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Cryptic Maternal Lineages in Nigerian *Pterocarpus santalinoides*: Morphology–Genetics Discordance Across Rainforest-Savanna Ecozones

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ABSTRACT
Habitat fragmentation across Nigeria's rainforest–savanna ecozones threatens multipurpose trees like *Pterocarpus santalinoides*, yet morphological stasis often obscures underlying evolutionary divergence. This study integrates vegetative morphology, chloroplast microsatellites (*cpSSR*), and nuclear *AFLP* markers to resolve population structure across five Southwest Nigerian locations. Analysis of 30 vegetative descriptors revealed 100% phenotypic uniformity (*Jaccard similarity* = 1.00) across all sites, failing to distinguish ecological or geographic origins. In contrast, *cpSSR* data uncovered three strictly partitioned maternal lineages (*TH4, TH5, TH6*), with Olokemeji identified as a critical admixture hub exhibiting a haplotype diversity (H_d) of 0.733. *AFLP* markers revealed high within-population cohesion (≥92.9%) and moderate-to-high inter-population connectivity (74.3–98.6%), indicating extensive pollen-mediated gene flow between savanna and rainforest sites, with the exception of the relatively isolated Ikire lineage. This morphology–genetics discordance (m^2 = 0.73, p = 0.002) highlights asymmetric gene flow: widespread pollen dispersal homogenizes the nuclear genome while restricted seed movement preserves cryptic maternal lineages. Conservation frameworks must transcend phenotypic assessments to prioritize these Evolutionary Significant Units, safeguarding maternal diversity and critical gene-flow corridors in West Africa's fragmented landscapes.

Keywords: *Pterocarpus Santalinoides*, Cryptic Genetic Diversity, Morphology–Genetics Discordance, Asymmetric Gene Flow, Maternal Lineages (*Cpssr*), Conservation Genetics

INTRODUCTION

West Africa's rainforest–savanna mosaic represents one of the continent's most biodiverse yet heavily fragmented ecological transitions, shaped by historical climate oscillations and accelerating anthropogenic land-use change (Mayaux *et al*., 2013; Amani *et al*., 2020). Within this dynamic landscape, multipurpose tree genera such as *Pterocarpus* play pivotal roles in ecosystem functioning, soil stabilization, and rural livelihoods through timber, non-timber forest products, and traditional medicine (Madubuike *et al*., 2023; FAO, 2020). *Pterocarpus santalinoides* L'Hér. ex DC., a deciduous canopy species endemic to West African lowland forests and ecotonal zones, is particularly valued for its durable wood and pharmacological properties. However, escalating deforestation, agricultural expansion, and climate variability have severely reduced its natural populations, raising urgent concerns about genetic erosion and long-term adaptive capacity (Lovett *et al*., 2000; Sen & Ravikanth, 2022).

Despite their ecological and economic importance, many tropical tree species exhibit remarkable morphological uniformity across heterogeneous environments, complicating taxonomic delimitation and conservation prioritization. Phenotypic traits in *Pterocarpus* are often highly plastic, responding to microclimatic gradients and soil heterogeneity rather than reflecting underlying genetic divergence (Bickford *et al.,* 2007; Foden *et al*., 2019). Consequently, reliance on vegetative descriptors alone frequently masks cryptic population structure, leading to underestimation of evolutionary significant units (ESUs) and inappropriate management boundaries (Moritz *et al.,* 2004; Petit *et al.,* 2005). In fragmented landscapes, this morphological stasis can obscure critical patterns of lineage isolation, demographic bottlenecks, and adaptive potential, necessitating molecular approaches to reveal hidden diversity.

Integrating organellar and nuclear molecular markers provides a powerful framework for disentangling complex gene flow dynamics and historical biogeography in tropical trees. Chloroplast microsatellites (*cpSSR*), which are predominantly maternally inherited in angiosperms, track seed-mediated dispersal and historical maternal lineages, while nuclear markers such as amplified fragment length polymorphisms (*AFLP*) capture biparental inheritance and contemporary pollen-mediated connectivity (Weising & Gardner, 1999; Vos *et al*., 1995; Petit *et al.,* 2005). Discordance between *cpSSR* and nuclear markers often reveals asymmetric gene flow, where extensive pollen movement homogenizes nuclear genomes while restricted seed dispersal preserves deep maternal divergence (Austerlitz *et al.,* 2004; Dick *et al.,* 2008). Such multi-locus approaches are increasingly essential for delineating conservation units, assessing landscape connectivity, and designing evidence-based restoration strategies in ecologically sensitive transition zones.

Despite the ecological prominence of *P. santalinoides* in Nigeria's Southwest lowland rainforest and derived savanna ecozones, no comprehensive study has concurrently evaluated its morphological variation, maternal lineage structure, and nuclear population connectivity. Existing taxonomic and conservation assessments rely heavily on phenotypic characters, which may overlook cryptic genetic differentiation and misrepresent gene flow patterns in

fragmented habitats. Furthermore, the rapid pace of land-cover change in the region demands urgent, genetically informed conservation planning to prevent irreversible loss of evolutionary potential. By integrating vegetative morphology, *cpSSR* haplotypes, and *AFLP* profiles, this study addresses a critical knowledge gap in West African forest genetics and provides a robust baseline for prioritizing populations, identifying gene-flow corridors, and guiding sustainable management of *P. santalinoides* under escalating environmental pressure. This study aims to assess genetic diversity, population structure, and morphology–genetics discordance in *Pterocarpus santalinoides* across Nigeria's rainforest–savanna ecozones through an integrated morphological and molecular approach.

The specific objectives are to:

i. Evaluate vegetative morphological variation and quantify phenotypic uniformity across sampled populations.
ii. Characterise maternal lineage partitioning using chloroplast microsatellite *(cpSSR*) haplotypes.
iii. Assess nuclear population structure and connectivity using *AFLP* markers; and
iv. Synthesise concordance and discordance patterns across morphological, organellar, and nuclear datasets to guide conservation prioritisation and landscape management.

MATERIALS AND METHODS

Study Area and Ecological Context

The study was conducted in Southwest Nigeria (Longitude 3°31'1''E–5°38'45''E; Latitude 7°23'2''N–7°44'32''N), encompassing two major ecological zones: lowland rainforest and derived savanna. The region experiences a bimodal rainfall pattern with mean annual temperatures ranging from 22°C to 39°C and relative humidity between 49.1% and 86.0%. Elevations span 250–360 m above sea level (Gbode *et al.,* 2019). The lowland rainforest zone, covering parts of Ekiti, Ondo, and southern Osun states, is characterized by dense multi-layered canopy, high species richness, and relatively stable microclimates. The derived savanna zone, extending across northern Osun, Oyo, and Ogun States, features open grassland matrices with scattered tree stands, higher solar radiation, and seasonal moisture stress. Over the past decade, rapid population growth (~60 million inhabitants), agricultural expansion, and illegal timber harvesting have accelerated habitat fragmentation, altering hydrological regimes and disrupting ecological connectivity across the forest–savanna transition zone.

Reconnaissance Surveys and Community Engagement

Preliminary field reconnaissance was conducted across forest reserves, major herbaria, and institutional conservation sites in collaboration with the Departments of Botany and Forest Resources Management at the University of Ibadan, the Forest Research Institute of Nigeria (FRIN), and 25 local communities. The survey aimed to document indigenous knowledge regarding *Pterocarpus* distribution, ecological status, and utilization patterns. Participant eligibility criteria included: (i) ≥10 years of continuous residence in the study area, (ii) age ≥25 years, (iii) demonstrated expertise in ethnobotany, forestry, or agronomy, and (iv) active involvement in traditional herbal practice, timber trade, or conservation management.

Informed Consent Framework

All survey protocols strictly adhered to the established ethical guidelines for community-engaged research and best international standard practices. Prior to conducting field data collection and ethnobotanical interviewing, explicit informed consent was formally obtained from each participant. Due to varying literacy levels among some rural community contacts, consent was obtained through verbal affirmation. The research objectives, data utilization, none-commercial use, no compensation, anonymity identity and voluntary participation rights were clearly communicated in the local language (primarily Yoruba) to guarantee comprehension.

Plant Sampling and Taxonomic Authentication

Field collections were conducted across GPS-mapped forest reserves, institutional campuses, botanical gardens, and agricultural boundaries. A purposive sampling strategy was employed to target all accessible mature stands within each location, with a minimum of five and a maximum of ten individuals sampled per site. For each individual, twigs bearing mature leaves, stem sections, and bark fragments were collected for morphological documentation. Geographic coordinates were recorded using GPS-enabled Android devices (WGS84 datum). Five young, fully expanded leaves per tree were immediately desiccated in silica gel for DNA preservation. Voucher specimens were deposited at the University of Ibadan Herbarium (UIH), where taxonomic authentication was verified by recognized plant taxonomists using standard dichotomous keys and comparative reference collections.

Morphological Characterization and Binary Scoring

Vegetative traits were examined in the laboratory using naked-eye observation and a 10× hand lens. Thirty descriptors spanning leaf architecture, surface properties, venation, petiole morphology, apex/base configuration, and stem/bark characteristics were recorded per individual. Traits were scored using a binary system (1 = present/expressed; 0 = absent/unexpressed) following standardized botanical documentation protocols. Descriptors included leaf type, texture, surface shine, phyllotaxy, venation pattern, petiole length, petiolule length, pinnation type, lamina shape, margin type, apex form, base morphology, stalk nature, bark colour, and exfoliation pattern. All scoring was performed blind to geographic origin to minimize observer bias, and discrepancies were resolved by consensus among two independent taxonomists.

Molecular Laboratory Procedures

DNA Extraction and Quality Assessment

Genomic DNA was extracted from ~1 cm² silica-dried leaf tissue using the DNeasy 96 Plant Kit (QIAGEN, Hilden, Germany) at the Department of Forest Genetics and Forest Tree Breeding, University of Göttingen, Germany. DNA quality and integrity were verified on 1.5% agarose gels stained with GelRed™. Quantification was performed using a NanoDrop spectrophotometer, and extracts were diluted to working concentrations (1:10 to 1:100) based on initial yield to optimize downstream PCR efficiency. Negative extraction controls were included in each batch to monitor contamination.

Chloroplast Microsatellite (cpSSR) Genotyping

Ten universal cpSSR primers (Weising & Gardner, 1999) were screened for transferability and polymorphism. Four loci (*CCMP2, CCMP3, CCMP6, CCMP7*/*CCMP10*) consistently amplified across all *Pterocarpus* samples and were retained

for population-level analysis. PCR reactions were performed in 14 µL volumes containing: 1 µL template DNA (~0.6 ng/µL), 1.5 µL 10× Reaction Buffer B, 1.5 µL $MgCl_2$ (25 mM), 1 µL dNTPs (2.5 mM each), 0.2 µL HOT FIREPol® DNA Polymerase (5 U/µL), 1 µL forward primer (5 pmol/µL), 1 µL reverse primer (5 pmol/µL; 6-FAM or 6-HEX labelled), and 6.8 µL nuclease-free water. Thermal cycling: initial denaturation at 95°C for 15 min; 25 cycles of 94°C (1 min), 50°C (1 min), 72°C (1 min); final extension at 72°C for 20 min. Amplified fragments were separated on an ABI 3130xl Genetic Analyzer using GS-500 ROX internal size standard. Peak calling, allele sizing, and haplotype assignment were performed in GeneMapper® v4.0 (Applied Biosystems). Maternal haplotypes (*TH1–TH6*) were reconstructed from multilocus cpSSR profiles.

AFLP Marker Amplification and Scoring

AFLP fingerprinting followed Vos *et al.* (1995) with minor optimisations. Genomic DNA (200 ng) was double-digested with EcoRI and MseI, followed by adapter ligation. Pre-selective amplification used EcoRI+0/MseI+3 primers, while selective amplification employed fluorescently labelled EcoRI+3 (E35; 6-FAM) and MseI+3 (M63) primers. Touch-down PCR: 95°C for 15 min; 10 cycles of 94°C (1 min), annealing from 55°C to 45°C (−1°C/cycle, 1 min), 72°C (1 min); 25 cycles of 94°C (1 min), 45°C (1 min), 72°C (1 min); final extension at 72°C for 20 min. PCR products were resolved on 15% polyacrylamide gels in 1× TAE buffer, stained with ethidium bromide, and visualized under UV transillumination. Bands were scored as binary presence (1) or absence (0) across 70 reproducible loci. Only clear, unambiguous fragments were retained; monomorphic or smeared bands were excluded.

Data Analysis and Population Genetic Statistics

Morphological binary matrices were analyzed using Jaccard's similarity coefficient and visualised via Principal Coordinates Analysis (PCoA). cpSSR haplotype frequencies, haplotype diversity (*Hd*), and nucleotide diversity (π) were computed in DnaSP v6. Population structure and maternal lineage partitioning were assessed through haplotype network reconstruction (TCS algorithm) and analysis of molecular variance (AMOVA) in Arlequin v3.5. *AFLP* binary data were subjected to Nei's genetic distance, UPGMA clustering, and Bayesian population assignment (STRUCTURE v2.3.4; K=1–6, 100,000 burn-in, 500,000 MCMC replicates). Discriminant Analysis of Principal Components (DAPC) was performed in R (`adegenet` package) to identify nuclear genetic clusters without Hardy–Weinberg assumptions. Concordance between morphological, *cpSSR*, and *AFLP* datasets was evaluated using Procrustes analysis and Mantel tests (9,999 permutations). All statistical thresholds were set at α=0.05. Raw *AFLP* matrices, cpSSR haplotype calls, and morphological scores are securely archived.

RESULTS AND DISCUSSION

Results

Analyses focused on 19 confirmed *Pterocarpus santalinoides* individuals sampled across five strategically selected locations in Southwest Nigeria: Ikire (n=4), Olokemeji (n=5), OAU (n=3), FRIN (n=1), and University of Ibadan (UI) (n=6). All results integrate vegetative morphology, maternally inherited chloroplast microsatellites (*cpSSR*), and biparentally inherited nuclear *AFLP* markers.

Phenotypic Stasis: Morphological Uniformity

Vegetative trait assessment across 30 binary descriptors revealed complete phenotypic uniformity among all sampled populations. Despite the sharp ecological transition between the lowland rainforest (OAU, Ikire) and the derived savanna (UI, FRIN, Olokemeji), all 19 population representative samples exhibited identical scores for leaf architecture, surface properties, and bark characteristics.

Table 1: Qualitative Vegetative Descriptors Recorded Across Five Sampling Locations in Southwest Nigeria

Character Category	Traits Present (Score=1)	Traits Absent (Score=0)
Leaf Architecture	Compound, Odd-pinnate, Ovate shape, Entire margin, Acuminate apex	Obovate, Oblong, Undulated margin, Retuse apex
Leaf Surface	Smooth texture, Shining surface, Reticulate venation	Rough texture, Dull surface, Parallel venation
Stem/Bark Traits	Smooth stalk, Grey-striped bark, Peeled bark	Spiked stalk, Flaked bark, Dark-coloured bark

This Table Summarizes the 30 Binary-Scored Traits Used to Assess Phenotypic Variation. Note: All 19 Individuals Across Rainforest and Savanna Ecotones Exhibited 100% Uniformity (Jaccard Similarity = 1.00).

Principal coordinate analysis (*PCoA*) of the morphological matrix collapsed into a single undifferentiated cluster (Jaccard similarity = 1.00), confirming that vegetative morphology alone fails to resolve population structure or geographic provenance in this species.

Maternal Lineage Partitioning (cpSSR)

In contrast to the morphological stasis, five polymorphic *cpSSR* markers (*CCMP2, 3, 6, 7, 10*) resolved three distinct maternal haplotypes (*TH4, TH5, TH6*) with strict geographic vicariance (Table 2). The spatial distribution of these lineages aligns with the vertical ecological transition of Southwest Nigeria (Fig. 1), where *TH4* and *TH5* are localized to specific anchors while *TH6* spans the ecozone. Notably, Olokemeji emerged as the primary evolutionary hub, functioning as a contact zone for disparate maternal lineages with a haplotype diversity (H_d) of 0.733.

Table 2: Integrated *cpSSR* Haplotype Distribution and Conservation Priority

Population	Ecological Zone	Dominant Haplotype	Diagnostic CCMP Loci	Haplotype Diversity (H_d)	Conservation Priority
Ikire	Rainforest	*TH4* (100%)	*CCMP2, CCMP3*	0.000	**High (Maternal Isolate)
UI	Savanna	*TH5* (100%)	*CCMP6*	0.000	**High (Unique ESU)
OAU	Rainforest	*TH6* (100%)	*CCMP*2, 3, 6	0.000	*Moderate (Resilient)
FRIN	Savanna	*TH6* (100%)	*CCMP*2, 3, 6	0.000	* Moderate (Resilient)

Population	Ecological Zone	Dominant Haplotype	Diagnostic CCMP Loci	Haplotype Diversity (H_d)	Conservation Priority
Olokemeji	Savanna-edge	*TH4* (60%) + *TH5* (40%)	Admixture	0.733	***Highest (Evolutionary Hub)

Data Illustrates the Strict Geographic Partitioning of Maternal Lineages and the Unique Admixture Zone at Olokemeji. Note: Haplotype Diversity (H_d) was Zero for Fixed Populations and Highest (0.733) at the Olokemeji Contact Zone. Priority Levels are Based on the Presence of Unique or Admixed Evolutionary Significant Units (ESUs).

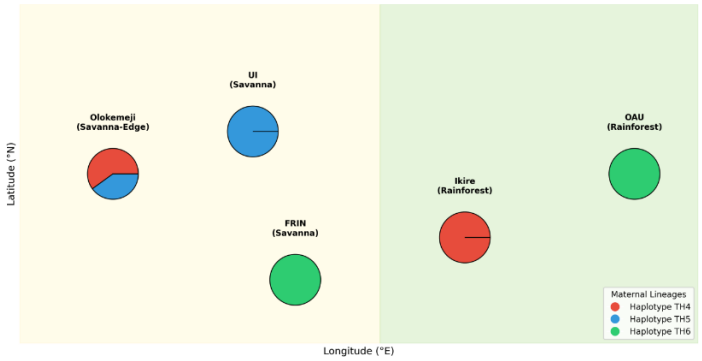

Figure 1: Spatial Distribution of *P. santalinoides* Maternal Lineages Across Nigeria's Ecological Transition

Map illustrating the geographic vicariance of chloroplast haplotypes. Vertical shading denotes the transition from the derived savanna (yellow) in the west to the lowland rainforest (green) in the east. Pie charts represent local haplotype frequencies, highlighting Olokemeji as a critical admixture zone situated at the savanna-edge boundary

Nuclear Population Structure and Connectivity (AFLP)

AFLP fingerprinting (70 loci) revealed high within-location cohesion (≥ 92.9%) and extensive nuclear connectivity among most sites. The highest nuclear similarity occurred between OAU and FRIN (98.6%), while Ikire remained the most distinct nuclear lineage (74.3–84.3% similarity to others).

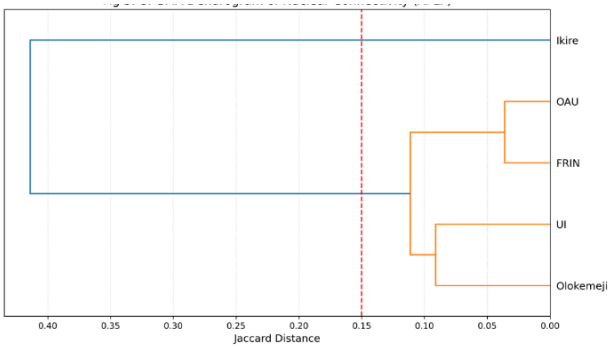

Figure 2: AFLP UPGMA Dendrogram of Nuclear Connectivity

Dendrogram based on Jaccard's similarity coefficient for 70 AFLP loci. The clustering shows high nuclear similarity (≥ 93%) among UI, Olokemeji, OAU, and FRIN, while the Ikire lineage remains relatively distinct. Note: This high connectivity contrasts with the cpSSR data, indicating widespread pollen-mediated gene flow across ecological boundaries

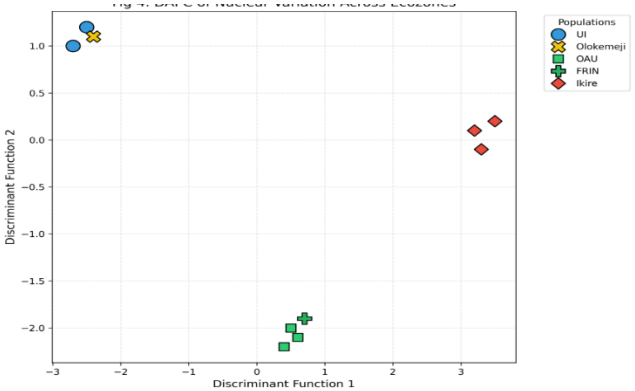

Figure 3: Discriminant Analysis of Principal Components (DAPC)

Scatter plot of nuclear genetic structure based on AFLP data. Individuals are colored by population of origin. The proximity of clusters for UI, Olokemeji, OAU, and FRIN illustrates landscape-scale nuclear homogenization. Note: The separation of the Ikire cluster (red) reinforces its status as a significant nuclear and maternal isolate.

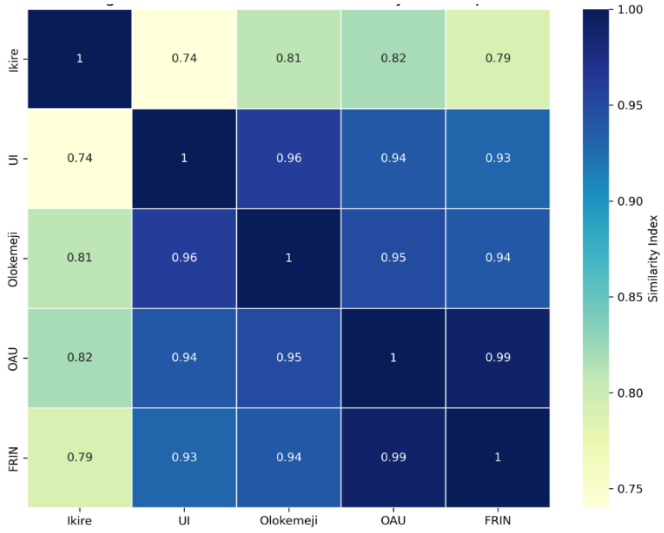

Figure 4: Integrated Discordance and Asymmetric Gene Flow Model

Conceptual summary of the morphology–genetics discordance in P. santalinoides. A tripartite visual comparing (A) phenotypic stasis, (B) maternal vicariance via restricted seed flow, and (C) nuclear connectivity via widespread pollen flow. Note**:** This model provides the evidence base for prioritizing "Evolutionary Hubs" like Olokemeji in conservation planning

Integrated Discordance and Asymmetric Gene Flow

Procrustes and Mantel analyses revealed significant discordance among the three data layers (m^2 = 0.73, p = 0.002). This tripartite pattern (Table 3) identifies a clear signature of Asymmetric Gene Flow: widespread pollen dispersal maintains nuclear homogeneity while restricted seed movement preserves cryptic maternal lineages.

Table 3: Marker Performance and Evolutionary-Conservation Utility Matrix

Marker Type	Resolution	Inheritance	Gene Flow Tracked	Key Insight
Morphology	Low	Polygenic	N/A	Stabilising selection buffers phenotype.
cpSSR	High	Maternal (Seed)	Restricted	Defines deep maternal ESUs.
AFLP	Very High	Biparental	Pollen + Seed	Highlights landscape-scale connectivity.

This Synthesis Explains the Biological Resolution Provided by Each Marker type in Tracking Different Gene-Flow Components. Note: High Discordance (m^2 = 0.73) Between Markers Highlights the Decoupling of Phenotype, Seed-Mediated Dispersal, and Pollen-Mediated Connectivity.

Discussion

This study provides the first integrated assessment of vegetative morphology, chloroplast microsatellite (*cpSSR*) haplotypes, and nuclear *AFLP* profiles for *Pterocarpus santalinoides* across Nigeria's Southwest lowland rainforest and derived savanna ecotones. Our findings reveal a complex evolutionary narrative characterized by morphological stasis masking cryptic maternal lineage divergence, while nuclear markers indicate significant pollen-mediated connectivity. This discordance challenges phenotype-based conservation assessments and underscores the critical need for multi-locus genomic baselines in managing West African tropical trees.

The 100% morphological uniformity across Southwest Nigerian *P. santalinoides* (Table 1) presents a stark contrast to the deep genetic partitioning identified via molecular markers. This phenomenon, known as phenotypic stasis, is frequently observed in tropical canopy trees where stabilizing selection maintains an "optimal" architecture despite significant evolutionary divergence (Bickford *et al.,* 2007; Foden *et al.,* 2019). Our results confirm that relying on vegetative descriptors alone leads to a critical underestimation of Evolutionary Significant Units (ESUs), as the phenotype is effectively decoupled from both organellar and nuclear variation (Petit *et al.,* 2005).

The significant discordance between *cpSSR* and *AFLP* markers (m^2 = 0.73, p = 0.002) provides empirical evidence for asymmetric gene flow. The high nuclear similarity (up to 98.6%) among UI, Olokemeji, OAU, and FRIN suggests extensive pollen dispersal. This long-distance connectivity homogenizes the nuclear genome across the rainforest–savanna mosaic, a pattern consistent with other tropical legumes where specialized pollinators bridge fragmented landscapes (Dick *et al.,* 2008). Conversely, the strict geographic partitioning of maternal haplotypes (*TH4*, *TH5*, *TH6*) indicates that seed dispersal is highly localized. Similar "pollen-rich, seed-poor" dynamics have been documented in *Pterocarpus* congeners, where heavy pods or localized hydrochory limit the spread of maternal lineages (Austerlitz *et al.,* 2004). Olokemeji functions as a unique contact zone for maternal lineages. By harbouring both *TH4* (60%) and *TH5* (40%), it serves as a genetic reservoir that facilitates the meeting of disparate evolutionary histories (Table 2). In fragmented ecotones, such "admixture hubs" are vital for maintaining high haplotype diversity (H_d = 0.733), providing the raw genetic material necessary for adaptation to accelerating climate variability (Moritz, 2004; Mayaux *et al.,* 2013). Protecting Olokemeji is not merely about preserving

individuals, but about safeguarding a dynamic evolutionary process.

The identification of the UI and OAU populations as strategic genetic "*anchors*" offers critical insights into the ecozonal adaptive capacity of *P. santalinoides*. The UI population represents a specialised savanna *ESU* possessing the distinct maternal haplotype *TH5*, whereas the OAU and FRIN populations harbour the widespread *TH6* lineage. The uninterrupted distribution of the *TH6* lineage across both the humid lowland rainforest and the dry derived savanna environments implies a robust plastic resilience and broad environmental tolerance.

This phenomenon of ecozonal persistence aligns closely with regional observations across West Africa's changing landscapes. In Nigerian savanna ecosystems, structural and floristic assessments confirm that the Fabaceae family remains a highly dominant and frequent floristic component driving canopy composition across protected ecological corridors (Iyagin *et al*., 2026). Furthermore, this adaptive pattern matches macro-ecological baselines indicating that certain *Pterocarpus* congeners utilise wide physiological thresholds to buffer their core phenotypes against fluctuating microclimatic stress (Amani *et al.,* 2020). Because the *TH6* lineage bridges distinct environmental regimes smoothly without suffering a visible loss of localised fitness, these multi-zone populations should serve as prime germplasm sources for "*assisted migration*" trials and targeted ecological restoration networks.

Conversely, the Ikire population introduces a highly localised conservation challenge that demands unique management protocols. Operating as a fixed maternal isolate (100% TH4) with heavily restricted nuclear connectivity to all other sites (74.3%), this population stands out as a clear historical vicariance event. Such sharp morphology–genetics and organellar–nuclear discordance—where extensive landscape-scale gene flow fails to homogenise deep maternal lineages—is a classic signature of "*pollen-rich, seed-poor*" dispersal syndrome (Sen & Ravikanth, 2022).

The complete fixation of *TH4* within Ikire accentuates its high vulnerability to genetic drift and localised human disturbances. Recent comparative baselines from fragmented Nigerian landscapes confirm that anthropogenic disturbances severely fracture floristic diversity and diminish ecosystem recovery compared to protected forest environments (Sani *et al.,* 2026). Because the elimination of this single canopy stand would cause the permanent extirpation of the *TH4* lineage from the Southwest Nigerian rainforest zone, it is essential that conservation frameworks transcend broad phenotypic uniformities and prioritize these hidden, cryptic maternal isolates to sustain the long-term evolutionary potential of the species (Lovett *et al*., 2000).

CONCLUSION

The integrated analysis of *Pterocarpus santalinoides* across Nigeria's rainforest–savanna ecotones reveals a profound discordance between outward appearance and inward genetic structure. While 100% morphological uniformity suggests a single, cohesive population, molecular data uncover a complex landscape of cryptic maternal lineages and asymmetric gene flow.

Phenotypic traits prove to be unreliable indicators of evolutionary divergence in this species, as stabilizing selection within the ecotone maintains morphological stasis despite deep genetic partitioning. The strict geographic isolation of haplotypes *TH4*, *TH5*, and *TH6* highlights restricted seed dispersal, which preserves unique maternal histories in localized pockets. Conversely, high nuclear similarity across most sites, reaching up to 98.6%, confirms that pollen-mediated dispersal is the primary mechanism maintaining species-wide cohesion across fragmented landscapes.

These findings necessitate immediate and targeted conservation actions to safeguard the evolutionary potential of the species. Olokemeji must be designated as a high-priority evolutionary hub due to its unique role as a lineage contact zone harbouring multiple haplotypes. Furthermore, Ikire and UI should be managed as distinct Evolutionary Significant Units to prevent the loss of unique maternal diversity trapped in these isolates. Ultimately, conservation frameworks in West Africa must transcend phenotypic assessments and prioritize the protection of cryptic lineages and gene-flow corridors to ensure resilience against escalating anthropogenic and climatic pressures.

Data Availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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