

Review

Unlocking the Hidden Biodiversity Trove: Gaps, Insights and Perspectives from DNA Barcoding in Nigeria

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Abstract

Global biodiversity is declining, while tropical regions remain disproportionately understudied despite their richness. Nigeria exemplifies one of Africa's complex and rich ecological zones, yet it remains poorly represented by molecular data, despite the availability of advanced techniques such as DNA barcoding. Here, we assess the current state of DNA barcoding in Nigeria and how well these efforts capture the national biological diversity. Nigeria currently has 7424 specimens and 7581 sequences in the Barcode of Life Database (BOLD), representing 1433 species—figures that fall short of the country's expected biodiversity and remain lower than those reported for several other African nations. Five standard DNA barcodes were associated with samples collected in Nigeria, including plastid *matK*, *rbcL*, and *trnL*; mitochondrial *COI*; and nuclear ITS. Our bibliographic appraisal identified only 47 publications employing DNA barcoding on samples from Nigeria, showing distinct taxonomic biases: 31 studies on Animalia (primarily fishes), followed by 7 on Plantae, 3 on Fungi, and 3 on Protista. Major drawbacks include inadequate sequencing infrastructure, limited expertise, low-quality data, insufficient funding, poor policy integration, incomplete documentation of sample provenance, publication outside globally indexed journals and unresolved issues under the Nagoya Protocol. We conclude that advancing DNA barcoding efforts requires addressing these gaps and establishing a national barcode database supported by regional molecular biodiversity centers that curate the repository to improve biodiversity discoverability in global analyses.

Keywords: genetic data coverage; molecular reference libraries; Nagoya Protocol; sampling disparities; Sustainable Development Goals



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1. Introduction

Global biodiversity is undergoing an unprecedented decline, driven by climate change, biological invasions, and accelerated anthropogenic pressures, including habitat destruction, overexploitation, and pollution [1]. Recent global assessments indicate that current extinction rates exceed background levels by more than an order of magnitude, posing significant threats to ecosystem stability and the essential services upon which human societies depend [2]. Notably, this crisis is most acute in regions with high biodiversity and endemism. Tropical and subtropical areas, particularly in the Global South, harbor a disproportionately large share of the world's biodiversity, yet are highly threatened and remain among the least studied and documented, and unknown species are often at risk [3]. As a result, many species may be lost before they are formally described, assessed, or incorporated into conservation frameworks. This challenge is further exacerbated by inadequate biodiversity documentation and characterization, driven by persistent limitations in taxonomic expertise, research infrastructure, funding, and access to modern molecular tools across much of the Global South [4]. Consequently, global biodiversity databases and reference libraries are strongly biased, with notable insufficiency of molecular data for many taxa from the Global South, thereby creating critical gaps in biodiversity knowledge.

To improve the documentation of biodiversity and save the unknown, a range of taxonomic tools has been developed, including the molecular approaches (hereafter DNA barcode) proposed by the Consortium of Barcode of Life [5]. DNA barcode uses short, standardized genetic markers including plastid regions for plants [maturase K (*matK*), and ribulose 1,5-bisphosphate carboxylase (*rbcL*)], nuclear ribosomal internal transcribed spacers (*nrITS*) for plants and fungi, and mitochondrial cytochrome c oxidase I (*COI*) Folmer fragment for animals. It is important to highlight the availability of these DNA barcodes in multiple molecular databases, such as Barcode of Life Data System (BOLD) and NCBI GenBank, although the BOLD system remains the core repository for DNA barcodes. These have emerged as a robust, complementary method for rapid and reliable species identification, effectively overcoming challenges associated with morphological similarity, phenotypic plasticity, and life-stage variation across diverse taxa [6]. More recently, the application of high-throughput molecular strategies such as superbarcodes—whole genome sequencing, e.g., Kipkoech et al. [7]—and environmental DNA (eDNA) metabarcoding have revolutionized the use of DNA barcodes. While the generation of superbarcodes involves the generation and utilization of a large amount of genomic data, such as plastomes (~120–160 kilobases in size), eDNA involves the extraction and sequencing of DNA directly from environmental samples, such as water, soil, or sediment, and has been widely recognized as a non-invasive tool that facilitates large-scale biodiversity surveys and ecological monitoring [8]. Although these DNA barcoding methods have substantially improved biodiversity assessments through barcode gaps, regions within the Global South—particularly the Afrotropics, which are both species-rich and taxonomically understudied—continue to lag behind in their application and representation. This disparity limits the full realization of molecular tools for comprehensive biodiversity documentation and constrains their effectiveness in informing conservation strategies at both regional and global scales.

Among Afrotropical regions, Nigeria stands out as one of the most biologically diverse countries, reflecting its wide range of ecosystems and biogeographical zones [9]. Extending from the mangrove forests and freshwater wetlands of the Niger Delta through lowland tropical rainforests to the Guinea and Sudan savannahs, the country supports exceptional plant and animal diversity, including numerous endemics and economically important and culturally significant taxa (Figure 1) [10]. With its ecological complexity, expansive landmass, and pronounced climatic gradients, Nigeria represents a biodiversity hotspot of significant conservation and scientific relevance. Across global genetic databases such

as GenBank and BOLD, taxa from Nigeria remain underrepresented [10], with existing molecular studies largely fragmented, taxon-specific, and geographically restricted [11]. This uneven distribution of data limits a comprehensive understanding of the breadth and depth of DNA barcoding efforts within the country. There is currently no clear, consolidated assessment of how many species have been successfully barcoded, or which taxonomic groups remain unexplored. Consequently, this inadequate systematic evaluation suggests significant knowledge gaps in the DNA barcoding landscape of Nigerian biodiversity, highlighting the need for a more integrative and comprehensive nationwide appraisal.

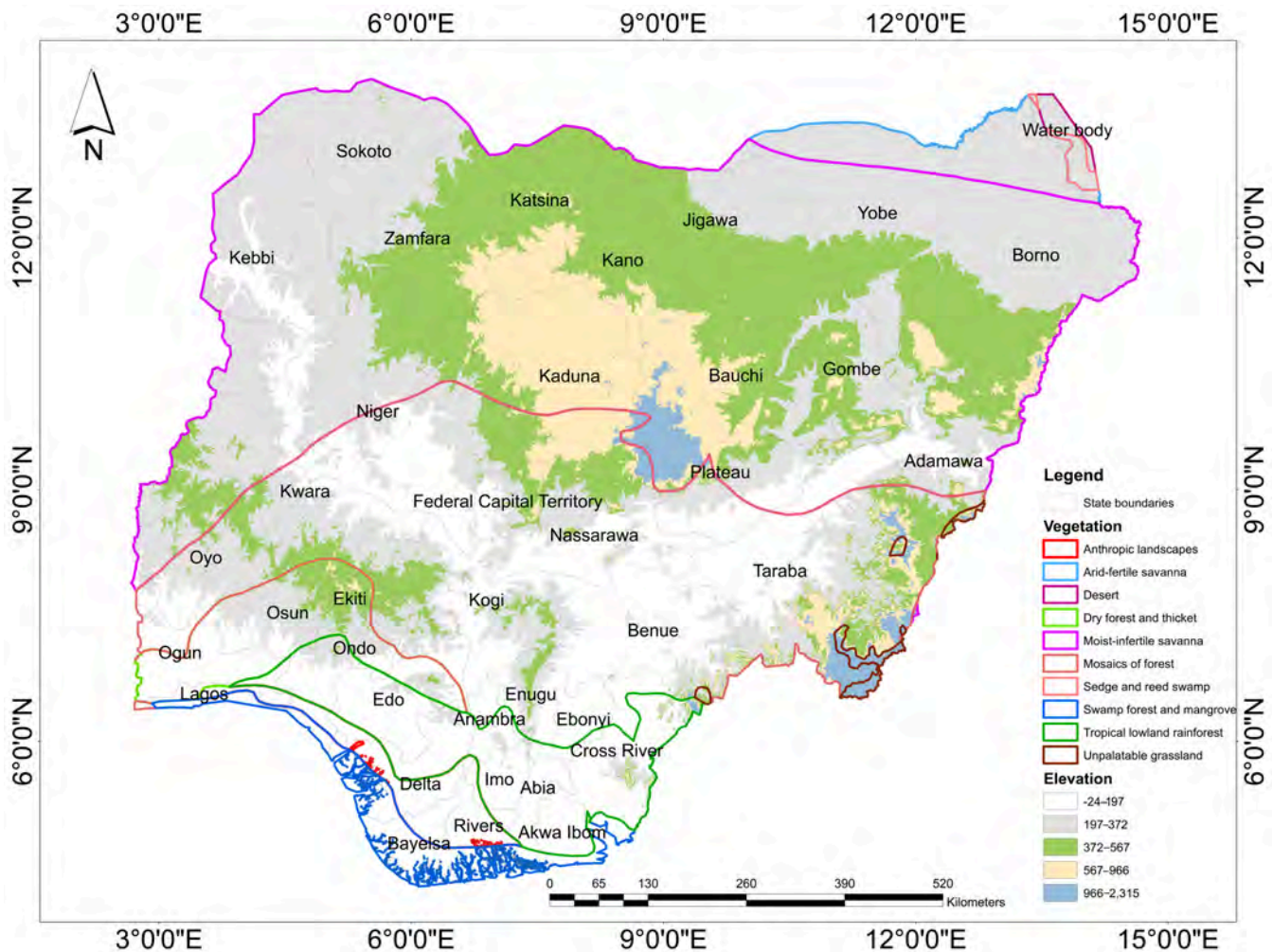


Figure 1. Distribution of vegetation types and elevation in Nigeria.

Given the high biological diversity in Nigeria that includes numerous endemic species and taxa of ecological and evolutionary significance, a comprehensive evaluation of its DNA barcoding landscape—particularly its representation in BOLD—is both timely and necessary to support improved conservation, bioresource management, and policy development. This study therefore aims to: (i) assess the current status and scope of DNA barcoding in Nigeria; (ii) identify critical gaps in genetic data coverage across major taxonomic groups; and (iii) propose an integrative framework to strengthen biodiversity documentation and molecular reference library development within the country. By addressing these gaps, this work seeks to provide a clearer understanding of the current state of DNA barcoding data in Nigeria and to guide future research priorities with targeted efforts in biodiversity documentation.

2. Overview of Nigeria's Biodiversity

2.1. Flora Diversity

Nigeria is estimated to possess one of the richest floras in West Africa, with vascular plant species richness commonly reported to range from approximately 6000 to 8000 [12,13]. This diversity reflects broad ecological gradients across Nigeria, each supporting distinct plant communities. The southern rainforest zone contributes a substantial proportion of this richness, with high levels of species turnover and localized endemism, and hosts emblematic species such as *Milicia excelsa* (Welw.) C.C.Berg and *Cola acuminata* (P.Beauv.) Schott & Endl. In contrast, the savannah regions support diverse assemblages of grasses, shrubs, and drought-adapted woody species [14,15]. Likewise, contrasting species compositions in montane and aquatic ecosystems—including littoral vegetation, freshwater, and mangrove—underscore the biodiversity in the region (e.g., Asuk et al. [16], Olowokudejo and Oyebanji [17], Oyebanji et al. [18]). Although these estimates show a rich floral composition, they are likely still underestimated due to uneven sampling effort, taxonomic uncertainties, and limited application of modern identification tools [4]. Many plant groups, particularly understory species, grasses, and non-timber forest plants, remain poorly documented or are represented only by old herbarium records. Moreover, lower green plants and fungi receive comparatively little attention, resulting in significant gaps in our understanding of their diversity. Furthermore, the scarcity of molecular reference data for Nigerian plants could underscore inaccurate species delimitation and obscure cryptic diversity. As a result, current estimates should be regarded as conservative, underscoring the need for comprehensive floristic surveys and integrative taxonomic approaches to better resolve the full extent of Nigeria's plant biodiversity.

Nigeria's plant diversity constitutes a foundational component of the socio-ecological system, delivering multiple ecosystem services across provisioning, regulating, and cultural domains. Medicinal plants exemplify critical provisioning services, sustaining primary healthcare needs for over 70% of the population and contributing to the treatment of infectious diseases, inflammatory conditions, and chronic ailments [19,20]. Furthermore, these plant resources contribute substantially to national and local economies through timber production, non-timber forest products, food crops, spices, fibers, and essential oils, including economically important species such as *Pentaclethra macrophylla* Benth., *Irvingia gabonensis* (Aubry-Lecomte ex O'Rorke) Baill. (bush mango), and *Garcinia kola* Heckel (bitter kola) [21,22]. Beyond material contributions, floristic diversity in Nigeria is embedded within biocultural systems, where indigenous knowledge, ethnobotanical practices, and cultural identities have co-evolved with local plant assemblages. From an evolutionary and conservation perspective, its rainforest and montane ecosystems harbor endemic and near-endemic plant species (e.g., *Garcinia smeathmannii* (Planch. & Triana) Oliv.) that contribute disproportionately to phylogenetic and functional diversity yet remain highly vulnerable due to their restricted distributions and habitat fragmentation. The erosion of these taxa, therefore, entails not only biodiversity loss but also the destabilization of linked socio-ecological processes. Within this framework, accurate taxonomic delimitation and integrative biodiversity assessment are indispensable for informing sustainable management strategies, safeguarding ecosystem service delivery, and maintaining biocultural resilience [23].

2.2. Fauna Diversity

Nigeria supports a highly diverse fauna and serves as a major center of faunal diversity in West Africa, with an estimated ca. 22,000 species [24]; the number of representative species has been previously reported by Happold et al. [25]. Quantitatively, there are numerous mammalian taxa—274 mammal species belonging to 13 orders, 42 families and

133 genera—including primates (over 20 species), ungulates, carnivores, and small mammals, many of which are strongly associated with forest and savannah habitats. Avifauna (ca. 839 species) is particularly high, with both resident and migratory species occupying forests, wetlands, savannahs, and montane regions [26]. Reptiles and amphibians (with ca. 109 snake species) are also well represented, especially in rainforest and wetland ecosystems, where high humidity and thermally stable conditions promote herpetofaunal diversity [27,28]. Insects constitute the most species-rich faunal group (ca. 20,000 species), playing essential ecological roles in pollination, nutrient cycling, and food web dynamics, yet they remain among the least studied and documented taxa in Nigeria [29].

Aquatic and coastal ecosystems also host diverse ichthyofaunal assemblages that support fisheries and livelihoods [30–32]. For instance, inland waters host families such as Cichlidae, Mormyridae, Clariidae, and Mochokidae, whereas coastal habitats harbor diverse elasmobranchs. These patterns highlight substantial ichthyofaunal diversity but also emphasize persistent knowledge gaps and limited conservation [31–33]. Within this broad faunal assemblage, Nigeria harbors numerous endangered, threatened, and endemic species of regional and global conservation concern. Forest-dependent mammals, amphibians, and birds, as well as aquatic elasmobranchs and teleosts, are particularly vulnerable to habitat loss, pollution, and fragmentation, while montane and wetland species often exhibit restricted distributions and specialized ecological requirements.

Endemism is especially pronounced in localized regions such as the Cross River and highland ecosystems, where species have evolved in relative isolation [34]. However, limited baseline data and sparse genetic documentation constrain accurate assessment of population status, species boundaries, and conservation priorities, particularly for cryptic or morphologically similar taxa. This taxonomic and genomic uncertainty biases biodiversity assessments and weakens conservation prioritization. Evidently, species of fauna face intense anthropogenic pressures—including the illegal wildlife trade, overfishing, bushmeat hunting, and unsustainable fishing—that erode population viability and ecosystem integrity [35,36]. Wildlife is often harvested for local consumption, traditional medicine, and commercial trade in unsustainable ways, while weak enforcement, limited capacity for species identification, and insufficient molecular reference data further constrain effective regulation and conservation. Strengthening biodiversity documentation and species identification frameworks, particularly through molecular approaches, is therefore essential for supporting the sustainable management and conservation of fauna in Nigeria.

3. Status of DNA Barcoding Studies in Nigeria

3.1. Assessment of Biodiversity Records in BOLD

Barcode of Life Data Systems (BOLD) play a central role in consolidating molecular data for species identification, conservation, and ecological research [37]. An assessment of Nigerian records in BOLD reveals substantial underrepresentation relative to the known biodiversity richness in the country. As of January 2026, searching the BOLD database for the keyword “Nigeria” indicates that Nigeria is represented by 7424 specimens (including fauna, flora, fungi, and protists), corresponding to 7581 DNA sequences from 1433 species (Figure 2). Compared with national biodiversity estimates, these figures suggest that BOLD contains a record for only a small fraction of the documented or estimated species. Notably, these records remain considerably lower than records available in NCBI when searched with “Nigeria, markers”, e.g., Nigeria ITS. It is parsimonious to explain this discrepancy as a demonstration of differences in data integration and submission leading to exclusion of “unverified” records, inconsistent metadata quality, and restrictions associated with data-sharing policies between the two data repositories. Consequently, many DNA barcodes

for Nigerian species that are accessible through NCBI are not fully represented in the BOLD system.

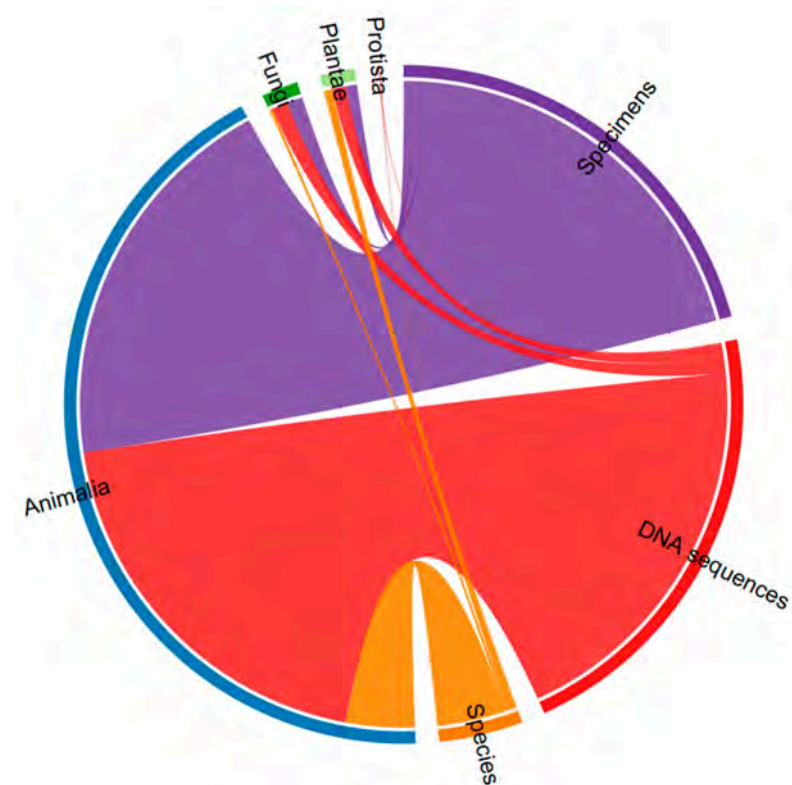


Figure 2. Taxonomic records of biodiversity from Nigeria are deposited in the BOLD systems. The data was collected from BOLD (<https://www.boldsystems.org/>). Access date: 30 January 2026.

Moreover, five types of DNA barcodes are represented in the BOLD database, including three plastid regions (*matK*, *rbcL*, and *trnL*), the nuclear ITS, and mitochondrial *COI*. Overall, the *COI* and nuclear ITS were the most frequently sequenced DNA barcodes for all the organisms, with *COI* especially prevalent in Animalia. The Barcode Index Number (BIN) system in BOLD clusters *COI*-5P sequences into RESL clusters (putative species units); BINs, therefore, provide a *COI*-based operational taxonomic framework for flagging cryptic diversity, assessing taxonomic concordance, and tracking unnamed or provisional species. The nuclear ITS was generally more frequently sequenced in fungi than in plants, whereas plastid markers such as *matK* and *rbcL* were predominantly sequenced for plant identification. Collectively, these patterns highlight a pronounced disparity between species richness and the availability of DNA barcoding efforts in Nigeria.

Although DNA barcode submissions to BOLD have recently experienced a gradual surge, a taxonomic breakdown of the records further reveals pronounced imbalances across major biological kingdoms and clear disparities in sequencing effort. We found that *COI* and nrITS are the most sequenced markers across taxa; *COI*, especially for animals, outpaced records for other organisms, and even higher records for fungi compared to Plantae are anomalous and highly unprecedented (Figure 2). These correspond to ca. 5.54% coverage of estimated animal diversity and only about 2.00% of its plant diversity, indicating substantial gaps in molecular representation. The limited representation of records is particularly striking, given their critical ecological, medicinal, and economic roles. Furthermore, reliable estimates for fungal and protist diversity in Nigeria remain lacking, signalling a broader neglect of these groups in national biodiversity research, underscoring the need for comprehensive taxonomic surveys and expanded molecular characterization of understudied taxa. These patterns also indicated that research on molecular biodiversity

has been largely shaped by opportunistic or externally driven initiatives rather than by coordinated national strategies. Such uneven taxonomic coverage constrains the utility of existing data for population-level analyses, phylogeographic studies, and informed conservation planning.

The institutional distribution of sequencing efforts and specimen deposition further reveals significant structural imbalances in Nigeria's DNA barcoding landscape. Notably, none of the DNA barcode records of animal species from Nigeria available in BOLD was generated by government agencies or sequencing facilities within the country. Most of the sequences were from foreign institutions, including the Centre for Biodiversity Genomics, the Wellcome Sanger Institute, the Royal Museum for Central Africa, and other international repositories (Figure 3). In total, 46 institutions have contributed animal samples from Nigeria, with the Swedish Museum of Natural History (SMNH) having the highest number of specimens, followed by Ebonyi State University, Nigeria (EBSU), and the Bavarian State Collection of Zoology (ZSM). This pattern indicates a strong dependence on external capacity for animal barcoding and highlights limited in-country sequencing infrastructure. In contrast, plant DNA barcode records demonstrate relatively greater involvement of Nigerian institutions, with most plant specimens deposited by local universities, particularly the University of Port Harcourt, Nigeria (UNIPORT), followed by the University of Lagos, Nigeria (UNILAG), and the Forestry Research Institute of Nigeria (FRIN). While this suggests growing domestic participation in plant barcoding, the overall dataset still reflects constrained national capacity, limited sequencing infrastructure, and weak institutional coordination. Strengthening in-country sequencing facilities, curatorial systems, and coordinated national DNA barcoding initiatives will be essential to improving the representation of Nigerian species in global genetic databases and fostering more equitable participation in biodiversity research.

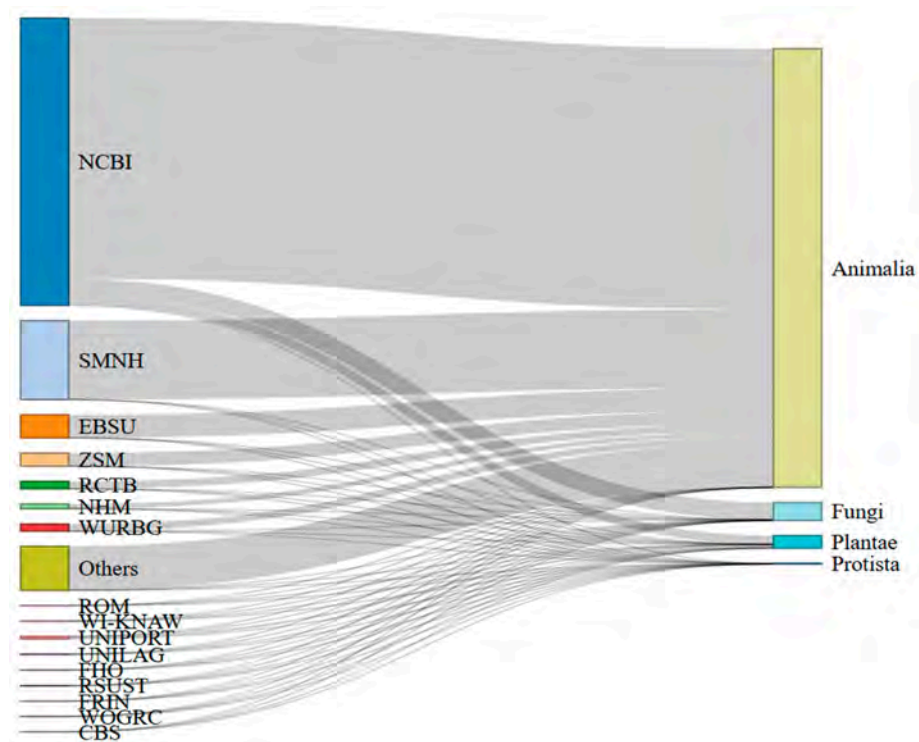


Figure 3. Assessment of institutional contributions to BOLD systems at the kingdom taxonomic rank. Abbreviations: NCBI—The National Center for Biotechnology Information; SMNH—Swedish Museum of Natural History; EBSU—Ebonyi State University; ZSM—Bavarian State Collection of Zoology; RCTB—research collection of Thierry Bouyer; NHM—University of Oslo Natural History Museum; WURBG—Wageningen University and Research Centre, Biosystematic Group; ROM—Royal

Ontario Museum; WI-KNAW—Westerdijk Fungal Biodiversity Institute; UNIPORT—University of Port Harcourt, Nigeria; UNILAG—University of Lagos, Nigeria; FHO—Daubeny Herbarium, University of Oxford; RSUST—River State University of Technology; FRIN—Forestry Research Institute of Nigeria; WOGRC—World Oomycete Genetic Resource Collection; and CBS—Centraalbureau voor Schimmelcultures. The data was collected from BOLD (<https://www.boldsystems.org/>). Access date: 30 January 2026.

A comparison of representation in the BOLD with other African countries reveals pronounced regional disparities in molecular biodiversity documentation, with Nigeria showing markedly lower presence than several nations of comparable or smaller land areas (Ghana: ~62,000 specimens and 63,366 sequences from 2158 species; Cameroon: ~3888 species; Kenya: 5390 species from >81,000 sequences; Uganda: 1567 species from ~12,000 sequences) and is dwarfed by the coverage from South Africa (776,000 specimens, 786,620 sequences, and 16,726 species) (Figure 4). The extensive molecular coverage in South Africa reflects long-standing and mature investment in biodiversity research infrastructure, coordinated national programs, and strong integration with global barcoding initiatives. Our explanation for these differences is not only the unwillingness of Nigerian researchers but also technical and institutional bottlenecks. Addressing this gap, therefore, requires pragmatic national investment in targeted and coordinated DNA barcode initiatives and the generation of high-quality DNA barcode markers alongside the standardized metadata on BOLD/NCBI for easy integration across platforms.

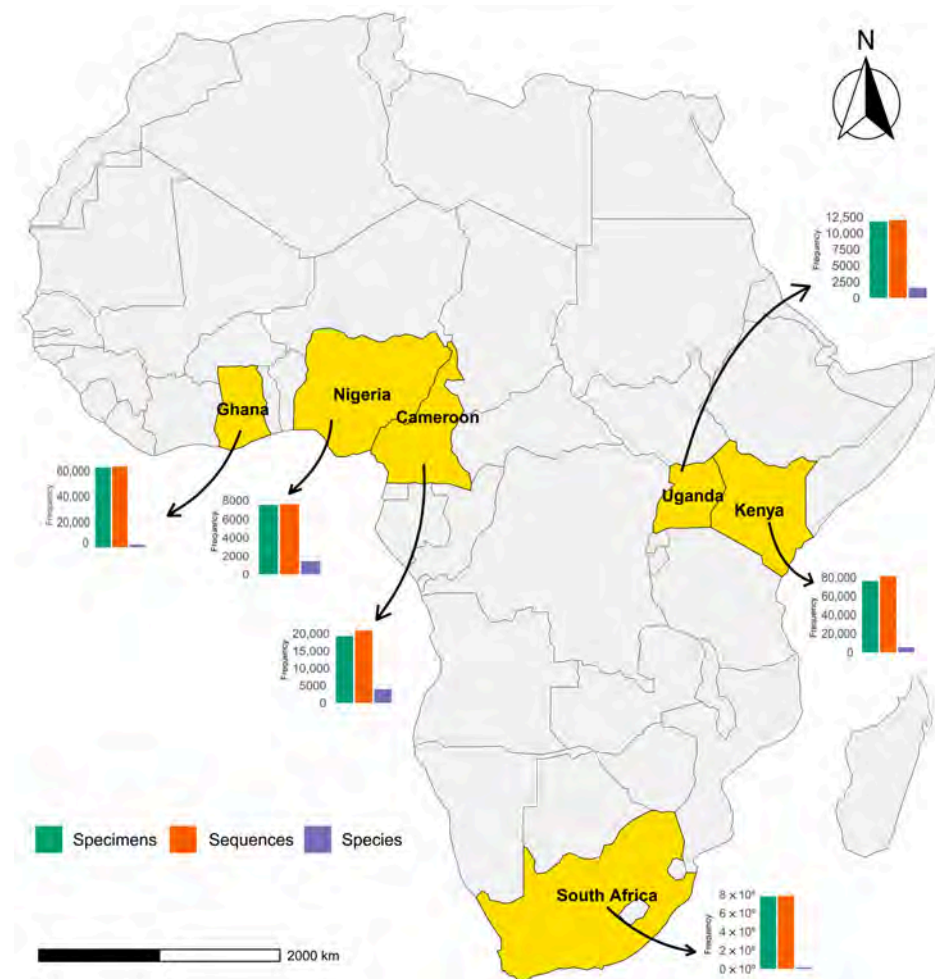


Figure 4. Comparative number of species, DNA sequences, and specimens for six African countries retrieved from BOLD. Histograms represent raw counts to highlight the sampling intensity. The data was collected from BOLD (<https://www.boldsystems.org/>). Access date: 30 January 2026.

3.2. Bibliography of DNA Barcoding-Based Studies

The application of DNA barcoding as a tool for documenting biodiversity remains limited and uneven (Table 1; Figures 5 and 6). A bibliographic assessment using the Scopus database, based on the search terms “DNA”, “DNA barcode*”, and “Nigeria”, yielded only 72 documents, highlighting the relatively small body of literature in this field (Figure 5). A closer examination of the abstracts revealed that only 47 of these documents directly addressed DNA barcoding studies conducted on Nigerian biological samples. While it is acknowledged that additional studies may exist in non-indexed local or regional journals, the low number of Scopus-indexed publications nevertheless indicates a substantial deficiency in the adoption and visibility of DNA barcoding research in the country.

Table 1. Selected examples from the literature on DNA barcoding in Nigeria.

S/N	Taxonomic Group	Family	Species	DNA Barcode	Reference
1.	Plantae	Fabaceae	<i>Senna</i> sp.	<i>psbA-trnH</i>	[38]
2.	Plantae	Fabaceae	<i>Albizia lebbek</i> , <i>Cassia fistula</i> , <i>Leucaena leucocephala</i> , <i>Parkia</i> <i>biglobosa</i> , and <i>Senna alata</i>	<i>MatK</i>	[39]
3.	Plantae	Fabaceae	<i>Senna</i> sp.	<i>matK</i> and <i>rbcL</i>	[40]
4.	Plantae	Fabaceae	<i>Isobertlinia</i> sp.	<i>rbcL</i> and <i>ITS</i>	[41]
5.	Animalia	Dasyatidae	<i>Fontitrygon garouaensis</i>	<i>COI</i>	[42]
6.	Animalia	Cichlidae	<i>Oreochromis</i> sp.	<i>COI</i>	[43]
7.	Animalia	Laelapidae	<i>Varroa destructor</i>	mtDNA <i>cox1</i>	[44]
8.	Animalia	Dasyatidae	<i>Fontitrygon</i> sp.	<i>COI</i>	[33]
9.	Animalia	Tenebrionidae	<i>Tribolium castaneum</i>	<i>COI</i>	[45]
10.	Animalia	Culicidae	<i>Anopheles gambiae</i>	<i>COI</i> and <i>ITS2</i>	[46]
11.	Animalia	Malapteruridae	<i>Malapterurus minjiriya</i>	<i>COI</i>	[47]
12.	Animalia	Apidae	<i>Apis mellifera adansonii</i>	<i>COI</i>	[48]
13.	Animalia	Schilbeidae	<i>Schilbe intermedius</i>	<i>COI</i>	[49]

Analysis of the taxonomic distribution across the 47 reviewed studies reveals a pronounced bias toward the kingdom Animalia, with 31 publications. In contrast, only seven studies focused on plant taxa, while fungi, protists, and bacteria were each represented by just three studies (Figure 6a). This uneven distribution may indicate a significant gap in taxonomic DNA barcoding research in Nigeria, particularly for plants and microbial groups. The substantial plant diversity and the critical ecological roles of fungi and microorganisms in processes such as nutrient cycling, soil health, and ecosystem functioning mean that their limited representation in molecular studies constitutes a major knowledge gap. This disparity has important implications for biodiversity conservation, agricultural sustainability, food security, and effective ecosystem monitoring.

Further examination of animal-focused studies indicates a strong research bias toward fish and other aquatic organisms, likely driven by the natural expansive hydrographic network (e.g., Niger–Benue catchment, Niger Delta, and coastal lagoons), socio-economic importance of fisheries, interests in fisheries management, aquaculture, and the assessment of aquatic biodiversity. While these studies have contributed valuable molecular data for Nigerian aquatic fauna in terms of population structuring in catfishes, cyprinids, mormyrids, and marine stingrays, the terrestrial vertebrates and invertebrates remain comparatively understudied. It is parsimonious to interpret this trend as an impediment to identifying disease vector populations (e.g., *Anopheles gambiae*), limiting the understanding of agricultural pest diversity. This is concerning because forest-dependent mammals, amphibians, insects, and other terrestrial taxa are particularly vulnerable to habitat loss, illegal trade, and cli-

mate change. Similarly, DNA barcoding studies on plant species in Nigeria remain scarce, fragmented, and taxon-specific, predominantly Fabaceae and selected medicinal species using the standard plastid and *nrITS* fragments. Our literature synthesis further indicates that existing research has often focused on very limited geographical coverage. Large portions of Nigeria's diverse flora, including endemic, threatened, and non-timber forest plant species, as well as alien species, remain unrepresented in global genetic databases. Thus, limited molecular characterization of these groups limits accurate species identification, population monitoring, and enforcement of wildlife protection regulations.

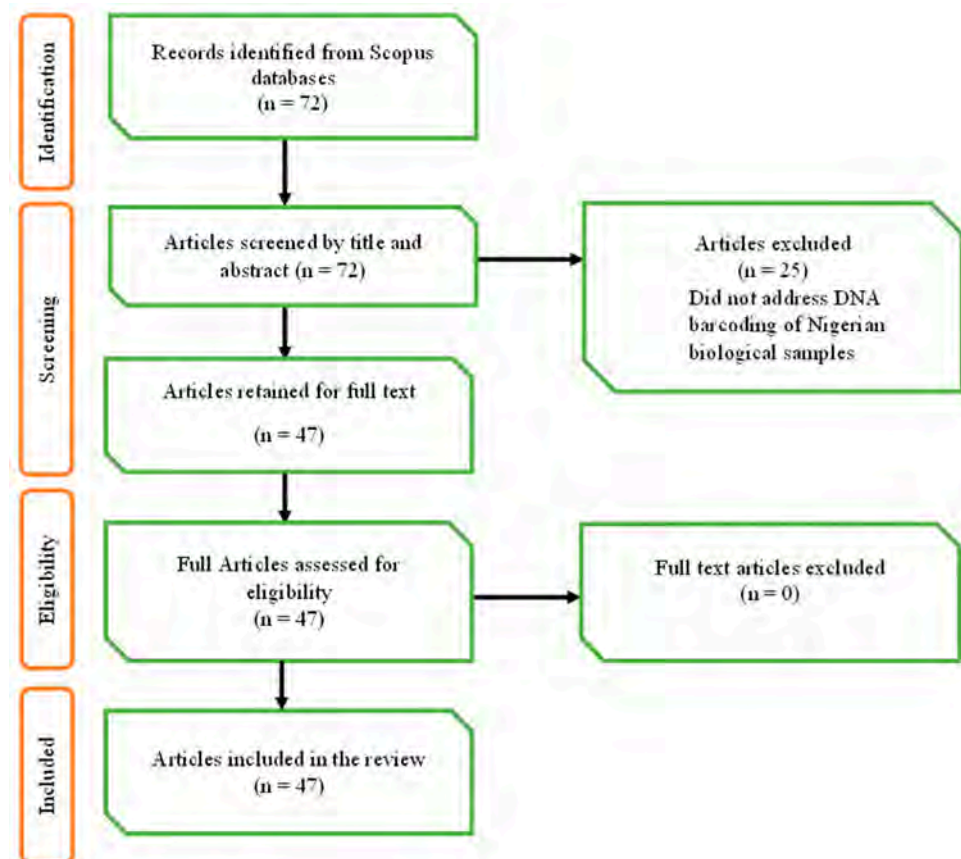


Figure 5. PRISMA flow diagram showing the identification, screening, eligibility assessment, and inclusion of publications in the bibliography.

A temporal analysis of publication output further highlights the slow, inconsistent growth of DNA barcoding research in Nigeria. The first Scopus-indexed publication on DNA barcoding of a Nigerian species appeared in 2009 (Figure 6b), marking a relatively late entry into the global barcoding movement. Publication output increased gradually over subsequent years, peaking at 8 publications in both 2020 and 2022. However, this momentum has not been sustained, with only two publications recorded in 2025 at the time of analysis. This fluctuating trend in the low visibility and discoverability of Nigerian barcode publications could be attributed to the publication of DNA barcoding papers in locally indexed journals, limited documentation of specimen provenance, and the low visibility of barcode publications.

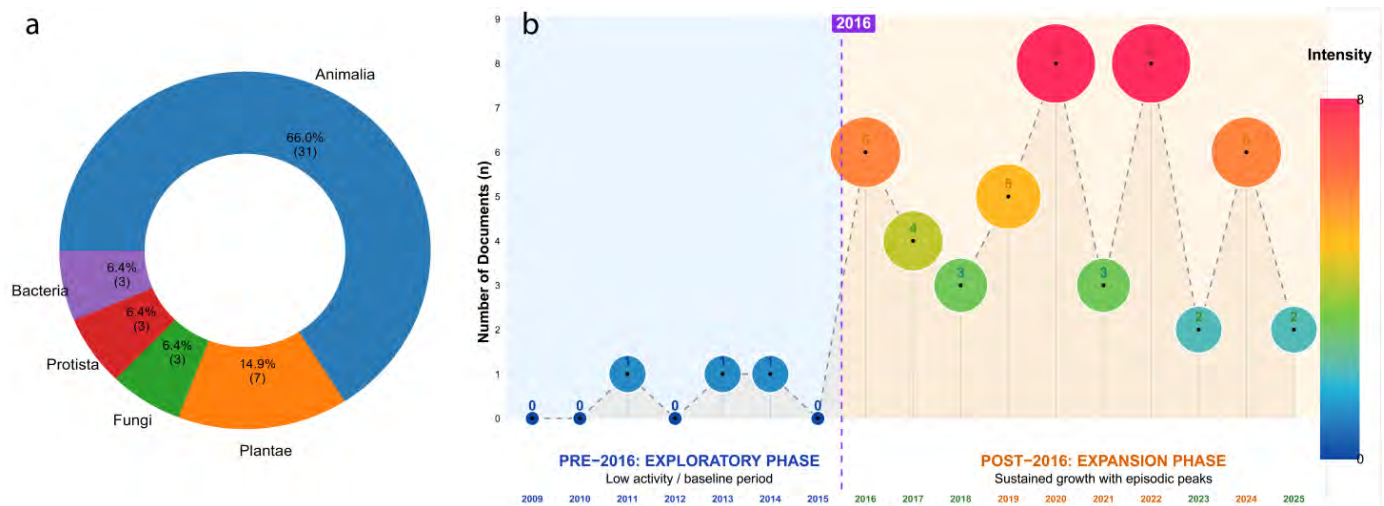


Figure 6. Bibliography of DNA barcoding-based studies. (a) Taxonomic groups and (b) temporal publication records.

Overall, the current state of DNA barcoding in Nigeria indicates a field still in its developmental stages, and the paucity of molecular reference data across plants, terrestrial animals, and microorganisms underscores the urgent need for coordinated large-scale barcoding initiatives.

4. Challenges Limiting DNA Barcoding of Nigerian Taxa

4.1. Technical and Infrastructure Constraints

Limited in-country sequencing capacity remains a major constraint to the advancement of DNA barcoding in Nigeria. High-throughput sequencing platforms, automated DNA extraction systems, and the bioinformatics infrastructure required for large-scale molecular biodiversity studies are available at only a few research centers, often with restricted capacity and inconsistent functionality. Consequently, most institutions are unable to generate DNA barcode data at scale independently, confining research efforts to small, short-term projects or externally supported collaborations. This limitation not only slows data generation but also restricts opportunities for training and capacity development in molecular taxonomy. Closely associated with this infrastructural gap is a pronounced dependence on foreign laboratories for DNA sequencing and advanced molecular analyses, which is evident in this review. As highlighted earlier, a substantial proportion of DNA barcode records for Nigerian taxa have been generated by institutions outside the country, reflecting reliance on international partners for sequencing, data processing, and deposition. While such collaborations are valuable, sustained dependence raises concerns about data sovereignty, equitable access and benefit-sharing, and the long-term sustainability of national biodiversity research. It also constrains its ability to respond efficiently to conservation priorities, biosecurity challenges, and regulatory demands, as sequencing workflows are subject to external timelines and funding cycles.

In addition, inadequate cold-chain and sample preservation infrastructure further limits the effectiveness of the DNA barcoding effort in Nigeria. The preservation of biological samples is critical for maintaining DNA integrity, particularly in tropical environments characterized by high temperatures and humidity. However, access to ultra-low-temperature storage, liquid nitrogen facilities, and a reliable power supply remains limited at many institutions and field stations. These constraints increase the risk of DNA degradation, reduce sequencing success rates, and hinder systematic sampling across diverse and remote ecosystems. Addressing these infrastructural limitations is therefore essential for improving data

quality, enhancing reproducibility, and enabling comprehensive DNA-based biodiversity assessments across Nigeria.

4.2. Human Capacity and Training Gaps

A major constraint to advancing DNA barcoding in Nigeria is the limited availability of trained molecular taxonomists capable of integrating classical taxonomy with modern genetic approaches [4,13]. Although the country has a strong foundation in morphology-based taxonomy, formal training in molecular systematics, bioinformatics, and DNA-based species delimitation remains inadequate. As a result, many researchers are either traditional taxonomists with limited molecular expertise or molecular biologists who require advanced learning in organismal taxonomy. This skills gap constrains the design, implementation, and interpretation of DNA barcoding studies and limits the development of reliable national reference libraries, which depend on accurate species identification and well-curated voucher specimens.

In addition, weak interdisciplinary collaboration among taxonomists, molecular biologists, ecologists, and bioinformaticians further impedes progress in DNA barcoding research. Effective DNA barcoding requires the integration of field sampling, taxonomic validation, laboratory sequencing, and computational analysis, yet such coordinated frameworks remain underdeveloped in many Nigerian institutions. Disciplinary silos, institutional fragmentation, and limited incentives for collaborative research restrict knowledge exchange and capacity building. Strengthening interdisciplinary collaboration through targeted training, integrated curricula, and national research networks will be critical for enhancing its capacity to generate high-quality DNA barcode data and apply them to conservation, policy, and sustainable development.

4.3. Data Quality and Misidentification

Data quality issues and species misidentification remain significant challenges in DNA barcoding, particularly in contexts where trained taxonomic expertise is limited. Such errors can propagate through reference databases, including GenBank and BOLD, compromising the reliability of downstream analyses. Evidence of these challenges has been reported in several Nigerian fauna barcoding studies [31,50], where discrepancies between query sequences and reference matches across databases have been observed. Instances in which sequences are assigned to different species names in GenBank underscore the need for rigorous taxonomic validation, integration of well-curated voucher specimens, and periodic revision of reference libraries. For example, this would be a vital complementary approach to rapidly monitor the estimated 1381 alien plant taxa—comprising 238 naturalized, 190 invasive, and 953 cultivated species—reported from Nigeria [51] and a huge contribution to the Kunming–Montreal GBF goals. Consequently, reliable biodiversity inventories depend not only on the availability of sequence data but also on the accuracy and taxonomic integrity of database records.

Once misidentified sequences are incorporated into reference libraries, they can introduce cascading errors across multiple applications, including ecological monitoring, regulatory enforcement, and forensic investigations. These errors are often difficult to detect without voucher specimens and expert taxonomic review. A persistent limitation of DNA barcoding in Nigeria is the incompleteness and insufficient curation of reference databases. For example, a study on Nigerian freshwater fishes reported that *COI*-based identification success varied markedly between databases, with 94.3% of species correctly identified using GenBank compared to 45.3% using BOLD at a $\geq 97\%$ similarity threshold, while 7.1% of cases showed conflicting species assignments between the two databases [48]. Similar challenges have been documented in Nigerian herpetofauna, where *COI* refer-

ence sequences for many African taxa remain underrepresented in both GenBank and BOLD [27].

4.4. Funding and Policy Limitations

Limited national funding remains a fundamental constraint on the advancement of DNA barcoding research in Nigeria. Biodiversity studies are often deprioritized within national science funding frameworks, with available resources largely directed toward applied sectors such as agriculture, public health, and extractive industries. Consequently, DNA barcoding initiatives frequently depend on short-term grants, international collaborations, or externally driven research agendas, which hinder continuity and long-term strategic planning. This funding gap affects all components of DNA barcoding, including field sampling, specimen curation, laboratory sequencing, data analysis, and the development and maintenance of reference libraries and publication in internationally indexed journals. Without sustained national investment, efforts to build comprehensive DNA barcode databases and develop local expertise in molecular taxonomy will remain limited. Here, we encourage funding what is necessary and not just what is famous.

In addition to financial constraints, the integration of molecular biodiversity data into conservation policy and environmental decision-making in Nigeria remains weak. Although DNA barcoding provides powerful tools for species identification, biodiversity monitoring, and enforcement of conservation regulations, its application within national biodiversity frameworks is still minimal. Conservation policies and management strategies continue to rely predominantly on traditional survey methods, with limited incorporation of genetic data to inform species assessments, habitat prioritization, or wildlife trade regulation. This disconnect reduces the perceived value of molecular approaches among policymakers and limits institutional demand for DNA-based tools. Strengthening linkages between researchers, conservation agencies, and policymakers will therefore be essential to ensure that DNA barcode data are effectively translated into actionable conservation outcomes and integrated into national environmental frameworks.

4.5. Ethical, Legal, and Biopiracy Concerns

Ethical and legal considerations play a critical role in shaping DNA barcoding research in Nigeria, particularly regarding Access and Benefit Sharing (ABS) frameworks. ABS mechanisms are designed to ensure that countries and local communities providing genetic resources receive fair and equitable benefits arising from their use. However, limited awareness of ABS principles among researchers, institutions, and local stakeholders has constrained their effective implementation. Inadequate institutional guidelines, unclear permitting procedures, and weak coordination among regulatory agencies often lead to inconsistencies in how biological samples are accessed, utilized, and shared. These challenges can erode trust among local communities, researchers, and international partners, and may hinder the development of transparent and equitable research collaborations.

Nigeria is a signatory to the Nagoya Protocol; however, translating its provisions into functional national frameworks for DNA-based research remains a significant challenge. Regulatory mechanisms governing prior informed consent, mutually agreed terms, and monitoring of genetic resource use are still evolving, and enforcement capacity remains limited. Consequently, compliance with the Nagoya Protocol is often inconsistent, particularly in projects involving international collaboration. Researchers frequently encounter uncertainties related to permitting requirements, timelines, and reporting obligations, which can delay research activities or encourage informal practices. These gaps reduce Nigeria's ability to effectively regulate access to its genetic resources and limit opportunities to leverage international partnerships for capacity building and technology transfer.

A related concern is the export of biological samples for sequencing and analysis without corresponding investment in local infrastructure or human capacity. As reflected in global genetic databases, a substantial proportion of DNA barcode data for Nigerian taxa has been generated in foreign laboratories, often without parallel development of in-country sequencing facilities or sustained training programs. While international collaborations remain essential, the continued externalization of sequencing activities risks reinforcing dependency and raises concerns regarding data ownership, equity, and biopiracy. Ensuring that the use of genetic resources is accompanied by meaningful capacity development, transparent data governance, and equitable benefit sharing is therefore essential for fostering ethical, sustainable, and nationally empowering DNA barcoding research in Nigeria.

5. Opportunities and Future Direction

5.1. Building National Reference Libraries and Consortium Initiatives

Several countries have established national DNA barcode reference systems to advance biodiversity research and conservation. For example, Australia's National Biodiversity DNA Library (NBDL) and South Africa's DNA barcoding consortium (the South African node of the International Barcode of Life, iBOL) are dedicated to generating standardized DNA barcodes across plants, animals, and microalgae to develop comprehensive, country-specific reference libraries that support species identification, biodiversity research, conservation, and biomonitoring [52,53].

Despite commendable progress in barcoding, a nationally coordinated initiative or consortium for a national DNA barcode reference library has not yet been fully established. This absence is not merely a technical gap; in essence, it poses a significant threat in light of four closely interrelated biodiversity challenges: illegal wildlife trafficking, incomplete biodiversity documentation, herbal medicine adulteration, and impaired ecosystem monitoring. Therefore, our recommendation to establish a DNA barcode library would be an invaluable step toward tackling these four problems simultaneously, since each is caused by a common factor (Figure 7). We iterate this strategy as the approach that would standardize and simultaneously strengthen species identification, traceability, and regulatory and conservation responses by providing voucher-backed reference data.

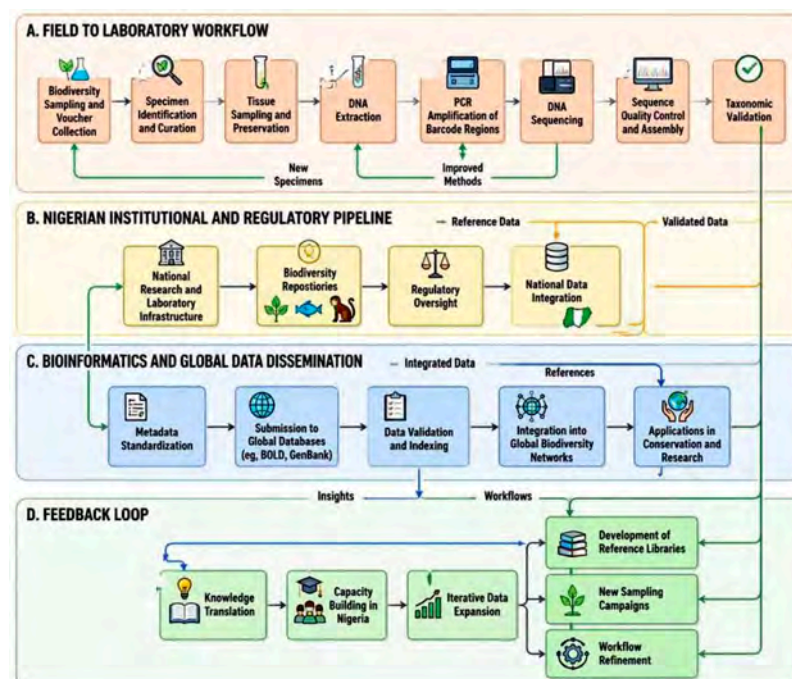


Figure 7. Proposed integrated workflow to enhance DNA barcoding activities in Nigeria.

5.2. Unified Strategies to Resolve Challenges Facing Diversity Assessment

The illegal wildlife trade requires urgent forensic identification. Nigeria is often cited as a main source and transit country for the illegal trade in wildlife (e.g., forest elephants, pangolins, and primates) [54,55]. Trafficked items such as pangolin scales, ivory carvings, or dried meat lose their physical identifying features through processing. Traditional methods are insufficient to enable conservation officers to monitor populations or conduct forensic investigations, implying that without the implementation of a DNA barcode library, it is difficult to monitor wildlife populations effectively or gather the forensic evidence that is needed to prosecute poachers and traffickers that are involved in the illegal wildlife trade, since the species can be accurately identified from a tiny tissue sample even after it has been processed. This method has proven effective for providing evidence to prosecute those who violate CITES (Convention on International Trade in Endangered Species) regulations [56,57]. For example, when DNA sequences from confiscated items are compared with regional genetic databases, matches can reveal the origin of organisms and identify “poaching hotspots,” enabling more focused law enforcement efforts. One of the frontier studies by Yeo et al. [58] on the illegal trade of African pangolins showed how DNA barcoding could help fight wildlife poaching, using DNA barcode sequences generated from portable MinION sequencing technology to identify the pangolin species present in a confiscated container in Singapore in 2019. Consequently, this approach facilitated rapid identification of pangolin species and provided valuable information on the geographical origin of confiscated pangolin scales. It also indicated a high level of poaching, which was primarily linked to West Africa, with Nigeria being one of the major source countries.

Equally pressing is the poor documentation of biodiversity, revealing a major challenge to biodiversity conservation in Nigeria. A recent investigation of Gashaka Gumti National Park highlighted “insufficient research data” as a key limitation, in addition to a “shortage of taxonomic experts” [59]. This finding reflects a worldwide issue known as the “taxonomic impediment”. It is characterized by a critical deficiency in taxonomic experts who can identify species using morphologically based techniques. Given Nigeria’s rapidly diminishing biodiversity, waiting to describe species the old way is a luxury Nigeria cannot afford. Consequently, in regions such as Cross River National Park, DNA barcoding has already uncovered potential new and undescribed moth and insect species that, despite their morphological similarity, exhibit genetic divergence, a phenomenon known as “cryptic species” [60]. DNA barcoding is now being used globally for rapid biodiversity documentation [37,61], helping countries to catalogue their biological resources more efficiently and to detect hidden diversity that would have remained unrecognized.

Herbal adulteration reveals a further dimension of this issue. Medicinal plants are widely used in Nigeria, e.g., in traditional medicine and in store-bought products. But these plants often come with a big problem: adulteration and contamination. This is a real risk for anyone relying on these remedies. Herbal products are sold with virtually no regulation, and many lack any real quality control. Sellers often substitute one quality plant species for another or label things inaccurately just to move their products. That is where DNA barcoding steps in. It is a solid way to check if medicinal plants are what people claim they are. Even if the herbs are already processed, DNA barcoding helps track down adulterants. This technology helps ensure people do not end up with toxic substitutes or ineffective herbal products. Globally, DNA has proven useful for protecting consumers and ensuring the safety of herbal products [62,63].

Difficulty in monitoring biodiversity in natural ecosystems ties together all previously mentioned challenges. Monitoring biodiversity in Nigeria’s ecosystems is a very difficult task to undertake. Some animals and plants are rare, hard to spot, or only come out at night. Others live in places people can barely reach, such as thick forests, swamps,

and deep rivers. Traditional surveys usually mean trapping, watching, or physically collecting specimens, and that takes time, money, and a lot of effort. Sometimes, it even puts the very species that are under study at risk. In addition, these traditional methods may fail to detect cryptic or low-abundance species, leading to incomplete biodiversity assessments. Metabarcoding, which employs DNA barcoding, facilitates the analysis of environmental samples, such as those collected from water or soil, to ascertain species presence in biodiversity assessments [64]. Rather than attempting to capture and identify every minute insect inhabiting a stream, researchers can filter a litre of water, sequence the entirety of its DNA (eDNA), and thereby compile a comprehensive inventory of all resident species. Consequently, this approach can offer a swift, non-invasive, and comprehensive method for monitoring the ecological status of Nigeria's rivers, forests, and parks over extended periods, thereby aiding the assessment of conservation initiatives [64,65].

Establishing a single national DNA barcode framework represents a critical opportunity to strengthen biodiversity documentation and conservation efforts in the country (Figure 7). A national DNA barcode library should prioritize endemic and threatened species, which are often the most vulnerable to extinction and are underrepresented in global genetic databases. Species with restricted distributions, particularly those in montane and wetland ecosystems, require urgent molecular characterization to support accurate identification, population monitoring, and legal protection [66]. Incorporating these taxa into a national reference system would also enhance conservation planning, wildlife trade regulation, and environmental impact assessments by providing reliable genetic tools for species verification.

5.3. Coordinated and Systematic Sampling Strategies

Structured sampling approaches that reflect ecological and biogeographical diversity are essential. Moving beyond opportunistic or taxon-specific collections toward structured, nationwide sampling would ensure more representative coverage of species and genetic variation. Such approaches would also capture intraspecific diversity and population structure, which are critical for understanding adaptive potential and resilience. Establishing standardized sampling protocols and linking regional collections to centralized national repositories would improve data quality, minimize duplication, and accelerate the development of a robust DNA barcode reference library capable of supporting research, conservation, and policy objectives at both national and global scales.

5.4. Strengthening Local Capacity

Strengthening local capacity is fundamental to advancing DNA barcoding in Nigeria and reducing long-term dependence on external expertise and infrastructure. Targeted training initiatives are needed to develop a critical mass of researchers with competencies in the fields of taxonomy, molecular laboratory techniques, bioinformatics, and biodiversity data management. Integrating molecular biodiversity components into undergraduate and postgraduate curricula, alongside specialized short courses and hands-on workshops for early-career scientists and technical staff, would significantly enhance national expertise. Such efforts should emphasize interdisciplinary training that bridges classical taxonomy and modern molecular approaches, ensuring that researchers are equipped to generate, interpret, and apply DNA barcode data effectively.

The establishment of regional molecular biodiversity hubs presents a practical strategy for decentralizing capacity and improving access to sequencing and analytical facilities. Strategically located hubs, linked to universities, research institutes, or natural history collections, could serve as centers for sample processing, sequencing, data analysis, and specimen curation. These facilities would also promote the adoption of standardized

protocols, strengthen quality control, and facilitate data sharing across regions, while reducing logistical challenges associated with long-distance sample transport. Aligning such hubs with Nigeria's major ecological or geopolitical zones would enable ecosystem-specific research priorities and foster stronger collaboration among institutions operating within similar environmental contexts.

5.5. Policy Integration

For DNA barcoding to achieve a meaningful impact in Nigeria, molecular data must be effectively translated into actionable conservation policies and management strategies. Integrating DNA barcode data into national biodiversity frameworks can enhance species identification, support the assessment of threatened taxa, and improve ecosystem monitoring and wildlife conservation [67,68]. These molecular tools provide reliable evidence that can inform environmental impact assessments, protected area planning, and enforcement of conservation regulations, particularly in cases involving cryptic species or processed biological materials [65]. Strengthening institutional linkages among researchers, conservation agencies, and policymakers is therefore essential to ensure that DNA barcode data are accessible, interpretable, and aligned with national conservation priorities.

Aligning DNA barcoding initiatives with the United Nations Sustainable Development Goals (SDGs) further enhances their relevance to national development agendas. Molecular characterization of plant and animal resources contributes directly to SDG 15 (Life on Land) by supporting biodiversity conservation, ecosystem restoration, and sustainable use of terrestrial resources [69,70]. By improving crop diversity, safeguarding wild relatives, and supporting sustainable fisheries and livestock systems, DNA-based approaches also contribute to SDG 2 (Zero Hunger) [71,72]. In addition, DNA barcode data can improve understanding of ecosystem resilience and adaptive responses to environmental change, thereby informing climate-related strategies under SDG 13 (Climate Action) [73]. Embedding DNA barcoding within policy frameworks that explicitly reference these SDGs can strengthen cross-sectoral collaboration, attract targeted funding, and position biodiversity research as a key driver of sustainable development in Nigeria.

6. Conclusions

Nigeria possesses exceptional biodiversity, supported by a wide range of ecosystems, including tropical rainforests, savannahs, wetlands, mangroves, and montane systems. These environments harbor thousands of plant and animal species of significant ecological, medicinal, and economic value. However, this biological richness is not matched by adequate molecular documentation. Evidence from bibliometric analyses and global databases such as BOLD indicates substantial gaps in DNA barcoding coverage, characterized by limited taxonomic representation, strong biases toward selecting animal groups, and minimal sequencing conducted within national institutions. These limitations constrain accurate species identification, biodiversity monitoring, and effective conservation planning. Ultimately, this perspective emphasizes that addressing identified critical gaps requires a paradigm shift from fragmented, taxon-specific studies toward integrated, cross-taxa approaches that capture ecosystem-level biodiversity and discoverability for a global species account and conservation framework. Frameworks that combine molecular tools with traditional taxonomy and ecological data are essential for detecting cryptic diversity, understanding population structure, and supporting evidence-based conservation. Advancing DNA barcoding in Nigeria will depend on coordinated national efforts, including sustained investment in infrastructure and capacity building, development of reference libraries, stronger policy integration, and equitable research partnerships. Such efforts

are critical for safeguarding biodiversity and improving Nigeria's contribution to global conservation initiatives.

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