https://doi.org/10.48047/AFJBS.7.6.2025.462-481

AFJBS

African Journal of Biological Sciences

Journal homepage: http://www.afjbs.com

Research Paper   Open Access

Molecular Genetic Diversity of Nigerian Fish Populations: A Systematic Review of Trends and Challenges

Usman, B.I.[2], *Abdul-Azeez, H.[1,2], Suleiman, A. M. [2], Mudi, Z.R. [2] and Aminu, M.U.[1,2]

[1.] Department of Fisheries and Aquaculture, Bayero University, Kano, PMB 3011, Kano State, Nigeria.
[2.] Department of Aquaculture and Fisheries Science, Africa Centre of Excellence in Aquaculture and Fisheries, Lilongwe University of Agriculture and Natural Resources (LUANAR), P O Box 219, Lilongwe, Malawi.
*Corresponding author: habdulazez.fac@buk.edu.ng, +2348071678669.

Volume 7, Issue 6, Jun 2025

Received : 15 April2025

Accepted : 05 May 2025

Published : 09 Jun 2025

doi :10.48047/AFJBS.7.6.2025.462-481

Abstract

Genetic diversity is a key factor in determining the adaptive potential and resilience of fish populations to environmental stressors. This review aimed to evaluate existing research on the molecular genetic diversity of Nigerian fish populations, with a focus on species studied, geographical coverage, and methodological approaches. The goal was to assess the suitability of these studies and identify knowledge gaps to guide future research and improve the monitoring and conservation of fisheries resources in Nigeria. A total of 42 relevant articles were retrieved from three academic databases following a screening process using predefined inclusion and exclusion criteria. The earliest study recorded (based on the selected databases and the search terms) was published in 2011, with a noticeable increase in publications over time. Approximately 70% of the studies focused on fish populations from the Southwest and South-South regions of the country. Inland water bodies and aquaculture environments accounted for 64% of the study settings. Taxonomically, catfishes and cichlids were the most frequently studied groups, with *Clarias gariepinus* representing nearly 60% of the catfish-related studies. The most commonly used molecular markers were mitochondrial DNA (mtDNA), simple sequence repeats (SSR), and randomly amplified polymorphic DNA (RAPD), with an average loci per population of 1.4 loci (mtDNA), 6.55 loci (SSR), and 5.14 loci (RAPD), respectively. The review highlighted the limited effectiveness of mtDNA for comprehensive genetic diversity assessments due to its narrow genomic coverage. It recommends the adoption of more robust molecular tools, particularly next-generation sequencing (NGS) technologies such as single nucleotide polymorphisms (SNPs). Furthermore, integrating landscape-level environmental data into population genetic studies is suggested to enhance the understanding and management of Nigeria's fish genetic resources.**Keyword**: Allele, Aquatic, Conservation, Evolution, Genome and Loci

INTRODUCTION

Fish are the most diverse group of vertebrates, inhabiting a wide range of aquatic environments and playing vital roles in ecosystem balance (Martinez *et al.*, 2018). However, their populations are increasingly threatened by environmental changes and human activities such as overfishing, pollution, habitat destruction, and the introduction of non-native species (Pauly and Zeller, 2016). Additionally, global climate change is driving ocean acidification and rising water temperatures, which affect salinity, dissolved oxygen levels, and circulation patterns in aquatic ecosystems (Crozier and Hutchings, 2014; Levitus *et al.*, 2012; O'Reilly *et al.* 2015).

Nigeria, a coastal country with abundant water resources, accounts for 0.28% of the world's inland water surface and has a coastline of 853 km (Abdullahi *et al.*, 2022; Nwuba *et.al*., 2022). Its fisheries sector relies on 14 million hectares of inland water bodies, including reservoirs, lakes, and rivers, contributing significantly to domestic fish production. Despite producing about 1.04 million tons of fish annually (75% from fisheries and 25% from aquaculture), Nigeria still need to augment the deficit of approximately 2.5 million tons through importation (Ogunji and Wuertz, 2023). This shortfall is partly due to declining fish stocks, driven by overfishing, harmful fishing practices, and pollution from oil spills and industrial waste (Amos and Peter, 2018; Oribhabor, 2016). Effective management strategies are needed to sustain the country's fishery resources.

Genetic information plays a crucial role in conservation and fisheries management by identifying genetically distinct populations, assessing connectivity, and detecting risks related to inbreeding and population decline (Pavlova *et al.*, 2017). Genetic diversity is a key factor in determining a species' ability to adapt to environmental changes. Measures such as heterozygosity (the presence of different alleles at a locus) and allele richness provide insights into population health (Frankham *et al.*, 2014). Reduced genetic diversity can lower population viability and increase the risk of extinction, particularly under environmental stress (Martinez *et al.*, 2018). Understanding patterns of genetic diversity can help predict which populations are most resilient or vulnerable to ecological pressures.

Molecular genetic studies utilize DNA markers to analyze genetic variation among fish populations. These techniques help fisheries researchers understand population structure, inbreeding levels, mating success, and the effects of natural and sexual selection (Abdul-Muneer, 2014). Molecular tools have been instrumental in conservation efforts by identifying species requiring urgent protection and selecting viable populations for conservation programs (Wang *et al.*, 2021).

Given the pivotal role genetic diversity assessment play in the management of fish stocks of both wild and aquaculture settings, this review study examines trends in intra-population molecular genetic diversity studies of Nigerian fish populations. It evaluates research progress over the years, the types of molecular markers and methods used, the fish species studied and the geographical locations of the populations. Finally, we identify knowledge gaps in fish genetic research and provide recommendations for future studies to guide conservation and fisheries management efforts.

MATERIAL AND METHODS

Search Strategy and Data Sources

This systematic review uses a structured approach to identify, evaluate, and synthesize molecular population genetic studies on Nigerian fish populations. Literature searches were conducted using Google Scholar (https://scholar.google.com/), ProQuest (https://www.proquest.com/) and ScienceDirect (https://www.sciencedirect.com/) database to access peer-reviewed journals and conference proceedings . A combination of relevant keywords and Boolean operators was used to refine the search. The search terms are: ("Genetic diversity" AND "fish" AND "Nigeria"), ("Molecular population genetics" AND "Nigerian fisheries"), ("Genetic structure of Nigerian fish species"), ("DNA markers" AND "fish populations in Nigeria"). Time duration was not attached to the search. Results of the search were exported in comma-separated values (CSV) or text (txt) files in to Rayyan software (Disner *et al.*, 2021; Ouzzani *et al.*, 2016) a web-based tool designed for systematic review screening.

Study Selection and Screening

A Double-blind review selection process was conducted by A.H. and M. Z.R. in Rayyan based on studies whose title and abstract reflect genetic diversity study of Nigerian fish populations using molecular technology. Reconciling differences in the selections was done after unblinding. All the authors finally downloaded the full-text articles papers and the full text screening. The inclusion criteria for the screening were: studies focusing on intra-population genetic diversity estimates of Nigerian fish species conducted using molecular markers such as microsatellites, mitochondrial

DNA, and SNPs, conducted on either wild/and aquaculture fish species. Published Peer-reviewed journal and conference articles on the subject matter are the ones considered. On the other hand, the exclusion criteria are; studies with no molecular genetic diversity data, genetic differentiation studies without diversity estimates, research not focusing Nigerian fish populations, review and case report papers and unavailable full-text or abstract only papers.

Data Extraction (Qualitative Data)

The following qualitative data were extracted from each selected study: the surname of the lead author, year of publication, type of water body (categorized as freshwater, brackish, or marine), geographic location of the water body, fish status (aquaculture or wild), fish species investigated, and the molecular marker(s) employed in the study.

Quantitative Data

The following quantitative variables were extracted for data analysis: sample size per population, number of molecular markers utilized, and the mean values of key genetic diversity metrics, including observed heterozygosity (Ho), haplotype diversity, nucleotide diversity, and number of alleles.

Statistical analysis

The extracted data were organized and processed using Microsoft Office Excel 2016, where descriptive statistics were computed. Linear regression analyses were conducted to model trends in the number of studies, fish populations examined, and sample sizes per population across the years. Additionally, relationships were assessed between the average number of molecular markers (loci), DNA fragments, and the average number of alleles recorded for each studied population against the corresponding genetic diversity metrics.

RESULTS

Data Search and Screening

The search across the three databases yielded a total of 911 articles. After removing duplicates and screening titles and abstracts, 838 articles remained (Figure 1). Subsequent full-text screening resulted in the inclusion of 42 studies, which were further expanded into 141 datasets based on the number of distinct fish populations examined within the studies.

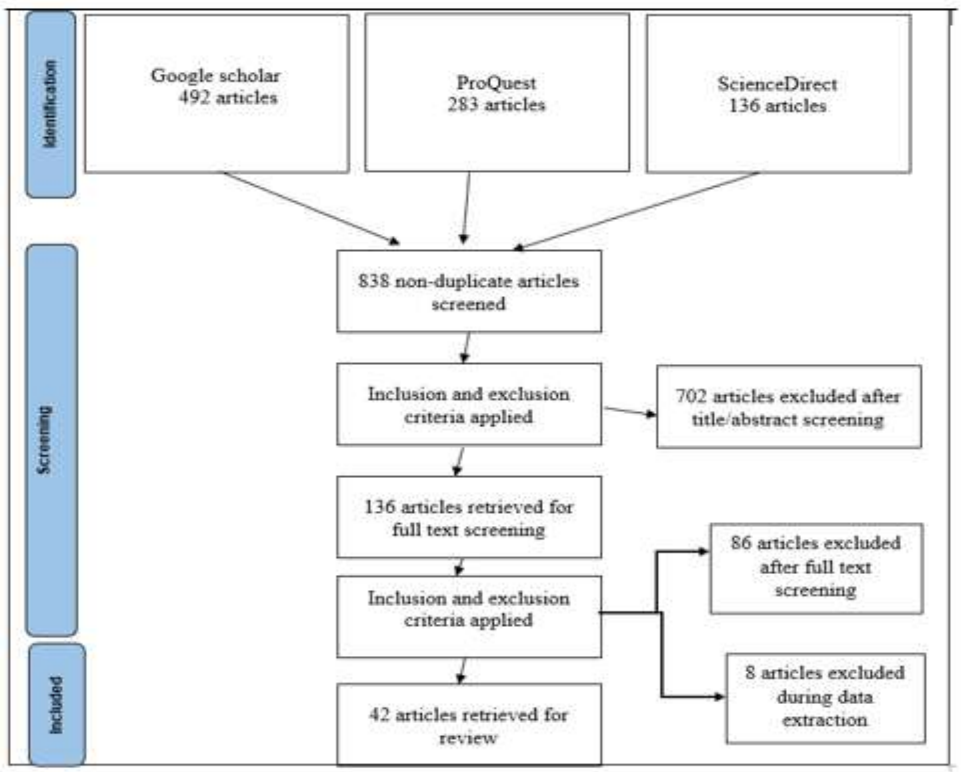

Figure 1: Flow Chart of the Search Database, the Screened and the Final Retrieved Articles using PRISMA Flow Chart.

Evolution and Geographic Spread of Fish Genetic Diversity Research in Nigeria

The earliest recorded publication on fish genetic molecular diversity retrieved from the three databases was in 2011 (Figure 2). Over the 14-year study period, there was a significant upward trend in the annual number of genetic diversity studies, as demonstrated by linear regression analysis ($R^2 = 0.5285$, $P = 0.0032$, Table 4). Similarly, the number of fish populations investigated each year also showed a strong positive trend ($R^2 = 0.6175$, $P = 0.0009$).

Analysis of the geographical distribution revealed that fish populations from Southwestern Nigeria were the most frequently studied, accounting for 50.0% of the total studies (Figure 2). In contrast, Southeastern Nigeria had the fewest studies on fish populations. Fish populations from the South-south region received considerable attention, representing 21.0% of the studies. Among the savannah-dominated regions of Northern Nigeria, fish populations from the Northcentral region were more extensively studied (12.0%) compared to those from the Northwest and Northeast regions.

Regarding habitat types, freshwater finfish inhabiting Nigeria's inland natural and artificial water bodies were the most studied group, comprising 64.0% of the total reviewed studies. In comparison, non-finfish species from freshwater and coastal environments received relatively less research focus (Figure 4).

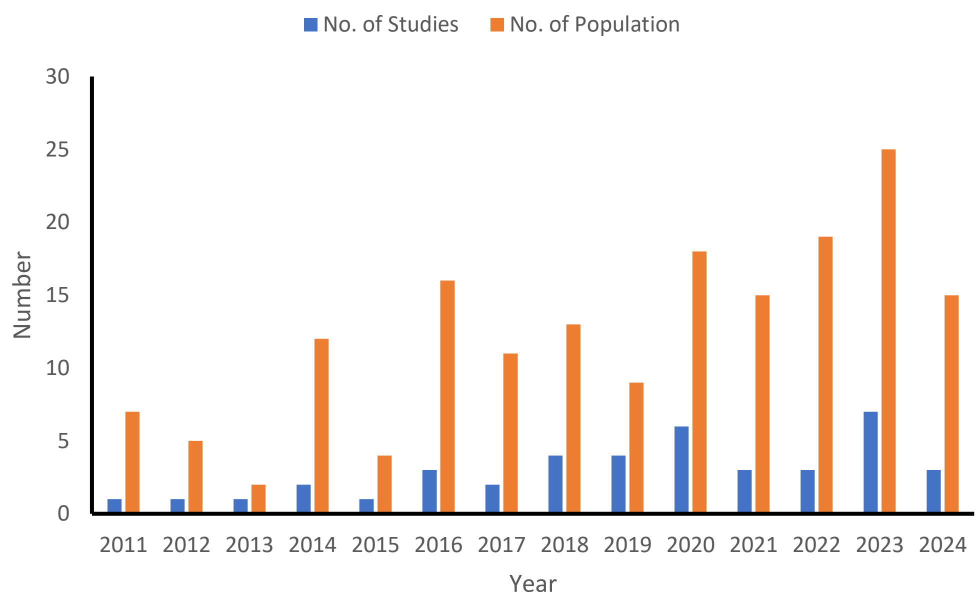

Figure 2: Trend of molecular genetic diversity studies published over the years

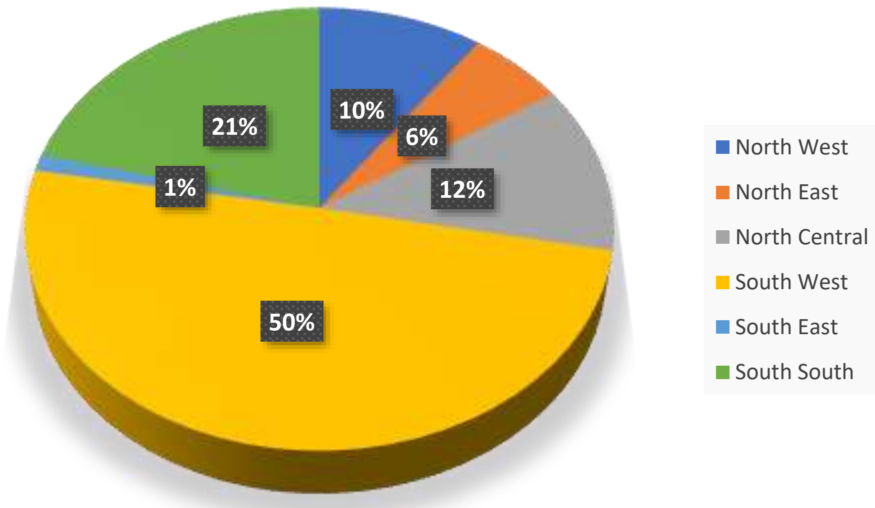

Figure 3: Geographical Distribution of the Location of the Studied Fish Populations

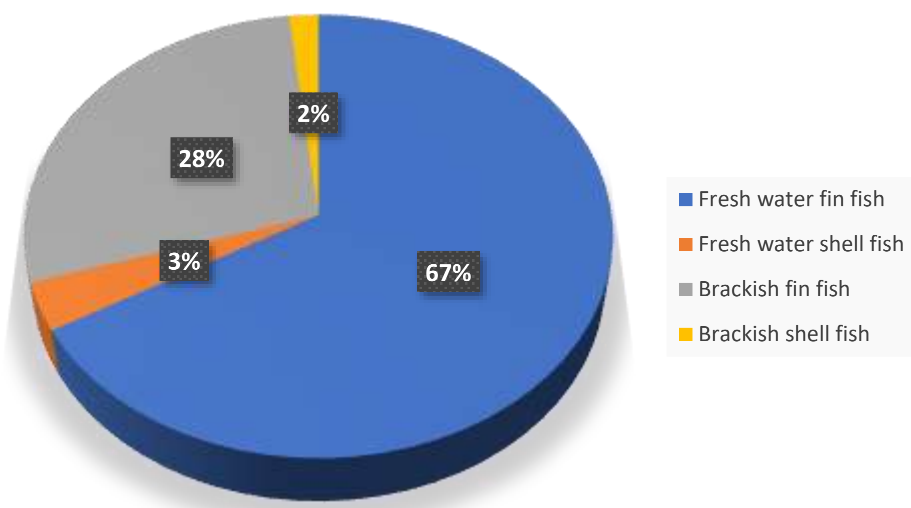

Figure 4: Proportion of Fin and Shell-fish Studied in Brackish or Fresh Waters

Taxonomic Distribution of Studied Fish Populations

The analysis of fish populations studied for genetic diversity revealed that species within the catfish group received the highest research attention, comprising 56.1% (n = 96) of all studied populations (Table 1). Among these, *Clarias gariepinus* populations represented over 60.0% of the catfish group. Furthermore, *Clarias gariepinus* from aquaculture systems accounted for 68.2% of all aquaculture species investigated for genetic diversity (Supplementary Data).

Cichlids were the second most frequently studied group, representing 29.8% (n = 51) of the total populations analyzed. Within the cichlids, *Tilapia guineensis* was the most commonly studied species, comprising 41.2% (n = 21) of the cichlid group, followed by *Oreochromis niloticus*, which constituted 29.4% (n = 15). In addition to finfish, three shellfish species were reported among the 17 total species studied, representing 5.3% (n = 9) of the populations assessed for their genetic diversity

Table 1: Fish Species and Proportion of the Studied Populations

Species	Common name	No. of population	Percentage (%)
Chrysichthys nigrodigitatus	Silver catfish	31	18.13
Heterobranchus longifilis	African catfish	6	3.51
Clarias gariepinus	African catfish	59	34.50
Oreochromis niloticus	Nile tilapia	15	8.77
Sarotherodon gallilaeus	Mango tilapia	1	0.58
Sarotherodon melanotheron	blackchin tilapia	4	2.34
Coptodon zillii	Red belly tilapia	4	2.34
Oreochromis aureus	Blue tilapia	1	0.58
Oreochromis. mossambicus	Mozambique tilapia	1	0.58
Tilapia spp (unidentified Spp)	Tilapia	4	2.34
Tilapia guineensis	Guinean tilapia	21	12.28
Lates niloticus	Nile perch	6	3.51
Heterotis niloticus	African bony tongue	4	2.34
Parachanna obscura	Snakehead fish	5	2.92
Bulinus globosus,	Fresh water snail	5	2.92
Callinectes amnicola,	Portunid crab	1	0.58
Egeria radiata	Common clams	3	1.75
	Total	**171**	**100.00**

Trends in Molecular Marker Usage and Sampling Strategies

An assessment of the types of molecular markers employed revealed that Simple Sequence Repeats (SSR) and Mitochondrial DNA (mtDNA) were the most commonly used, each accounting for 29.3% (n = 12) of the studies and collectively evaluating over 60.0% of the studied fish populations (Figure 5). Additionally, electrophoresis of blood serum and homogenized tissue was utilized in 8.8% (n = 15) of the populations to assess genetic diversity.

Analysis of the number of fish samples and molecular markers used indicated that SSR studies had the highest mean number of fish samples per population (mean = 20.09), with sample sizes ranging from as few as 4 to as many as 120 individuals (Table 2). However, no significant trend was observed in the annual number of samples used in SSR studies (linear regression; $R^2 = 0.0045$, $P = 0.6261$, Table 4). Similarly, although mtDNA studies reported a mean sample size of 17.51 (ranging from 1 to 100 individuals), no clear increasing trend over the years was detected (linear regression; $R^2 = 0.0396$, $P = 0.1377$).

Analsis of the number of loci indicated Single Nucleotide Polymorphisms (SNPs) and mtDNA studies exhibited the lowest mean loci per study (mean = 1.00 and 1.49, respectively), while Randomly Amplified Polymorphic DNA (RAPD) and SSR markers utilized the highest (mean = 9 loci per population). Despite the relatively high mean observed heterozygosity recorded in SSR-based studies (Ho = 0.568; Table 3), there was no significant linear relationship between the number of loci used and the recorded genetic diversity for either SSR ($R^2 = 0.0001$, $P = 0.9357$, Table 4) or RAPD markers ($R^2 = 0.0038$, $P = 0.7782$).

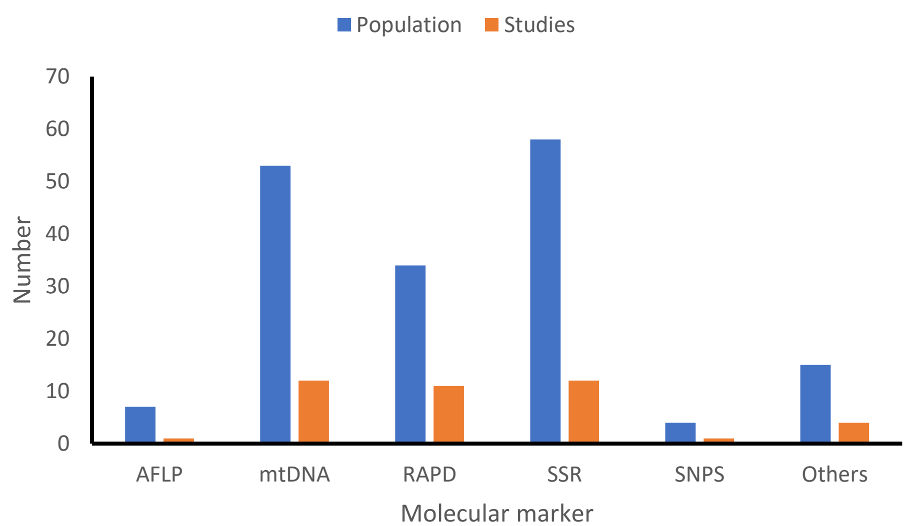

Figure 5: Proportion of Molecular Markers and Fish Populations in Genetic Diversity Studies.

Table 2: Descriptive Statistics of the Number of Fish Samples and Molecular Marker

DNA marker	Fish sampled/population			Number of DNA marker/population		
	Mean	Min.	Max.	Mean	Min.	Max.
AFLP	12.57	10.00	15.00	4.00	4.00	4.00
mtDNA	17.51	1.00	100.00	1.49	1.00	2.00
RAPD	15.27	5.00	40.00	5.14	3.00	9.00
SNPS	10.00	10.00	10.00	1.00	1.00	1.00
SSR	20.09	4.00	120.00	6.55	2.00	9.00
Others	19.11	10.00	30.00	5.00	5.00	5.00

Table 3: Descriptive Statistics of the Genetic Diversity Recorded Based on Marker Type

DNA marker	Fish population genetic diversity level		
	Mean	Min	Max.
AFLP (Nei's gen. Div.)	0.118	0.0216	0.2464
mtDNA (i.e., Nucl. Div.)	0.031	0.001	0.21
RAPD(i.e., Ho)	0.294	0.056	0.67
SNPS (i.e., Tajima's div.)	1.029	1.005	1.101
SSR (i.e., Ho)	0.568	0.125	1.00

Table 4: Linear Regression Analysis Outputs

S/N	Dependent variable (Y)	Independent Variable (X)	Intercept (a)	Gradient (b)	R^2	P-value
1	No. of study	Year	-648.879	0.321	0.529	0.003
2	No. of population	Year	-2422.090	1.207	0.618	0.001
3	Sample size (SSR)	Year	784.566	-0.378	0.005	0.626
4	Sample size (mtDNA)	Year	-2061.620	1.030	0.039	0.138
5	Ho (SSR)	No. of DNA marker	0.906	-0.051	0.213	0.000
6	Ho (RAPD)	No. of DNA marker	0.319	-0.005	0.004	0.778

Ho=Observed heterozygosity

DISCUSSION

Evolution and Geographic Spread of Fish Genetic Diversity Research in Nigeria

Assessing genetic diversity is a central objective in molecular ecology and plays a crucial role in conservation planning. It informs decisions such as prioritizing populations for protection, selecting stock for restocking efforts, or determining sample sizes needed to conserve genetic variation both in situ and ex situ (Cossu *et al.*, 2022).

Since their introduction nearly seven decades ago, molecular techniques have significantly advanced our understanding of population genetic structure and diversity(Shahnawaz and Chinnathangam, 2016). One of the earliest documented applications of the techniques in African fish genetic diversity studies-based on accessible online records-is the investigation of *Lates niloticus* populations from Lake Victoria, Nabugabo, Kyoga, Albert and Turkana in East Africa (Hauser *et al.*, 1998). Similar efforts in Nigeria appear to have begun much later. According to the reviewed papers, the earliest published Nigerian studies date back to 2011. Nonetheless, this timeline may not fully reflect the actual onset of genetic research in the country, as earlier works might remain unpublished or inaccessible online.

The southwestern region of Nigeria, has emerged as a focal point for fish genetic research. This is likely influenced by the concentration of biotechnology facilities and research institutions, including the National Centre for Genetic Resources and Biotechnology (NACGRAB), which is mandated to conserve indigenous plant, animal, and microbial genetic resources (Borokini *et al.*, 2010). The availability of such infrastructure, along with a dense network of private biotech companies, likely reduces the cost and increases the feasibility of molecular analyses in this region (Glaeser and Gyourko, 2018). In contrast, although biotechnology laboratories are present across various universities and research institutes nationwide, access and affordability may still be limited in regions with fewer service providers (Delphonso *et al.*, 2025).

Geographically, the 14-million-hectare Nigeria's inland waters-comprising rivers, lakes, reservoirs, and streams-span across most of the states in the country (Nwuba *et al.*, 2022). On the other hand only around 853 kilometer coastline stretch consisting of inshore waters, coastal lagoons, estuaries and mangrove in the Niger Delta region are the main brackish waters of the country (Jimoh and Lemomu, 2010). This widespread distribution of freshwater systems likely explains the dominance of studies focused on freshwater fish species.

Importantly, although the number of fish genetic diversity studies and the number of the studied fish populations increased over time, current efforts remain insufficient in light of Nigeria's rapid population growth and rising demand for fish (Olowa and Olowa, 2016). Strengthening the monitoring of genetic diversity in fish populations is therefore essential to support sustainable fisheries management and to safeguard the genetic resources vital for food security and biodiversity conservation (Cossu *et al.*, 2022).

Taxonomic Distribution of Studied Fish Populations

Nigeria's inland waters are home to 260 documented fish species, with major commercial catches dominated by genera such as *Lates*, *Tilapia*, *Citharinus*, *Chrysichthys*, *Mormyrus*, and *Clarias* species (Olopade *et al.*, 2017). Despite this richness, the sector has experienced a steady decline in fish yields. This decline is largely attributed to overfishing-exacerbated by the use of improved fishing gear-alongside environmental pollution and the continued use of destructive and illegal fishing methods (Sogbesan, and Kwaji, 2018). In contrast to this high species diversity, the present review identified only 17 fish species that have been the focus of population genetic diversity studies in Nigeria. This limited representation, when viewed against the backdrop of declining fisheries productivity from the captured fisheries and increasing anthropogenic pressures, highlights a significant gap in research and management (Eyo and Ahmed, 2005).

The current state of fisheries resource management in Nigeria's inland waters-which contribute approximately 82% of the nation's domestic fish production-remains inadequate and fails to reflect the ecological and economic significance of these resources (Olopade *et al.*, 2017). The limited number of genetically studied species indicates that many native fish populations are still unexplored and potentially at risk, highlighting an urgent need for broader taxonomic representation and more inclusive, genetics-informed conservation strategies.

Trends in Molecular Marker Usage and Sampling Strategies

This review revealed that mitochondrial DNA (mtDNA) and simple sequence repeats (SSR or microsatellites) are the most commonly used molecular markers in fish genetic diversity studies in Nigeria. While SSRs and amplified fragment length polymorphisms (AFLPs) are among the most often applied molecular markers globally (Leipold *et al.*, 2018), their use in Nigerian fish genetic diversity studies appears uneven.

Simple sequence repeats remain popular due to their high variability at the locus level, making them highly informative for assessing genetic diversity (Leipold *et al.*, 2018). In the past, developing suitable primers for SSR analysis was time-consuming, but advancements in next-generation sequencing (NGS) have significantly streamlined this process(Taheri *et al.*, 2018; Zalapa *et al.*, 2012). Despite their advantages, the high cost and technical demands of SSR analysis may limit their broader adoption in resource-constrained settings (Adhikari *et al.*, 2017).

AFLPs, although used less frequently in the reviewed Nigerian studies, are still considered valuable in conservation genetics due to their cost-effectiveness and independence from prior sequence data (Leipold *et al.*, 2018). When applied with a sufficiently high number of loci, AFLPs offer broad genome coverage and can outperform SSRs in some diversity estimates. However, limitations such as their dominant nature and lower reproducibility may hinder their wider use (Eidesen *et al.*, 2007; Gaudeul *et al.*, 2004; Leipold *et al.*, 2018). Cutting edge technology such as Single nucleotide polymorphisms (SNPs) are rarely used in Nigerian fish genetics diversity research. This underuse is likely due to the high cost of DNA sequencing associated with the use of the marker.

The frequent use of mtDNA in Nigeria may be attributed to its affordability and simplicity, making it a practical choice for initial assessments of population genetic structure(Galtier *et al.*, 2009). However, mtDNA has limitations. It reflects only maternal inheritance and compared with other markers, can be considered to have low rate of recombination, which can limit its ability to represent total genomic diversity which reduces the effective population size and thus increases the sensitivity to genetic drift (Moritz, 1994). More critically, there is no established empirical link between mtDNA diversity and overall population fitness or nuclear genome diversity. Cases like the northern elephant seal and parthenogenetic geckos show that low mtDNA diversity can still occur in genetically healthy or expanding populations (Moritz, 1994). Nonetheless, mtDNA remains valuable for phylogenetic studies, as it helps trace evolutionary lineages and identify cryptic species(Galtier *et al.*, 2009).

Random Amplified Polymorphic DNA (RAPD) also showed reasonable usage in reviewed studies. RAPD is advantageous due to its simple protocol, minimal DNA requirement, ability to detect polymorphism, and broad genome coverage. Its relatively low cost and rapid execution make it an attractive option for genetic diversity studies in Nigeria, especially in settings with limited resources (Cui *et al.*, 2017).

Sample Size and Loci Number

Accurately estimating genetic diversity in large natural populations using finite sample sizes is a central concern in population and conservation genetics. Small or poorly designed sampling strategies can introduce significant errors, compromising the validity of estimates and, by extension, the effectiveness of genetic conservation efforts (Bashalkhanov *et al.*, 2009). For conservation programs to be sustainable across generations, it is essential that the sampled population retains sufficient allelic richness and includes a minimum number of individuals carrying each allele. Failure to meet these criteria can undermine the long-term viability of the conservation initiative (Mclaughlin and Winker, 2020).

The appropriate sampling strategy for assessing genetic diversity depends on several factors, including population structure, the distribution of traits or alleles, the statistical metric used for measuring diversity, and the desired level of precision. The optimal sample size is influenced by the underlying genetic variation in the population-commonly described through genotype and allele frequencies, heterozygosity, allelic richness, and linkage disequilibrium (Singh *et al.*, 2006).

Despite recognition of the critical role that sample size and number of loci play in genetic studies, there remains no universal scientific consensus on the minimum thresholds (Leipold *et al.*, 2018). For instance, Bonin *et al.*, (2007) suggested that the number of loci analyzed may not significantly affect diversity estimates. In contrast, Hollingsworth and Ennos (2004) emphasized that up to 250 loci may be necessary for accurate phylogenetic analyses of weakly differentiated populations. Sinclair and Hobbs (2009) further observed that increasing sample sizes led to higher levels of detected polymorphism.

In practice, the trend in genetic studies is toward the inclusion of more individuals and loci, whether using dominant or codominant markers(Sánchez-montes *et al.*, 2017). However, financial constraints-particularly in developing countries like Nigeria-often limit the feasibility of large-scale molecular analyses. To maximize efficiency, studies must carefully balance the number of individuals and loci sampled with the resources available (Leipold *et al.*, 2018).

The number of loci required is also influenced by how many individuals are genotyped. Electrophoresis-based surveys have shown that more loci are needed when fewer individuals are sampled. For instance, to achieve accurate estimates of gene diversity, 20–30 individuals may be necessary if only 20 loci are assayed. Conversely, sampling 5–6 individuals may suffice when using a dense panel of around 250 loci (Singh *et al.*, 2006).

Recent guidelines aim to strike a balance between cost and data robustness. For example Leipold *et al.* (2018) recommended that 120 AFLP fragments (including both polymorphic and monomorphic bands) are adequate to estimate a population's genetic diversity, with diminishing returns beyond this point. Additionally, a mean of 23.4 ± 1.20 individuals per population was also found sufficient to capture 95% of total genetic variance. Similarly, Mittell *et al.*(2015) demonstrated that a median of 10 microsatellite loci is typically sufficient to characterize molecular genetic variation in populations.

Based on these recommendations, the results of this review suggest that only a few SSR-based studies in Nigeria meet the minimum recommended sample size, and even fewer approach the ideal number of loci required for robust diversity estimates. This highlights a critical gap in methodological rigor, which may compromise the interpretability and conservation value of such studies.

Future Directions of Fish Genetic Diversity Studies

The review revealed that most fish genetic studies in Nigeria have disproportionately focused on a limited number of species, notably *Clarias gariepinus*, *Tilapia guineensis*, and *Oreochromis niloticus*, while many indigenous and ecologically significant finfish and shellfish species remain largely understudied. Future research should aim for broader taxonomic coverage that includes species from diverse aquatic habitats across Nigeria's inland and coastal waters, to better reflect the country's rich biodiversity potential. Additionally, there is a pronounced regional bias in the spatial distribution of studies, with a heavy concentration in southwestern Nigeria, while the southeastern and northern regions are significantly underrepresented. This has resulted in notable spatial knowledge gaps in both wild and cultured fish populations.

Our review also uncovered an overreliance on mitochondrial DNA (mtDNA) for estimating intra-population genetic diversity, despite its limitations and general unsuitability for comprehensive diversity assessments (Galtier *et al.*, 2009). Moreover, many studies did not adhere to recommended sampling standards, particularly in terms of sample size and the minimum number of loci required to generate robust and reliable genetic diversity estimates. A strong dependence on traditional molecular markers such as microsatellites and RAPDs were also observed. To enhance resolution and analytical depth, future studies should adopt next-generation sequencing (NGS) technologies, including SNP genotyping and whole-genome resequencing, which offer more comprehensive insights into population structure, local adaptation, and evolutionary history (Kumar *et al.*, 2019).

Furthermore, few reviewed studies investigated adaptive genetic variation or gene-environment interactions. It is essential for future research to integrate landscape-level heterogeneity into population genetic studies to better understand how environmental variation influences gene flow and genetic structure within and among populations. The review advocates for stronger interdisciplinary collaboration among geneticists, ecologists, policymakers, and local stakeholders-particularly riparian communities-to ensure that genetic research findings are effectively translated into sustainable fisheries management and biodiversity conservation strategies.

CONCLUSION

The present systematic review highlights the emerging yet limited scope of molecular genetic studies on Nigerian fish populations. While there has been steady progress since 2011, research remains heavily concentrated in southern Nigeria and disproportionately focused on a few commercially important species. The predominant use of traditional molecular markers such as mtDNA, SSRs, and RAPDs, along with suboptimal sampling strategies, constrains the robustness of the current genetic diversity assessments. To address these gaps, future studies should prioritize broader species and regional coverage, adhere to recommended sampling standards, and adopt advanced genomic tools like SNPs genotyping and whole-genome sequencing. Strengthening interdisciplinary collaboration and integrating genetic data into fisheries policy will be necessary for the conservation of Nigeria's aquatic biodiversity and the sustainability of its fisheries resources.

Funding Statement: This study was funded by the Institutional Based Research (IBR) grant (**No: BUK/DRIP/TETF/024)** of Tertiary Education Trust Fund (TETFund).

REFERENCES

Abdul-Muneer, P. M. (2014). Application of Microsatellite Markers in Conservation Genetics and Fisheries Management: Recent Advances in Population Structure Analysis and Conservation Strategies. *Genetics Research International*, *2014*, 1–11. https://doi.org/10.1155/2014/691759

Abdullahi, T.I., Oladimeji, Y.U. & Hassan, A. A. (2022). Economics of sole fish and integrated fish-vegetable production and its optimum inputs combination in Kaduna State, Nigeria. *Ife J. Agric.*, *34*, 19–34.

Adhikari, S., Saha, S., Biswas, A., Rana, T. S., Bandyopadhyay, T. K. & Ghosh, P. (2017). Application of molecular markers in plant genome analysis: a review. *Nucleus (India)*, *60*(3), 283–297. https://doi.org/10.1007/s13237-017-0214-7

Amos, S. O. & Peter, K. B. (2018). Sustainable artisanal fisheries practices in Nigeria. *Oceanography & Fisheries Open Access Journal*, *6*(1), 8–19.

Bashalkhanov, S., Pandey, M. & Rajora, O. P. (2009). A simple method for estimating genetic diversity in large populations from finite sample sizes. *BMC Genetics*, *10*, 1–10. https://doi.org/10.1186/1471-2156-10-84

Bonin, A, Ehrich, D. & Manel, S. (2007). Statistical Analysis of Amplified Fragment Length Polymorphism Data: A Toolbox for Molecular Ecologists and Evolutionists. *Mol Ecol*, *16*, 3737–3758.

Borokini, T. I., Okere, A. U., Giwa, A. O., Daramola, B. O. & Odofin, W. T. (2010). Biodiversity and conservation of plant genetic resources in Field Genebank of the National Centre for Genetic Resources and Biotechnology , Ibadan , Nigeria. *International Journal of Biodiversity and Conservation*, *2*(3), 37–50.

Cossu, P., Mura, L., Dedola, G. L., Lai, T., Sanna, D., Scarpa, F., Azzena, I., Fois, N., & Casu, M. (2022). Detection of Genetic Patterns in Endangered Marine Species Is Affected by Small Sample Sizes. *Animals*, *12*(20), 1–19. https://doi.org/10.3390/ani12202763

Crozier, L. G. and Hutchings, J. A. (2014). Plastic and evolutionary re sponses to climate change in fish. *Evolutionary Applications*, *7*, 68–87. https://doi.org/https://doi.org/10.1111/eva.12135.

Cui, C., Li, Y., Liu, Y., Li, X., Luo, S., Zhang, Z., Wu, R., Liang, G., Sun, J., Peng, J. & Tian, P. (2017). Determination of genetic diversity among Saccharina germplasm using ISSR and RAPD markers. *Comptes Rendus - Biologies*, *340*(2), 76–86. https://doi.org/10.1016/j.crvi.2016.11.005

Delphonso, B. T., Kayode-Isola, T. M. & Lalekan, A. A. (2025). The Role of Biotechnology Education in Nigeria's Industrialization and Sustainable Development. *International Journal of Research and Scientific Innovation (IJRSI)*, *12*(1), 862–875. https://doi.org/10.51244/IJRSI

Eidesen, P., Alsos, I., Popp, M., Stensrud, Ø., Suda, J. & Brochmann, C. . (2007). Nuclear vs. plastid data: complex pleistocene history of a circumpolar key species. *Mol Ecol*, *16*, 3902–

3925.

Eyo, A.A. and Ahmed, Y. B. (2005). *Management of inland capture fisheries and challenges to fish production in Nigeria. Paper presented at: 19th Annual Conference of Fisheries Society of Nigeria (FISON); Ilorin, Nigeria.*

Frankham, R., Bradshaw, C. J. A. & Brook, B. W. (2014). Genetics in conservation management: Revised recommendations for the 50/500 rules, Red List criteria and population viability analyses. *Biological Conservation*, *170*, 56–63. https://doi.org/. https://doi.org/10.1016/j. biocon.2013.12.036.

Galtier,N., Nabholz, +S. & Hurst, G. D. D. (2009). Mitochondrial DNA as a marker of molecular diversity : a reappraisal. *Molecular Ecology*, *18*, 4541–4550. https://doi.org/10.1111/j.1365-294X.2009.04380.x

Gaudeul, M., Till-Bottraud, I., Barjon, F. & Manel, S. (2004). Genetic diversity and differentiation in Eryngium alpinum L. (Apiaceae): comparison of AFLP and microsatellite markers. *Heredity*, *92*, 508–518.

Glaeser, E. and Gyourko, J. (2018). The Economic Implication of Housing Supply. *Journal of Economic Perspectives*, *32*(1), 3–30. https://pubs.aeaweb.org/doi/10.1257/jep.32.1.3

Hauser, L., Carvalho, G. R., Pitcher, T. J. & Ogutu-Ohwayo, R. (1998). Genetic affinities of an introduced predator: Nile perch in Lake Victoria, East Africa. *Molecular Ecology*, *7*(7), 849–857. https://doi.org/10.1046/j.1365-294x.1998.00399.x

Hollingsworth, P.M. and Ennos, R. . . (2004). Neighbour joining trees, dominant markers and population genetic structure. *Heredity*, *92*, 490–498.

Jimoh, A.A. and Lemomu, I. P. (2010). Shellfish resources in Nigeria. *FISON EKO 2010*, *Ceda 1997*.

Kumar, K. R., Cowley, M. J. & Davis, R. L. (2019). Next-Generation Sequencing and Emerging Technologies. *Seminars in Thrombosis and Hemostasis*, *45*(7), 661–673. https://doi.org/10.1055/s-0044-1786397

Leipold, M., Tausch, S., Hirtreiter, M., Poschlod, P. & Reisch, C. (2018). Sampling for Conservation Genetics: how many loci and individuals are needed to determine the genetic diversity of plant populations using AFLP? *Conservation Genetics Resources*, *12*(1), 99–108. https://doi.org/10.1007/s12686-018-1069-1

Levitus, S., Antonov, J. I., Boyer, T. P., Baranova, O. K., Garcia, H. E., Locarnini, R. A., & Zweng, M. M. (2012). World ocean heat content and thermosteric sea level change (0–2000 m), 1955 2010. *Geophysical Research Letters, 39*, 10603. https://doi.org/https://doi. org/10.1029/2012GL051106.

Martinez, A. S., Willoughby, J. R. & Christie, M. R. (2018). Genetic diversity in fishes is influenced by habitat type and life - history variation. *Ecology and Evolution*, *8*(23), 12022–12031. https://doi.org/10.1002/ece3.4661

Mclaughlin, J. F. and Winker, K. (2020). *An empirical examination of sample size effects on population demographic estimates in birds using single nucleotide polymorphism (SNP)* *data*. 1–16. https://doi.org/10.7717/peerj.9939

Mittell, E.A., Nakagawa, S. & Hadfield, J. D. (2015). Are Molecular Markers Useful Predictors of Adaptive Potential? *Ecol Lett*, *18*, 772–778.

Moritz, C. (1994). Applications of mitochondrial DNA analysis in Conservation: a critical review. *Molecular Ecology*, *3*, 401–411.

Nwuba,L.A., Ude, E.F. & Ogbonnaya, H. F. (2022). Current trends in fisheries and aquaculture. *Int. J. Agric. Food Biodivers*, *1*, 64–69.

O'Reilly, C. M., Sharma, S., Gray, D. K., Hampton, S. E., Read, J. S., R., R. J. & Zhang, G. (2015). Rapid and highly variable warming of lake surface waters around the globe. *Geophysical Research Letters, 42*, 10773–10781. https://doi.org/https://doi.org/10.1002/2015GL066235.

Ogunji, J. and Wuertz, S. (2023). Aquaculture Development in Nigeria: The Second Biggest Aquaculture Producer in Africa. *Water (Switzerland)*, *15*(24), 1–17. https://doi.org/10.3390/w15244224

Olopade, O. A., Taiwo, I., & Dienye, H. E. (2017). Management of Overfishing in the Inland Capture Fisheries in Nigeria. *Journal of Limnology and Freshwater Fisheries Research*, *3*(3), 189–194. https://doi.org/10.17216/limnofish.335549

Olowa, O. W and Olowa, O. A. (2016). Food demand forecast for Nigeria (2016-2028). *Scientia Agriculturae*, *15*(1), 340–343. https://doi.org/10.15192/pscp.sa.2016.15.1.340343

Oribhabor, B. J. (2016). Impact of human activities on biodiversity in Nigerian aquatic ecosystems. *Science International*, *4*(1), 12–20.

Pauly, D. & Zeller, D. (2016). Catch reconstructions reveal that global marine fisheries catches are higher than reported and declining. *Nature Communications, 7*, 10244. https://doi.org/https://doi.org/10.1038/ncomms10244.

Pavlova, A., Beheregaray, L. B., Coleman, R., Gilligan, D., Harrisson, K. A., Ingram, B. A., Kearns, J., Lamb, A. M., Lintermans, M., Lyon, J., Nguyen, T. T. T., Sasaki, M., Tonkin, Z., Yen, J. D. L. & Sunnucks, P. (2017). Severe Consequences of Habitat Fragmentation on Genetic Diversity of an Endangered Australian Freshwater Fish: A call for assisted gene flow. *Evolutionary Applications*, *10*(6), 531–550. https://doi.org/10.1111/eva.12484

Sánchez-montes, G., Ariño, A. H., Vizmanos, J. L., Wang, J. & Martínez-solano, Í. (2017). Effects of Sample Size and Full Sibs on Genetic Diversity Characterization : A Case Study of Three Syntopic Iberian Pond-Breeding Amphibians. *Journal of Heredity*, *00*(00), 1–9. https://doi.org/10.1093/jhered/esx038

Shahnawaz, A. and Chinnathangam, S. (2016). Perspective Chapter: Molecular Approach for the study of Genetic Diversity and Conservation Prioritization of Fish Population. In *IntechOpen* (p. 4). https://doi.org/http://dx.doi.org/10.5772/57353

Sinclair, E.A. and Hobbs, R. J. (2009). Sample size effects on estimates of population genetic structure: implications for ecological restoration. *Restor Ecol*, *17*, 837–844.

Singh, M., Chabane, K., Valkoun, J. & Blake, T. (2006). Optimum sample size for estimating gene diversity in wild wheat using AFLP markers. *Genetic Resources and Crop Evolution*, *53*, 23–33. https://doi.org/10.1007/s10722-004-0597-6

Sogbesan, O. A. and Kwaji, B. P. (2018). Sustainable Artisanal Fisheries Practices in Nigeria. *Oceanography & Fisheries Open Access Journal*, *6*(1), 1–12. https://doi.org/10.19080/ofoaj.2018.06.555677

Taheri, S., Lee, A. T., Yusop, M.R., Hanafi, M.M., Sahebi, M., A. P. & Shamshiri, R, R. (2018). Mining and Development of Novel SSR Markers using Next Generation Sequencing (NGS) Data in Plants. *Molecules*, *23*(2), 399.

Wang, W., Ma, C., Ouyang, L., Chen, W., Zhao, M., Zhang, F., Fu, Y., Jiang, K., Liu, Z., Zhang, H. & Ma, L. (2021). Genetic diversity and population structure analysis of Lateolabrax maculatus from Chinese coastal waters using polymorphic microsatellite markers. *Scientific Reports*, *11*(1), 1–11. https://doi.org/10.1038/s41598-021-93000-6

Zalapa, J.E, Cuevas, H, Zhu, H, Steffan, S, Senalik, D., Zeldin, E., M. B., Harbut, R. & Simon, P. (2012). Using Next-generation Sequencing Approaches to Isolate Simple Sequence Repeat (SSR) Loci in the Plant Sciences. *Am J Bot*, *99*(2), 193–208.