Assessment of Genetic diversity in populations of *Parkia biglobosa* in Derived and Guinea Savanna Zones of Nigeria

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Abstract: *Parkia biglobosa* (African locust bean) is a valuable multipurpose tree species widely used by local communities across West Africa for food, medicine, and income generation. Despite its importance, its natural populations are declining due to overexploitation and poor regeneration, putting its genetic resources at risk."This study assessed the genetic diversity of *P. biglobosa* in three populations (Benue, Kogi, and Nasarawa States), which were purposively selected based on the intensity of utilization and marketing of its products located in two savanna ecological zones (derived and guinea) of Nigeria, using nuclear simple sequence repeat (nSSR) markers. Leaf samples were collected, and genomic DNA was extracted from silica gel-dried leaf tissue. Polymerase Chain Reaction (PCR) was performed using five nSSR primers (Parpan3, Parpan4, Parpan9, Parpan13, and Parpan15). The amplified DNA fragments were separated using 2% agarose gel electrophoresis. Fragment sizes were estimated using ladder – DNA sizing marker and analyzed with CERVUS 3.0.7 software. The number of alleles per locus ranged from 2 - 7, observed heterozygosity ranged from 0.000 to 0.333, while expected heterozygosity ranged from 0.533 to 0.923 within populations. Polymorphic Information Content (PIC) values within populations ranged from 0.346 - 0.840, indicating that the markers were highly informative. Across populations and ecological zones, allelic richness ranged from 6.6 to 12.8, observed and expected heterozygosities ranged from 0.0000-0.0686 and 0.8339-0.9217, respectively. Despite high expected heterozygosity, observed heterozygosity was low, most likely due to the presence of null alleles and inbreeding arising from restricted gene flow within fragmented populations. The results show high genetic variation within and between populations, though not fully expressed at the phenotypic level. The SSR markers (Parpan 3, 9 and 13) used proved effective and are recommended for future genetic studies on *P. biglobosa*. However, broader sampling across the species range is needed for more comprehensive conclusions. This study highlights the need for urgent conservation and sustainable management strategies, including habitat protection and plantation development outside the natural range of the species.
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1. Introduction

Parkia biglobosa (African locust bean tree) is one of the indigenous tree species used in agroforestry systems across Sub-Saharan African countries, due to its multiple uses. The species is a leguminous tree that belongs to the Fabaceae family and Mimosoideae subfamily (Amusa *et al*, 2014; Houndonougbo *et al*, 2020), which is widely distributed from Senegal in West Africa to Uganda in Central Africa and thrives in derived savanna, guinea savanna, and Sudan savanna climatic zones (Lompo *et al*., 2018). Onyekwelu *et al*. (2015) listed some indigenous tree species that produce important fruit trees such as *Chrysophyllum albidium, Irvingia gabonensis and Garcinia kola* and other Non-Timber Forest Products (NTFPs) which are important to the populace.

Parkia biglobosa is an important multipurpose indigenous fruit tree that plays an important role in the livelihoods of rural communities in Nigeria and beyond. It provides food, nutrition, medicine, income, and other ecosystem services. The seeds are fermented to produce "dawadawa" or "iru", a protein-rich traditional condiment used as a substitute for animal protein (Lamien *et al*., 2011; Nyadanu *et al*., 2017). Pods and fruit pulp are rich in proteins, vitamins (A, B, C), carbohydrates, lipids, and minerals (Nyadanu *et al.*, 2017; Agbani *et al*., 2018), while the leaves, bark, and roots are used in traditional medicine to treat various ailments, including hypertension, malaria, and wounds (Ouedraogo, 1995; Dedehou *et al*., 2016).

Besides its socio-economic benefits, *P. biglobosa* contributes to ecological functions such as soil fertility improvement through nitrogen fixation (Teklehaimanot, 2004). Despite its nutritional, economic and ecological importance, this species is genetically threatened as a result of overharvesting,

deforestation, bushfires, and unsustainable land-use practices. Natural of *P. biglobosa* is noted to be poor, and its populations are declining due to ageing of the trees and lack of adequate management (Ræbild *et al*., 2012; Padakale *et al*., 2015). Many fruit trees are currently being overexploited in their natural habitats due to high demand, continuous harvest, declining tree populations, ageing of existing trees, unsustainable farming systems, high human pressure, absence of livelihood options as well as poverty. The decline of fruit trees poses threats to food security as well as the environment, wildlife, traditional medicine and human livelihoods (Boboye *et al.,* 2021). The ongoing threats from land-use change, fruit tree overharvesting, and climate variability necessitate urgent investigation and conservation efforts.

Parkia biglobosa has been noted to exhibit moderate to high genetic diversity across its natural range in West and Central Africa (Amusa *et al*., 2014; Lompo *et al*., 2016). Preserving the genetic diversity of the species is fundamental for its adaptability, resilience, survival and future use in breeding and afforestation programs especially in the face of increasing habitat fragmentation, overexploitation, and climate change. Genetic diversity enables a species to withstand environmental changes and stress, making it essential for sustainable forest management and conservation (Oluwajuwon *et al*., 2022). Lawal *et al.* (2023) noted that genetic diversity connotes the richness of the hereditary information in the gene pool of a given species. However, sustainable utilization and effective conservation requires a clear understanding of the genetic structure and variability of tree species for developing conservation strategies.

Molecular markers, especially **simple sequence repeats (SSR)** have proven to be highly effective in assessing genetic diversity in plant populations. Utilizing microsatellites (SSR) for tree species is optimal because they are codominant, multiallelic, highly polymorphic and may reveal dominant molecular marker of good potential and have been widely used due to their ability to detect detailed genetic differences (Ahmad *et al*., 2018). Previous studies have applied SSR and other molecular markers to investigate the genetic diversity of *P. biglobosa* in West Africa, revealing a range of genetic diversity levels across regions (Amusa *et al*., 2014; Adesoye and Apo, 2015; Lompo *et al*., 2016; 2018; Popoola *et al*.,2020). For this study, nuclear SSR marker was used to assess variability within and between *P. biglobosa* populations because it has been proven effective for *P. biglobosa* population as reported by Koura *et al*., (2019).

Despite the widespread distribution and utilization of *P. biglobosa* in Nigeria, there is still limited research on its genetic diversity in the country. The present study was undertaken to evaluate the genetic diversity of *P. biglobosa* populations in the derived and guinea savanna ecosystems of Nigeria, specifically focusing on Benue, Kogi, and Nasarawa States due to the prevalence, utilization and marketing of *P. biglobosa* in them. The findings will support the conservation of *P. biglobosa* genetic resources, inform sustainable management strategies, and guide the selection of superior genotypes for domestication, afforestation, and breeding programs in Nigeria and beyond.

2. Material and Methods

Study area

The study was carried out in three populations (Benue, Kogi and Nasarawa) of of *P. biglobosa* from two ecological zones in Nigeria (Figure 1). Benue State is situated between Longitude 7° 4' and 10° 0' E and Latitude 6° 25' and 8° 8' N. The climate is tropical, with two distinct seasons: rainy season and dry seasons. The rainy season lasts from April to October with an average annual rainfall of 1120 to 1500 mm. The dry season starts in November and ends in March (Alapa, 2019). The climate is characterized by high temperature, with temperature range of 26 - 37^{o}C. The relative humidity is dependent on the seasons but varies from 50 to 80% with dry season having the lowest and the rainy season having the highest. The vegetation is characterized by open woodland with tall trees that typically have short and wide leaves. Kogi State extends from Latitude 6.33 ^{o}N to 8.44 ^{o}N and from Longitude 5.40 ^{o}E to 7.49 ^{o}E. The Niger and Benue rivers, which converge at Lokoja, are the primary sources of drainage for the State. These rivers have vast flood plains. The State has two distinct seasons: the rainy season, which lasts from April to October, and the dry season, which lasts from November to March (Odekunle, 2004). Mean annual rainfall ranges from 800 to 1100 mm (Sani and Haruna, 2010) while mean daily temperature ranges from 24.4 to 33.8^{o}C. Rrelative humidity is highest during the rainy season with mean value of 82.2 and 61.1% during the dry season. The soil is characterized by the cretaceous sediments and sandstone (Fatoye, 2018). Nasarawa State is situated in the central part of Nigeria, it is located between latitude 7^{o} 45' and 9^{o} 2''N of the equator and between Longitudes 7^{o} and 9^{o} 37'E of the Greenwich meridian. There are two distinct seasons are the rainy and the dry seasons. The rainy season commences at the beginning of May and lasts till October. The dry season is experienced between November and April. Mean annual rainfall varies from 1100 mm to 2000 mm. Daily temperature range between 20 and 34°C. Relative humidity ranges between 65% and 85 % during the rainy season and 25% and 55% during the dry season.

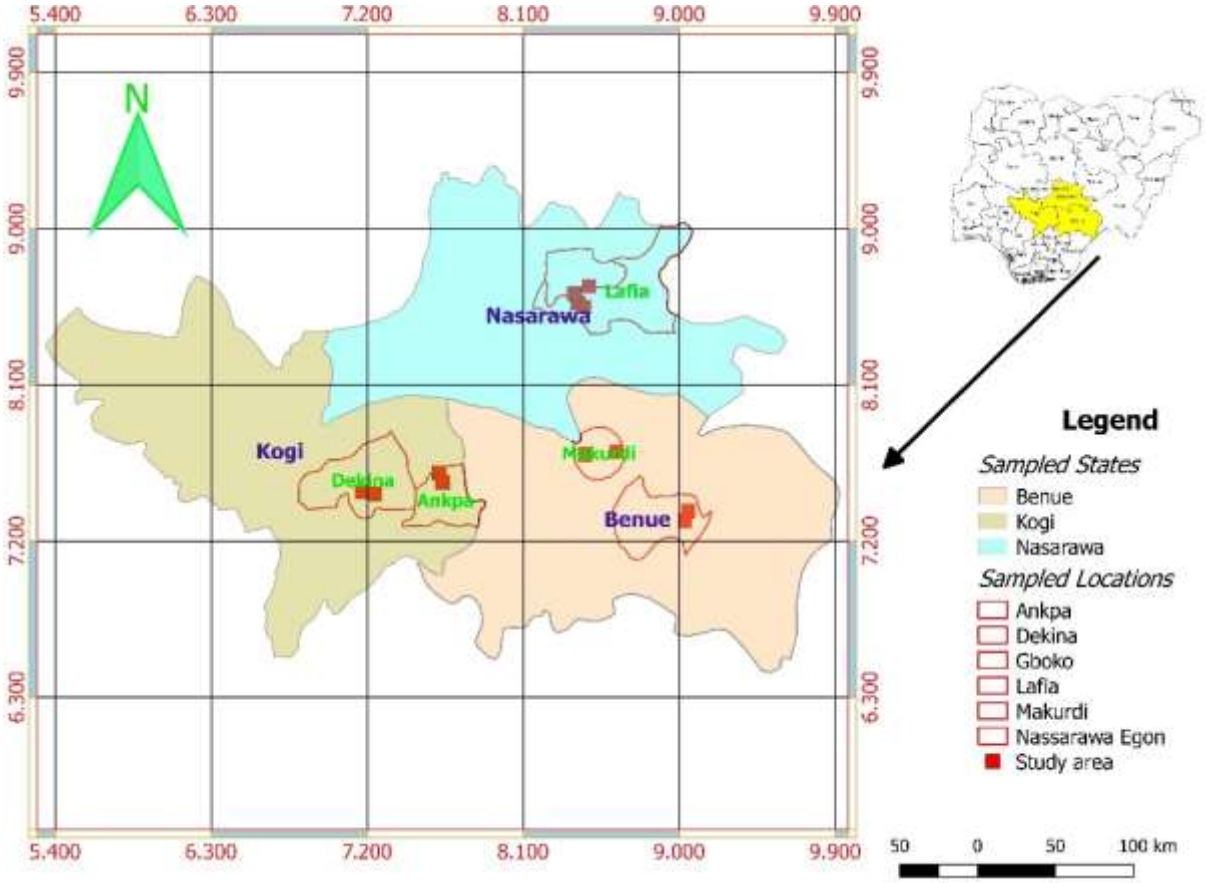

Figure 1: Map of central Nigeria showing the selected states ecological zones of study.

Collection of Plant material

Parkia biglobosa leaf samples from adult trees were collected from derived and guinea savanna ecosystems across Benue, Kogi and Nasarawa States (Figure 1 above). The leaves were cleaned, dried and preserved in silica gel in sealed and well-labeled zip-lock bags and brought to Inqaba Biotech West Africa laboratory in Ibadan, Nigeria and stored at -20^{0}C for DNA Extraction.

Genomic DNA Extraction Protocol

Total genome DNA was extracted from 0.02g powdered silica gel dried *P. biglobosa* leaves put in 20 ml tube using plant mini extraction kit protocol according to the manufacturer's instruction at Inqaba Biotech Africa laboratory Ibadan, Nigeria. The DNA quality and quantity were evaluated using 1% agarose gel electrophoresis in a nanodrop spectrophotometer and stored at -20 °C for PCR amplification

PCR amplification and Electrophoresis

Five out of the ten nuclear microsatellite primers (SSR) developed for *Parkia panuresis* (Luettman *et al*., 2010) and transferable to *P. biglobosa* population study (Koura *et al*., 2019) were selected and used for this study. The primers ten bases (F/R) were supplied by Inaqba Biotech West Africa laboratory with the code number: NG2024/55508. The locus name and sequences are presented in Table 1.

The PCR amplification was performed using a volume of 25µl in a DNA thermal cycler (eppendorf. master Master cycler Gradient). The reaction mixture contained 3µl of genomic DNA, 12.5 µl of GoTag green master mix. 2x (Promega), 0.5µl each of forward and reverse primers and 8.5µl Nuclease free water. The cycling conditions were:

1 cycle at 94°C for 3 min; followed by 35 cycles at 94°C for 30s, 30s at 50°C annealing temperature, and extension at 68°C for 1 min.; with final extension lasting 1min at 68°C. The PCR products were stored at 4°C until analysis. Amplified PCR products were separated by electrophoresis using 2% agarose gel in 1 Xtbe (Triss base EDTA) buffer stained with 5ul ethidium bromide and visualized under uv light. Fragment size was estimated using 50-10000bp bench Top PCR marker (ladder-DNA sizing marker).

Table 1: Characteristics of the nuclear microsatellite loci transferable by Koura *et al*. (2019) and used for this study

Primer	Primer sequence	Annealing Temperature(^{0}C)	motif	Repeat	Size range
Parpan 3	F:CACGTTAATTCAATCAAAATGGTG R: TTTTGCCTTTTTCGGACTTG	56.5		$(GT)_{15}$	155-209
Parpan 4	F:TAMRATTGATGGGAGTGGGAAAA R: CAGGAGGTGGTCTCTTCAGG	54,0	AG	$GT_{13}(GA)_{15}$	148-210
Parpan 9	F: FAM-GGGGCTTGTGTCTCTCACTG R: ACTTTGAAGGCACGAGATGG	58.0		$(AC)_{12}$	204-262
Parpan 13	F: TAMRA-CCTCCCTCGCTTCACAATC R: CACATGCAAATGAAAATGGTG	58.5	$_{17}$TT(GT)$_8$	(GT)	86-194
Parpan 15	F: HEX-TGGCCTCACTGCATACTGAC R: TGGGATGAACAAAACTGTGC	55.0		$(AC)_{24}$	104-152

Data Analysis

Scoring was done using the gel output files under Photo Light. Each primer pair was considered as 'locus' to refer to an nSSR site (defined by the terminal of a PCR primer pair), and the length of variants at a site was treated as an allele. Bright and scorable bands were traced and scored as discrete numbers (absent = 0, present = 1). The Cervus 3.0.7 software (Kalinowski *et al.*, 2007) was used to estimate genetic diversity parameters. The frequencies of the bands were used to calculate the number of alleles (A) per locus, number of individuals at the locus, observed (Hobs) and expected (Hexp) heterozygosity and polymorphic information content (PIC).

3. Results

Genetic diversity within the *P. biglobosa* population in the derived and the guinea savanna ecosystems

The genetic diversity of the *P. biglobosa* population within the derived and guinea savanna ecosystems is presented in Table 2. In the Benue population, the number of alleles (K), which is referred to as allelic richness, ranged from 2 to 7 per locus in the derived savanna and 3 to 6 in the guinea savanna, with a mean of 4.4 alleles. The observed heterozygosity (Hobs) was 0.000 across all loci. The expected heterozygosity ranged from 0.533 to 0.923 and 0.714 to 0.879 with a mean of 0.7694 and 0.8012 in the derived and guinea savanna ecological zones, respectively. The highest genetic diversity in terms of K, HExp in the two ecological zones was observed in parpan 13 (K=7, HExp=0.923), while the lowest value was recorded in parpan 4 (K=2, HExp=0.533). The Polymorphic Information content (PIC) (which is the primer's discriminating power) value ranged from 0.346 to 0.840 in the derived savanna zone and 0.555 to 0.791 in the guinea savanna. The highest PIC was recorded in Parpan 13 (0.840), while the lowest value was obtained in Parpan 4 (0.346).

In the Kogi population, the allelic richness (K) ranged from 4 to 7 per locus in the derived savanna and 2 to 6 in the guinea savanna, with a mean number of 5.4 and 3.8 alleles, respectively. The observed heterozygosity (HObs) ranged from 0.000 – 0.333, with a mean of 0.117 in the derived savanna and 0.000 in the guinea savanna. The expected heterozygosity (HExp) ranged from 0.821 to 0.900 and 0.667 to 0.879 in the derived and guinea savanna, respectively, with respective means of 0.8719 and 0.7816 for the two ecological zones. The highest genetic diversity in terms of K, HExp, in the two ecological zones of Kogi State

was observed in parpan 13 (K=7, HExp=0.900), while the lowest was recorded in parpan 4 (K=2, HExp=0.667). The Polymorphic Information Content (PIC) ranged from 0.671 to 0.825 in the derived savanna zone and 0.375 to 0.791 in the guinea savanna. The highest PIC was recorded in parpan 13 (0.825) while the lowest was in parpan 4 (0.375).

In the Nasarawa population, the **allelic richness (k)** ranged from 3 to 6 and 3 to 7 alleles across all loci, with a mean allelic richness of 4.4 and 4.6 within the derived and guinea savanna, respectively. The **observed heterozygosity (HObs)** was **extremely low (0.000–0.014)** across all loci in the two ecological zones. The **HExp** remained high (0.800–0.909 in derived savanna and 0.714 to 0.890 in guinea savanna across all loci). The highest genetic diversity was observed in parpan 3 (K=7; HExp=0.909) while the lowest was recorded in parpan 15 (K=3; HExp=0.714). The Polymorphic Information content (PIC) **values** were 0.593–0.810 in the derived savanna and 0.555-0.805 in the guinea savanna in all loci. The highest mean PIC was observed in Parpan 13 (0.810), while the lowest was obtained in Parpan 15 (0.555).

Table 2. Comparison of genetic diversity within the populations of *Parkia biglobosa* in the derived and guinea savanna ecological zones of Benue, Kogi and Nasarawa State

Population	Ecological zones		Derived Savanna			Guinea savanna		
		Locus	exp	obs	IC	exp	0bs	IC
	Benue	Parpan 3	.857	.000	.703	.879	.000	.791
		Parpan 4	.533	.000	.346	.714	.000	.555
		Parpan 9	.867	.000	.786	.837	.000	.756
		Parpan 13	.923	.000	.840	.788	.000	.671
		Parpan15	.667	.000	.535	.788	.000	.671
	Kogi	Parpan 3	.923	.000	.840	.848	.000	.744
		Parpan 4	.867	.333	.671	.667	.000	.375
		Parpan 9	.821	.250	.667	.800	.000	.593
		Parpan 13	.900	.000	.825	.879	.000	.791
		Parpan 15	.848	..000	.744	.714	.000	.555
	Nasarawa	Parpan 3	.802	.014	.715	.899	.000	.768
		Parpan 4	.800	.000	.593	.800	.000	.593
		Parpan 9	.857	.000	.793	.890	.014	.805
		Parpan 13	.909	.000	.810	.791	.000	.700
		Parpan 15	.800	.000	.593	.714	.000	.555

K allelic richness, N =number of individuals typed, Hobs- Observed heterozygosity, HExp- Expected Heterozygosity, PIC =Polymorphic Information Content

Genetic Diversity between *P. biglobosa* populations

The genetic diversity of *P. biglobosa* populations in derived and guinea savanna ecosystems in Nigeria is presented in Table 3. The number of individuals sampled in each ecological zone varied from 34 in the derived savanna to 38 in the Guinea Savanna. The mean Allelic richness (K) was 12.8 in the derived savanna and 11 in the guinea savanna, which were not significantly different. The mean observed heterozygosity was significantly higher in the derived savanna (0.0460) than in the Guinea savanna (0.0106) at 5% probability (Table 3). The mean expected heterozygosity was 0.9217 in the derived savanna and 0.9129 in the guinea savanna, both of which were not significantly different.

The genetic diversity of the *P. biglobosa* population in Benue, Kogi and Nasarawa states is presented in Table 4. The number of individuals

sampled from each population was 20 in Nasarawa State, 25 in Kogi State, and 27 in Benue State. Mean Allelic richness was equal in Kogi (7.8) and Nasarawa (7.8) states, both of which were higher than the mean alleleic richness in Benue (6.6), but mean alleleic richness was not significantly different across states. The mean observed heterozygosity was low across the States, with Kogi state (0.0686) having the highest value, followed by Nasarawa (0.0348). The lowest value (0.000) was recorded for Benue state. The mean expected heterozygosity obtained in the Nasarawa population (0.8860) was slightly higher than the mean expected heterozygosity recorded in *P. biglobosa* populations in Kogi state (0.8803) and Benue (0.8339). However, the mean expected heterozygosity did not differ significantly across the three states.

Table 3: Comparison of genetic diversity between the *Parkia biglobosa* populations in the derived and guinea savanna ecological zones

Ecological zones	N	Number of loci	K	Hobs	HExp
Derived savanna	34	5	12.8[a]	0.0460[a]	0.9217[a]
Guinea Savanna	38	5	11.0[a]	0.0106[b]	0.9129[a]
***p*-value**	-	-	**0.2606**	**0.02554**	**0.2427**

Note: Columns with different superscripts (alphabets) are statistically different at the 0.05 level. K allelic richness, N =number of individuals typed, Hobs- Observed heterozygozity, HExp- Expected Heterozygosity,

Table 4: Comparison of genetic diversity among different populations of *Parkia biglobosa*

Population	N	K	No. of loci	Hobs	HExp
Benue State	27	6.6[a]	5	0.0000[b]	0.8339[a]
Kogi State	25	7.8[a]	5	0.0686[a]	0.8803[a]
Nasarawa State	20	7.8[a]	5	0.0348[a]	0.8860[a]
***p*-value**	-	**0.331**	-	**2.29e-05**	**0.265**

Note: Columns with different superscripts (alphabets) are statistically different at the 0.05 level.

K= allelic richness, N =number of individuals typed, Hobs- Observed heterozygozity, HExp- Expected Heterozygosity

Discussion

Genetic diversity of the *Parkia biglobosa* population

Genetic diversity is fundamental to sustaining the adaptive capacities of species, the loss of which can potentially compromise the survival potential of affected populations or species (Pauls *et al*., 2013; Wang *et al*., 2023). Molecular markers play a crucial role in modern plant breeding by allowing breeders to identify and track desirable traits to evaluate genetic diversity (Salgotra and Chauhan, 2023). Understanding genetic diversity is essential for conservation and effective breeding strategies in tree species like *P. biglobosa*. This study revealed valuable insights into the genetic structure of *P. biglobosa* populations across three states (Benue, Kogi, and Nasarawa) within two savanna ecological zones (guinea and derived) in Nigeria.

The allelic richness (number of alleles (K), which reflects genetic variability and long-term potential for adaptability and resilience) was lower in this study compared to previous reports by Lompo *et al*. (2016) (k=5-15) and Popoola *et al*. (2020) (17-50 in *Parkia biglobosa*. However, our results are in line with values presented for tree species like *Vitellaria paradoxa* (Abdulai *et al*., 2012), k=4.06 in Ghana; *Parkia multifuga* (Phurailatpam *et al*.,2022), k=5.33 in Manipur; *Khaya grandifolia* (Soares *et al*., 2020), k=5.9 in Brazil and *Theobroma speciosum* (Dardengo *et al*., 22018), k=7.88-8.67 in Brazil.

A notable result from this study is the observed low heterozygosity (Ho**)**, particularly in the Benue population, where it was completely zero. This suggests a high level of homozygosity, likely caused by inbreeding, small population sizes, reduced or restricted gene flow, possibly as a result of habitat fragmentation or overexploitation. The lack of

observed heterozygosity also suggests that individuals may be more genetically similar than expected under natural conditions. Similar trends have been reported in *P. biglobosa* populations facing anthropogenic pressure (Sina, 2006; Ho=0.26; Popoola *et al*., 2020, Ho=0.28) and other species such as *Prunus sibirica* (Wang *et al*., 2023, Ho=0.32) and *Adansonia digitata* (Abate *et al*., 2025, Ho=0.065-0.077).

Despite observed low heterozygosity, high expected heterozygosity (He) values were recorded within and between populations, indicating a rich underlying gene pool. This pattern, where expected heterozygosity is high but observed heterozygosity is low, may reflect historical genetic diversity that is no longer fully expressed due to population pressures or recent environmental changes and outcrossing mechanisms, which are typical of insect-pollinated, outcrossing tree species like *P. biglobosa* (Lompo *et al*., 2016). High expected heterozygosity have been recorded in *P. biglobosa* (Akin-Idowu *et al*., (2018) (0.41-0.93); Lompo *et al.*, 2018 (0.79); and related species like *Fraxinus angustifolia* (0.72) (Temunovic *et al.*, 2013), *Fagus sylvatica* (0.407-0.880) (Szasz-Len and Konnert, 2018), *Vitellaria paradoxa* (0.5-0.7) and *Adasonia digitata* (0.6-0.8) (Boboye *et al*., 2021*)*, *Celtis zenkeri* (0.78) (Olamidayo *et al*., 2021). The results of Soares *et al*. (2020), He=0.56; Sexton *et al*. (2015), He=0.64 and Tsipidou *et al*. (2021), He=0.622 are within the range of this study. Several studies reported very low expected heterozygosity in *Theobroma speciosum* (Dardengo *et al*., 2018; He=0.21-0.26), *P. biglobosa*. (Sina, 2006; He=0.34), *Cunninghamia lanceolata* (Jin *et al*., 2023; He=0.233), which contradicts our results.

The Polymorphic Information Content (PIC) values recorded in this study indicate that most of the nuclear SSR markers (Parpan 3, 9 and 13) used were highly informative and reliable for detecting genetic variation, as noted by Koura *et al*. (2019). These values are comparable to those reported by Popoola *et al*. (2020) (0.51-0.89) in *P. biglobosa* and higher than PIC values from other studies like Attikora *et al*. (2024) (0.24) for *Fraxinus angustifolia*, Mohammed *et al*. (2022) (0.3092-0.5658) for *Vitellaria paradoxa* and Denis (2025) (0.45) for *Kigelia africana*.

The expected heterozygosity values in derived and guinea ecological zones and across the three states ranged from 0.8339 to 0.8860, indicating generally high genetic diversity as opined by de Lafontaine *et al*. (2013), who noted that the expected heterozygosity value range of 0.6-0.8 is high. Thus, the overall estimates of genetic diversity of *P. biglobosa* were high with low observed heterozygosity. Areas experiencing high deforestation and human pressure often display reduced observed heterozygosity despite retaining relatively high expected values. High heterozygosity is often linked with greater evolutionary potential, improved adaptability, and reduced risk of inbreeding (Odebunmi *et al*., 2017; Frankham, 2022). However, the discrepancy between observed and expected heterozygosity in all populations of the species, especially in Benue, may point to an excess of homozygotes, which could reflect inbreeding, small population sizes, or habitat fragmentation (Hartl and Clark, 2007). It also suggests that, while the population harbours genetic potential, actual genetic variation is not fully expressed in the individuals observed. This trend highlights a broader issue of **genetic erosion in tree species** facing habitat loss, reduced pollination, and human exploitation.

Some previous studies (Adesoye *et al.,* 2013; Adesoye and Apo, 2015; Ouedraogo, 2015) have documented wide genetic variation in *P. biglobosa*, emphasizing the role of environmental factors and genetic makeup, which agrees with this study. However, if this diversity is not maintained through adequate management and conservation, the evolutionary potential of the species could be severely reduced. The findings of this study contradict studies that reported low genetic diversity in *P. biglobosa* and other tropical species, such as Amusa *et al*. (2014) for *P. biglobosa*; Boboye *et al*. (2018) for *Chrysophylllum albidium*; Akinnagbe *et al.* (2019) for *Mansonia altissima*; Lawal *et al*. (2023) for Khaya species. It was observed in this study that populations of *P. biglobosa* in derived savanna showed slightly higher genetic diversity than those in the Guinea savanna. This may be due to better gene flow, less habitat fragmentation, or historical differences in land use. Katumo *et al*. (2022) noted the role of human activity, pollinator availability, and landscape structure in shaping the genetic diversity of plants.

The overexploitation of *P. biglobosa* could have threatened their genetic diversity and, hence, could limit their conservation and evolutionary development of the remaining populations. Cui *et al*. (2022) reported that genetic diversity is a prerequisite for future adaptive change and evolution and has a profound effect on species conservation. Our results highlight the urgent need for conservation actions for *P. biglobosa* in the savanna regions of Nigeria, especially in Benue State, where genetic diversity is at risk. Maintaining high genetic diversity is crucial for the long-term survival of *P. biglobosa*, particularly under the growing threats of climate change, habitat loss, and unsustainable harvesting.

Conclusion

This study revealed high genetic diversity in *Parkia biglobosa* populations across the Guinea and Derived savannas of Benue, Kogi and Nasarawa States, despite low observed heterozygosity, especially in Benue State.

The high expected heterozygosity suggests that the species retains considerable genetic potential. However, the discrepancy between observed and expected heterozygosity raises concerns about inbreeding, habitat fragmentation, and genetic erosion. The high polymorphism in most of the markers indicates that the nuclear SSR markers used are effective in detecting subtle genetic differences among populations, offering a powerful tool for monitoring genetic diversity and guiding breeding and afforestation programs. Therefore, maintenance of *P. biglobosa* genetic diversity is essential for its adaptive capacity, long-term survival, and sustainable use, given its economic and ecological value. There is an urgent need for in-situ conservation efforts, implementing restoration programs in more vulnerable populations like Benue state, where observed heterozygosity was completely absent. These identified genetic diversities can be prioritized in breeding programs to select high-performing individuals for seed production and propagation, especially populations from Nasarawa and Kogi states. Protecting the remaining natural habitats and promoting regeneration and ensuring interconnected conservation corridors for gene flow become essential. Strategies such as promoting natural regeneration, protecting pollinators, and encouraging community-based conservation can help restore genetic stability and connectivity among populations.

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