield components in sesame (*Sesamum indicum* L, Pedaliaceae family) was done at the Jaboticabal campus, in the Screen house and Molecular laboratory of Universidade Estadual Paulista, (Unesp) Brazil. This was aimed to elucidate the diversity among some sesame varieties (*Sesamum indicum* L) in Nigeria using agro-morphological parameters and Inter-simple sequence repeats (ISSR) molecular markers. Eight sesame varieties: NCRIBEN-01M, NCRIBEN-02M, NCRIBEN-04E, NCRIBEN-05E, Black seeded, E8, Gujarat, and Yandev-55 were planted in the screen house. Leaves were collected at 12 days after planting and processed for molecular evaluation. Furthermore, each variety were evaluated morphological agronomic parameters in screen house potted experiment the varieties varied in seed coat colour of four groups: black, brown, light brown, white and ovate leaf lobe in E8 variety. Plant height (cm) ranged from 96.4±1.1 to 144.3±2.0, days for 50% flowering and days to maturity ranged from 55±1.0 to 68±1.0 and 91±1.0 to 130±2.0 days respectively. Yield influencing parameters had ranges of 35±2.0 to 63±1.0 for capsule per plant, 52±2.0 to 76±2.0 for seed per capsule and 2.12±1.56 to 4.43±0.1 for 1000 seed weight (g). Principal components matrix revealed that the PC1, which accounted for the highest variability was mostly related to yield related traits like number of capsules plant', number of primary branches plant$^{-1}$ and 1000 seed weight. PC2 was dominated by growth related traits. Dissimilarity dendrogram of the studied sesame genotypes, established using Agglomerative clustering at 0.821 coefficient, revealed three clusters. These results showed variability in yield traits of these sesame varieties studied. Eleven ISSR primers were used for analysis eight different sesame -populations from Nigeria. The primers showed legible and reproducible genomic profiles. The 11 primers amplified 472 bands of which 228 (48.3 %) were polymorphic. PIC (Polymorphic Information Content) PIC in this study with 11 sesame genotypes varied from 0.330 to 0.50 an indication of the informativeness of ISSR markers as well as their relevance in discriminating the populations studied. There is therefore diversity among the sesame genotypes studied. Further studies on genetic diversity of Nigerian sesame accessions using ISSR markers using greater numbers of markers and genotypes will further unravel their degree of diversity is recommended

**Keywords:** Genetic characterization, molecular markers, Sesame varieties, Polymorphism.

## Introduction

Sesame (*Sesamum indicum* L. Pedaliaceae) is one of the prehistoric oilseed crops, dating back to 3050- 3500 BC and has been cultivated from ancient times (Bedigian, 2003). It is one of the first oilseed crops used by humans, occupying the ninth position among the most cultivated in the world (Bezerra *et al*., 2010; Perin *et al*., 2010; Mesquita *et al*., 2013; Pinto *et al*., 2014; Silva *et al*., 2014). Originating from East Africa and in India (Nayar and Mehra, 1970; Bedigian, 2003) sesame thrives well on moderate temperatures (25 and 30 ºC), lowland (below 500 m) and low rainfall (500 to 650 mm) (Arriel *et al*., 2009). It is extensively cultivated worldwide and naturalized in dry habitats of tropical and subtropical regions of the old world (Bedigian, 2003). The crop is highly drought tolerant, grows well in most kind of soils, regions and is well suited to different crop rotations. Subsistence farmers grow sesame using low inputs and in low and less water (Cagirgan, 2006). Major world leading producers of sesame are Sudan, Myanmar, India, Tanzania, Nigeria, China, Ethiopia and Burkina Faso (FAO, 2021). Asian and African countries cultivate about 90 percent of the world sesame production area.

Sesame is one of the most important oil seed crops in the world widely used in baked goods, confectionery products (because it is stable against oxidative changes than other vegetable oils), pharmaceutical industries (Falusi and Salako, 2001) and alternative medicine (Mushtaq *et al*., 2020). Oil extract is used the industry to produce soap, perfume, carbon paper and pharmaceutical products (Adu-Gyamfi *et al*., 2019). Its edible nutritious seeds and leaves are used for making vegetable soup and oil cake for animal feed (Kafiriti and Deckers, 2001; Alam *et al*., 2007).

Despite its much priced position in food and oil production with great export potential, sesame yield has been low. In Nigeria, for instance 788.5 kg average yield in 2020 is far below its potential of 1,800 kg/ha. The fact that average yield per hectare in Nigeria from 2011 to 2020 was above the mean for Africa and world (FAO, 2021) lays credence to poor sesame yield the world over.

The most important challenging traits of sesame the world over include lack of widely adapted varieties, poor stand establishment, susceptibility to diseases and pests, poor responses to fertilizer, lack of profuse branching, non-synchronous maturity, shattering of capsules at maturity and low harvest index (Wijnands *et al*., 2007; Mahajan *et al*., 2007). One other reason for low seed yield and reduced acreage under cultivation is the persistent use of traditional practices and lack of improved varieties for use by the farmers. Even when modern varieties are present, their **c**ultivation is reported to be limited due to insufficient genetic information on them (Alege *et al*., 2021).

Limited genetic variability in sesame germplasm is a result of long history of domestication, continuous cultivation on rain fed marginal lands, hence survival via natural selection (Tripathy *et al*., 2019). Genetic drift and selection by nature have reduced diversity. Therefore, possible using broad-based genetic resources of wild types, land races and improved varieties offers better opportunity for sesame genetic improvement. This is because broad based genetic resources provide important genepool of untapped genetic resource for abiotic and biotic stress resistance and yield increase as well as maintaining and enhancing resilience of production systems (Tripathy *et al*., 2019).

## Conclusion

This current study evaluated the genetic diversity of eight sesame genotypes using their agromorphological performance and eleven ISSR markers. The results showed significant variations among the genotypes especially in the yield related traits but less variation in the morphology. The black sesame and E8 performed better in number of capsules per plant. The black sesame also had significantly highest number of seeds per capsule and was early in maturity This is earliness is a good triat for draught escape especially giving the current issues with climate change in its attendant negative impacts of draught. The studied genotypes also were diverse based on the use of molecular markers. The ISSR markers used for the first time on these Nigerian genotypes were very informative and efficient on detecting the diversity of the studies genotypes. Further studies on genetic diversity of Nigerian sesame accessions using ISSR markers using greater numbers of markers and genotypes will further unravel their degree of diversity is recommended.

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