World Journal of Aquaculture Research & Development

ISSN 2688-5581

Review Article

The Population Structure and Genetic Diversity of the African Catfish (*Clarias gariepinus*) Species: Implications for Selection and Long-Term Genetic Enhancement. A Review

Negesse Kebtieneh[1,2*], Kefyalew Alemayehu[3] and Gashaw Tilahun[4]

[1]*Department of Fisheries and Aquaculture, College of Agriculture and Environmental Studies, Bahir Dar University, Ethiopia*

[2]*Department of Biology, College of Natural and Computational Science, Debre Tabor University, Ethiopia*

[3]*Department of Animal Sciences, College of Agriculture and Environmental Studies, Bahir Dar University, Ethiopia*

[4]*Department of Fisheries and Aquaculture, School of Fisheries and Wildlife, Bahir Dar University, Ethiopia*

Abstract

In most Asian and Sub-Saharan countries, the African catfish, Clarias gariepinus, is the second most commonly cultivated fish species. The quantification of genetic diversity and population structure is essential for the interpretation, understanding, and management of populations and individuals. Due to its rapid growth rate, capacity to adapt to a variety of culture conditions, and high fertility, African catfish, C. gariepinus was first genetically improved in the 1950s and then adopted as the best catfish for African aquaculture in the middle of the 1970s. Numerous molecular markers, such as allozyme, mtDNA, SNPs, RAPD, Microsatellite, and SDS-PAGE markers, have been used in African catfish genetics and breeding studies to evaluate genetic divergences and similarities in order to ensure genetic improvement and a selective breeding programme of C. gariepinus fish species. Quantifying the genetic differences within and between populations of the fish species C. gariepinus is also accomplished through the use of genetic diversity and population structure assessments. These are important to formulate genetic conservation and management strategies, to sustainably manage economically important aquaculture fish species like C. gariepinus. Genetic improvement and marker assisted selective breeding programs are essential to have extensive knowledge of economically significant strains.

Keywords: African catfish; Genetic diversity; Population structure; Genetic improvement and molecular marker

Introduction

African catfish, *C. gariepinus* is one of a crucial inland water fish species, use for aquaculture production in parts of sub-Saharan Africa, North Africa, South America, Asia, and Europe [1]. By volume, it is the second-most widely grown fish production in Africa [2]. Because of its high fertility rate, fast growth rate even at high stocking densities, eat a variety of foods, are disease-resistant, and can withstand a variety of environmental conditions [1]. These all-natural behaviors have helped African catfish, *C. gariepinus* spread to many areas outside of its native range particularly Thailand, Malaysia, and the Netherlands, where it was introduced for aquaculture practices and new strains like the Dutch strain were created [3-5]. African catfish, *C. gariepinus* is the most important and suitable catfish species for tropical aquaculture in Africa [5,6]. It is also generally considered to be one of the economically important freshwater fish species for rearing, whose aquaculture potential has been documented [7].

Genetic variation is beneficial and important for the long-term survival of natural populations as it ensures the provision of high fitness levels, allowing populations to adjust to new environmental conditions [8], and it has resulted in a fascinating phenomenon that is anticipated to be the consequence of mutation or migration to a genetically dissimilar population [9]. Genetic degradation is caused by a lack of understanding in the field of fish farming [10]. It results in an excess of homozygosity in the population and a drop in productivity and is caused by inbreeding, negative selection, and hybridization. Genetic diversity is necessary for the natural population of African catfish, *C. gariepinus* populations to function as intended by evolution and to be preserved for future generation [8]. However, migration, genetic drift, extinction of genetically distinct wild populations and spontaneous mutation contribute to genetic changes in African catfish, *C. gariepinus* populations [11].

The identification of the species and its genetic makeup are essential to understanding *C. gariepinus*'s economic significance. The traditional method of the characterization of *C. gariepinus* has been used to evaluate this species, and it has not been found to be a reliable method for species identification [12]. However, using molecular markers are reliable method for the genetic identification of fish species. Using a single primer with an arbitrary nucleotide sequence, different investigators have observed distinct molecular markers for polymorphisms based on allele frequency and amplification of DNA segments. The levels of DNA polymorphisms can be detected using

Citation: Kebtieneh N, Alemayehu K, Tilahun G. The Population Structure and Genetic Diversity of the African Catfish (*Clarias gariepinus*) Species: Implications for Selection and Long-Term Genetic Enhancement. A Review. World J Aquac Res Development. 2024; 4(1): 1019.

Publisher Name: Medtext Publications LLC

Manuscript compiled: Jan 22nd, 2024

***Corresponding author:** Negesse Kebtieneh, Department of Fisheries and Aquaculture, College of Agriculture and Environmental Studies, Bahir Dar University, Bahir Dar, Ethiopia

molecular markers method by the presence or absence of amplification products when two strains or individuals are compared [13-17].

Several studies have been carried out to determine the genetic diversities and characterization of African catfish, *C. gariepinus* species using molecular markers such as RAPD [9,18]; microsatellite markers [6,16-24]; SNP [25]; Isozymes [26]; and Mitochondrial DNA marker [6,27]. On the other hand, a concise analysis on the genetic diversity and population structure of *C. gariepinus*, an African catfish, shows the need for selection and long-term genetic development for future prospects. In order to facilitate selection and long-term genetic improvement, this paper presents the genetic diversity and population structure of African catfish, *C. gariepinus*.

Objective

This review objective is to evaluate the population structure and genetic diversity of the African catfish, *C. gariepinus*, in order to determine the implications of selection and long-term genetic improvement.

Overview of African Catfish Population Structure and Genetic Diversity

Genetic diversity

For the purposes of genetic improvement initiatives, conservation, and resource management, natural population genetic monitoring is vital. Therefore, it is necessary to assess the amount of genetic diversity and the structure of diversity in samples and populations [28]. From individual fitness to ecosystem function, genetic diversity is crucial for ecological and evolutionary processes [29]. The loss of genetic diversity in the cultured population may be due to strict breeding practices that may have genetically isolated the stock from other populations, while the loss of genetic diversity in the wild population may be due to overfishing, poaching, population division, genetic drift, and natural selection [9,17].

In order to comprehend the genetic diversity of the fish population, especially in different catfish species, it is necessary to know mean number of alleles per locus (A), mean effective number of alleles (Ae), nucleotide diversity (p), haplotype diversity (h), percentage of polymorphic loci, observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (Ar), inbreeding coefficient(Fis), Shannon's information index (Si), Unbiased expected heterozygosity (UHe), and Nei's genetic identity (Ni) [6,8,9,11,16,18,22,26,30-32].

Genetic variation within *C. gariepinus* populations was has been reported as moderate and accounted mean number of Alleles (A), mean effective number of Alleles (Ae), Allelic richness (Ar), observed Heterozygosity (Ho), and expected Heterozygosity (He) ranges from 4.67-12.17; 3.15-5.80; 4.67-9.65; 0.50-0.69; 0.67-0.80, respectively [22]. Low allelic diversity was found in North African catfish populations from Thailand (A ranged from 6.00-7.00; Ae ranged from 3.43 - 4.59) while heterozygosity was moderate (Ho ranged from 0.52-0.72; He ranged from 0.67-0.77) [16]. Aliyu and Diyaware [30] reported the effective number of alleles with in *Clarias gariepinus* populations was 1.689 from Nigeria, which is fewer than that of the reported value ranging from 0.450 ± 0.050 and 0.442 ± 0.127 between *C. gariepinus* and *Heterobranchus bidorsalis* populations respectively in the same country Nigeria [19].

The endangered catfish populations in Bangladesh were found to have a high level of genetic diversity. This was indicated by the mean and effective number of Alleles (Ae), observed Heterozygosity (Ho), Shannon's information index (Si), and polymorphic information content, which varied from 41-44, 9.96-37.46, 0.57-0.76, 2.09-2.30, and 0.84-0.88, respectively [20]. Whereas low allelic diversity and moderate heterozygosity were reported from North African catfish, *C. gariepinus* populations in Thailand, as the mean number of alleles (A), the effective number of Alleles (Ae), observed heterozygosity (Ho), and expected heterozygosity (He) ranged from 6.00-7.00; 3.43-4.59; 0.52-0.72; 0.67-0.77), respectively [16]. Similar results were reported within African catfish, *C. gariepinus* populations in Hungary as the observed and expected overall heterozygosities were between 0.519 and 0.544, respectively [21].

The mean observed Heterozygosity (HO) was reported as moderate, ranging from 0.7975 ± 0.05 in natural to 0.6975 ± 0.045 in cultured *C. gariepinus* populations in Kenya. The mean number of alleles per locus (Na) was higher in farmed than in natural populations, ranging from 9.25 ± 2.9575; 6.9925 ± 2.5875, respectively. On the other hand, the mean predicted heterozygosity was marginally higher than Ho values, ranging from 0.7675 ± 0.0475 in natural populations to 0.8175 ± 0.04 in *C. gariepinus* populations that were cultured [24]. The genetic diversity values within farmed and wild African catfish, *C. gariepinus* populations were 0.4522 and 0.4018 respectively in Nigeria [9]. Whereas, the genetic diversities of bighead catfish populations were reported across three countries of Cambodia, Vietnam and Malaysia. Hence, the result showed that the higher genetic diversity in the mainland populations (Cambodia, He=0.761 to 0.813 and Vietnam, He=0.759 to 0.789 with mean number of alleles of 10.13 to 13.88) compared to Peninsular Malaysia (He=0.519 to 0.699 with mean number of alleles of 4.5 to 10.75) [33].

Moderate genetic diversity was determined in yellow catfish populations, with the observed Heterozygosity (Ho) ranging from 0.42 to 0.49 and the expected Heterozygosity (He) ranging from 0.51 to 0.61 in Chain [34]. The average observed Heterozygosity (Ho) and expected Heterozygosity (He) in the eight Channel catfish populations ranged from 0.504 to 0.767 and from 0.6 to 0.781, respectively [32]. The findings demonstrated the significant genetic variation among the eight populations of channel catfish.

The genetic diversity of Fare East catfish (*Silurus asotus*) was studied and reported as the average expected Heterozygosity (He) of the wild and cultured catfish sampled populations showed were 0.907 and 0.875 respectively in Korea [31]. Similarly in Kenya, higher observed and expected heterozygosity were reported in samples of natural than the cultured African catfish, *C. gariepinus* populations [6]. These investigations verified that a high degree of genetic diversity was preserved in both wild and cultured catfish populations. Because the nearby fish research institutes consistently released fry, it was successful in preserving variation in the wild catfish populations. But the genetic diversity in culture populations decreased. Maintaining high genetic diversity allows species to adapt to future environmental changes and avoid inbreeding, while maintain low genetic diversity the species has a small gene pool, and presences of inbreeding, which happens when there are small, isolated populations, can reduce a species' ability to survive and reproduce [35].

Haplotype diversity and nucleotide diversities are necessary to comprehend the knowledge of genetic diversities in fish species such as catfish populations [28]. Several researchers showed each diversities within and among catfish populations such as in Indian catfish, the recorded haplotype and nucleotide diversities were found ranged from 0.06897 to 0.76322 and 0.00019 to 0.00208, respectively

in India [36]; in *Clarias macrocephalu*, the recorded over all haplotype (0.479) and nucleotide (0.00058) diversities were found in Philippines [37], which shows alarmingly low genetic diversities compared with other fresh water fish populations (0.011) [38], in African catfish, *C. gariepinus* populations the nucleotide diversity was found 0.000869 in river and a tributary in northeast Nigeria [26], in North African catfish population, greater haplotype diversity (0.99930) and nucleotide diversity (0.07270) ware found in the three geographical isolated Rivers of Nigeria [10]. The formulation of conservation and management plans for wild fish populations benefited greatly from the knowledge of this genetic diversity, which also has consequences for fish species selection and long-term genetic improvement. Similarly, in Kenya, with in African catfish, *C. gariepinus* population the haplotype diversity was found highest in Lake Victoria (LV), and lowest in River Sosiani (SR), while, nucleotide diversity was highest in Lake Kamnarok (LKA) and lowest in Lake Victoria (LV) [39]. These demonstrate the presence of genetically diverse populations of *C. gariepinus*, necessitating spatially explicit management measures including lessening pollution, minimizing habitat degradation and fragmentation, and reducing fishing pressure in order to ensure sustainable stock utilization.

Percentage of polymorphism, allelic richness, inbreeding coefficient, Shannon's information index, unbiased expected heterozygosity and Nie's genetic identity are important parameters to understand the genetic diversity of fish species [28]. The research was conducted to examine the genetic diversity of African catfish, *C. gariepinus* population in northeast Nigeria and reported the percentage of polymorphism from farmed and wild populations ranged from 47.3% to 75.9%, respectively and the mean numbers of inbreeding coefficient (FIS) were 0.083 and 0.053 in the farmed and wild populations, respectively [10]. The findings show that northeast Nigeria has a notable degree of genetic diversity, which is helpful for the *C. gariepinus* breeding program's selection and long-term genetic improvement.

The percentage of polymorphic loci, gene diversities and Shannon's information index values in the three slender walking catfish, *Clarias nieuhofii* populations were found 75.00%, 0.2252, and 0.3443 for Surat Thani; 86.59 %, 0.2982, and 0.4441 for Narathiwat, and 96.25%, 0.3371, and 0.5049 for Phatthalung, respectively in southern Thailand [40]. The genetic difference between the Surat Thani and Narathiwat populations was determined to be the largest (0.2213) among the three populations. The findings showed that Clarias nieuhofii from several communities in southern Thailand exhibited a high degree of genetic variation. Building suitable breeding programmes and preserving populations that might serve as sources for stock management, restocking initiatives, and sustainable usage would both benefit from this information. Lal et al. [26] found that the percent polymorphism 50% and 31.25% respectively in samples from India and Thailand of exotic African catfish, *C. gariepinus* populations. The findings suggest that the *C. gariepinus* found in India may be a hybrid of many populations from several genetic lineages.

Population structure

In cases when evolutionary processes lead to genetic differentiation or genetic population structure, FST comparison is utilized as a metric by means of differentiation within and between populations as a key insight [41]. According to Holsinger and Weir [41], FST magnitude values range from 0 to 0.05 for minimal differentiation, 0.05-0.25 for moderate differentiation, and more than 0.25 for high population differentiation. The genetic structure of catfish is ascertained by estimating the differences across populations using the estimated coefficients of genetic differentiation (Fst) and gene flow (Nm) values. Hence, different authors reported the FST and Nm values in different catfish populations, (FST=0.1622, Nm=1.2909 [18] for African catfish, *C. gariepinus*; (FST=0.130, Nm=0.298 - 47.786 [33]) for Bighead catfish *Clarias macrocephalus*; (FST=0.038, Nm=12.79 [15]) for Bighead catfish; (FST=0.2815, Nm=1.2762 [40] for Slender Walking Catfish, *Clarias nieuhofii*; (FST=ranging from 0.203-0.129, Nm=0.9490 [9]) for African catfish, *C. gariepinus*; (FST=0.011, Nm=24.333 [20]) (Table 1). These indicate that there are significant factors between populations and gene flows are the main genetic differentiations.

Genetic distance is a measure of the genetic divergence between species or between populations within a species, whether the distance measures time from common ancestor or degree of differentiation [42]. Hence, genetic distance (D) also showed the significant genetic differentiation within and among groups of catfish populations and determines the population structure. Genetic distance between populations of catfish reported by different authors reviewed as showed in (Table 1). Genetic distances varying from 0.036-0.144 between population in the species of African catfish, *C. gariepinus* in Thailand [22]; varying from 0.087-0.161 between populations in the same species in the other part of the same country [16]; from 1.5798-3.4526 between populations in African catfish in India [18], from 0.007-0.019 between populations of bighead catfish in Viet Nam [15]; from 0.1381 - 0.2213 between populations of Slender Walking Catfish, Clarias nieuhofii in Thailand [41]; from 0.008-0.0519 between population of North African catfish, *C. gariepinus* in Nigeria [10], from 0.120-0.256 between populations of Endangered catfish, Rita rita in Bangladesh [20], from 0.080-0.273 between populations of Yellow catfish, *Pelteobagrus fulvidraco* in north to south Chain [43]; from 0.055-0.148 between populations of striped catfish, *Pangasianodon hypophthalmus* in Thailand [44]; 0.5213 between populations of African catfish , *C. gariepinus* in Nigeria [45]; 0.1038 between populations of African catfish, *C. gariepinus* in Nigeria [9]. These indicate that catfish populations with many similar alleles have small genetic distances. While catfish populations with different allele may have high genetic distances.

The applications of molecular markers for genetic diversity and population structure of African catfish

The most commonly used molecular markers in aquaculture include Allozymes, mitochondrial DNA (mtDNA), Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), microsatellites, Expressed Sequence Tag (EST) and Single Nucleotide Polymorphism (SNP) [46]. Microsatellite marker, RAPD, SNPs, mitochondrial DNA (mtDNA), and Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis (SDSPAGE) are used for African catfish, *C. gariepinus* species genomic studies (Table 2).

Due to their frequency, SNPs are the most often utilised marker in population genetic studies involving African Catfish, *C. gariepinus*. Isa [23] used SNPs marker to identify *C. gariepinus* from its closest relative *Clarias anguillaris* from Nigeria, for conservation and management purposes. Mitochondrial DNA marker is used for study the population genetic structure and genetic diversity of wild and farmed African catfish, *C. gariepinus* fish species populations in

Table 1: Estimated sources of genetic variations, coefficients of genetic differentiations and average gene flow of different catfish populations.

Country	Species	Sources of variations in %		Estimated mean F_{ST} values	Estimated genetic flow (Nm)	Estimated genetic distances (D)	Over all differentiation	References
		Among populations	Within populations					
Kenya	African catfish, *C. gariepinus*	22	88	0.22	-	-	Moderate	Echessa [24]
Nigeria	African catfish, *C. gariepinus*	1	99	0.19	-	0.5213	Moderate	Awodiran, Adeniran [45]
India	Indian catfish, *Clarias magur*	34.01	65.99	0.34014	-	-	High	Sahoo, Barat [36]
Thailand	African catfish, *C. gariepinus*	-	-	0.144 ± 0.026	-	0.036 to 0.144	Moderate	Wachirachaikarn, Rungsin [22]
Thailand	North African catfish, *C. gariepinus*	15.76	84.24	0.096 ± 0.034	-	0.087 to 0.161	Moderate	Wachirachaikarn and Na-Nakorn [16]
India	African catfish *C. gariepinus*	18	82	0.1622	1.2909	1.5798 to 3.4526	Moderate	Ezilrani and Christopher [18]
Kenya	African catfish, *C. gariepinus*	17.22	86.69	0.133	-	-	Moderate	Alal, Barasa [39]
Malaysia	Bighead catfish, *Clarias macrocephalus*	13.37	86.63	0.13	0.298 to 47.786	-	High	Nazia, Tam [33]
Nigeria	African catfish, *C. gariepinus*	8	92	0.01	-	-	Low	Ola-Oladimeji, Awodiran [12]
Viet Nam	Bighead catfish	-	-	0.038	12.79	0.007 to 0.019	Low	Nguyen and Duong [15]
Thailand	Slender Walking Catfish, *Clarias nieuhofii*	-	-	0.2815	1.2762	0.1381 to 0.2213	High	Pechsiri and Vanichanon [40]
Nigeria	North African catfish, *C. gariepinus*	75.73	24.27	0.75726	5.85	0.008 to 0.0519	high	Popoola [10]
Nigeria	African catfish *C. gariepinus*	72	28	0.719	0.098	-	high	Awodiran and Afolabi [17]
Bangladesh	Endangered catfish, *Rita rita*	1	99	0.11	24. 333	0.120 to 0.256	low	Ali, SALAM [20]
Nigeria	African catfish *C. gariepinus*	4	96	0.203 to 0.129	0.949	0.1038	Variable	Suleiman, Diyaware [9]
Philippines	*Clarias macrocephalus*	80.05	19.95	0.8005	-	-	high	Tan, Jumawan [37]
Thailand	Striped catfish, *Pangasianodon hypophthalmus*	17.57	82.4	0.167	-	0.055 to 0.148	moderate	Na-Nakorn and Moeikum [44]
China	Yellow catfish, *Pelteobagrus fulvidraco*	3.1	96.9	0.031	-	0.080 to 0.273	Variable	[43]

Uganda [47]; for analysis the population genetic differentiation and genetic diversity of *C. gariepinus* in the three water bodies of Southwest Nigeria [10] and for analysis the genetic diversity and population structure of *C. gariepinus* population in Kenya [6]. Random Amplified Polymorphic DNA (RAPD) is also used for the genomics studies of African catfish, *C. gariepinus* species for different purposes like for the assess the population genetic structure, genetic diversity and allelic richness of wild and farmed African catfish populations in Nigeria [8]; for gene characterization of wild and farmed African Catfish populations, *C. gariepinus* [9], which useful for genetic and breeding program in northeastern Nigeria and for analysis of genetic diversity of wild and cultured African catfish, Clarias gariepinus populations in Nigeria [17]. Aliyu and Diyaware [30] showed Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis (SDS PAGE) marker used to assess the genetic diversity of African catfish, *C. gariepinus* populations from the two lakes in Nigeria.

Microsatellite markers are used increasingly in aquaculture fish species due to their elevated Polymorphic Information Content (PIC), co-dominant mode of expression, Mendelian inheritance, abundance and broad distribution throughout the genome [48]. Microsatellite markers have also been developed in *Clarias gariepinus* fish species for desirable traits like growth enhancement, disease resistance, etc. [23]. Some authors used microsatellite marker for different genomic studies in African catfish, *Clarias gariepinus* species like demonstrating genetic differentiation and population structure in Kenya [6]; for genetic variations and differentiations in India [18]; for strain selection in Thailand [22]; for analysis the genetic diversity and population structure in Hungary [21]; for analysis the genetic diversity and population structure of North African catfish in Thailand [16], for separation of *C. gariepinus* (*Siluriformes*, *Clariidae*) fish populations [45] and for analysis the genetic diversity of wild and cultured populations in Nigeria [17] as indicated below in Table 2. Microsatellites are regarded as extremely dependable due to their high Polymorphism Information Content (PIC) values. When comparing the populations of fish rose in hatcheries and the wild, these molecular markers are useful. Therefore, the use of molecular markers is essential for the genetic improvement and sustainable management of *C. gariepinus* fish resources.

Marker assisted selective breeding in African catfish, *C. gariepinus* fish species

Marker-Assisted Selection (MAS) is the process of using

Table 2: Applications of molecular markers in the genetic diversity and population structure of the African catfish species, *C. gariepinus*.

Species	Molecular markers	Applications	References
North African Catfish, *C. gariepinus*	mtDNA	In order to investigate the genetic diversity and population genetic structure of African catfish populations in Uganda, both wild and cultivated.	[47]
African Catfish, *C. gariepinus*	SNPs	To differentiate between *C. gariepinus* and it's nearest related Nigerian *C. anguillaris* in Nigeria.	Isa [23]
North African Catfish, *C. gariepinus*	mtDNA	In order to offer information for the creation of conservation and management strategies for wild fish populations, it was necessary to demonstrate the genetic diversity and population genetic differentiation of *C. gariepinus* in the three water bodies located in Southwest Nigeria.	Popoola [10]
African Catfish, *C. gariepinus*	RAPD	To evaluate the genetic diversity, allelic richness, and population genetic structure of African catfish populations in Nigeria, both in the wild and under cultivation.	Suleiman, Moruf [8]
African Catfish, *C. gariepinus*	RAPD	In order to support the genetic and breeding programmes of *C. gariepinus* in northeastern Nigeria, it is necessary to characterize the genes of populations of African catfish that are raised and wild.	Suleiman, Diyaware [9]
Exotic African catfish, *C. gariepinus*	Allozyme	In order to differentiate between the genetic varieties of exotic catfish, samples of *C. gariepinus* were taken in India and Thailand.	Lal, Singh [26]
African Catfish, *C. gariepinus*	mtDNA and Microsatellite	To exhibit the *C. gariepinus* population's genetic diversity and population structure, which is utilised in Kenyan aquaculture and conservation methods.	Barasa, Mdyogolo [6]
African Catfish, *C. gariepinus*	SDS-PAGE	to evaluate the two lakes in Nigeria's African catfish population's genetic diversity.	Aliyu and Diyaware [30]
African Catfish, *C. gariepinus*	Microsatellite	To illustrate the genetic differentiations and variations that are important for managing India's fish resources and for the investigation of genetic diversity.	Ezilrani and Christopher [18]
African Catfish, *C. gariepinus*	Microsatellite	For strain selection in Thailand	Wachirachaikarn, Rungsin [22]
African Catfish, *C. gariepinus*	Microsatellite	For the purpose of population and conservation genetics of naturally occurring and bred African catfish populations in Hungary, it is useful to examine the genetic diversity and population structure of African catfish populations.	Sipos, Bakos [21]
North African catfish, *C. gariepinus*	Microsatellite	To examine the North African Catfish's genetic diversity and population structure, as these will be helpful in creating a foundational population for a genetic enhancement initiative in Thailand.	Wachirachaikarn and Na-Nakorn [16]
C. gariepinus (Siluriformes, Clariidae)	Microsatellite	This is used to analyse the genetic diversity and population structure of *C. gariepinus* populations in Nigeria in order to separate the populations.	Awodiran, Adeniran [45]
African catfish, *C. gariepinus*	RAPD and Microsatellite	To examine the genetic diversity of groups of African catfish kept in captivity and the wild in Nigeria.	Awodiran and Afolabi [17]

morphological, biochemical, or DNA markers as indirect selection criteria for selecting important traits in fish breeding [49]. In breeding programmes, this procedure is used to increase the efficacy or efficiency of selection for the desired traits.

The choice of economically important traits for genetic improvement largely depends on the consumer's preference, the farmers (yield, growth, diseases resistances and survival) and the feasibility of techniques or methods involved in farmed fish species like *C. gariepinus* species [50]. For instances, in Indonesia, the mutiara strain of African catfish, *C. gariepinus* was performed 10% to 40% better in growth, 15% to 70% better in productivity, 2-9 times higher in benefit-cost ratio, shorter growing period (45-60 days), lower feed conversion ratio (0.6-0.8) in nursery and (0.6-1.0) in grow out) and higher survival rate (60% to 70%) and it was much more resistant to disease than the local strain counterpart [51], useful for genetic improvement program.

Selective breeding for increased production is expected to enhance efficiency of resource utilisation of a production system, through correlated changes in feed efficiency or shorter production period [52]. Common steps using a selective breeding program of aquaculture fish species including African catfish, *C. gariepinus* are presented by Figure 1 [53].

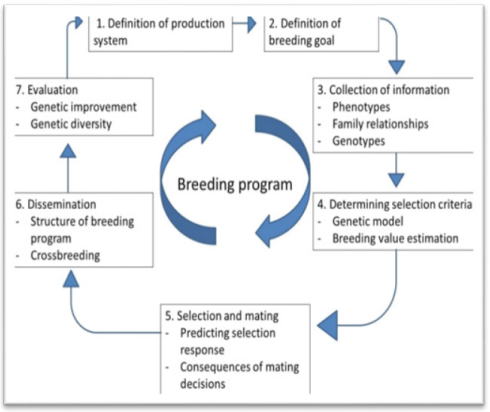

Figure 1: Steps using a selective breeding program adopted from Oldenbroek and van der Waaij [54].

Sustainable genetic improvement

According to estimates, just 10% of the world's aquaculture industry uses genetically modified stocks [54]. Choice of breeds, cross breeding, and selective breeding are some of the current techniques for genetic improvement used in aquaculture, while sex reversal, sterilization, and triploidization are more recent techniques used to improve fish production in aquaculture industry [51]. Genome-editing technologies such as CRISPR/Cas9 experiments with cultured fishes have focused on improving growth rate and disease resistance, achievement of reproductive confinement, and other valued traits [55,56].

Infectious disease is one of the primary constraints to aquaculture

production and, therefore, a major target for selective breeding and genome-editing approaches [56]. Host resistance to certain pathogens is a suitable trait for the use of genome-editing technologies due to the difficulty in non-destructive measurement of the trait in breeding candidates, the plausibility of utilizing cell culture genome-wide pooled CRISPR screens, and the frequent availability of early life *in vivo*-established challenge models [57]. Applications of genome editing fall into several categories: (i) finding causative variants underlying one or more Quantitative Trait Loci (QTLs) affecting traits of interest, followed by using editing to fix the favourable alleles; (ii) introducing favourable alleles from other populations, strains, or species into closed breeding systems through editing; and (iii) creating and utilising de novo alleles that positively affect the trait of interest.

The industry would benefit from the use of genome-editing technologies, such as CRISPR/Cas9, to annotate the protein pathways relevant to aquacultures, such as disease resistance, growth, development, adaptation, and sex determination, and to piece together the genomes of strains of *Clarias macrocephalus* and *C. gariepinus* cultured in Thailand, down to the chromosome level. Therefore, Clariid bio resources are important for genetic improvements in sustainable catfish farming [58]. The other report revealed that gene editing of channel catfish for the reproductive confinement of gene-engineered, domestic, and invasive fish to prevent gene flow into the natural environment appears promising [59]. These are important for genetic improvement of *C. gariepinus* provides promise in improving production. Strains of African catfish, *C. gariepinus* species that grow faster, exhibit greater disease resistance, and have other more favorable characteristics for aquaculture have been produced through selective breeding [51].

Economically significant genetic strains of *C. gariepinus* species include those that exhibit traits associated with aquaculture performance, such as growth, Feed Conversion Ratio (FCR), productivity, resistance to disease, resistance to stress, size uniformity, and benefit/cost ratio [51], used for the sustainable genetic improvement for the future generations (Table 3). Catfish production qualities have been successfully improved using selection, intraspecific crossbreeding, interspecific hybridization, and genetic engineering [60]. Interspecific hybridization, in contrast, really improved more features in a single cross compared to previous breeding programmes. However, more genetic improvement was produced by mass selection combined with crossbreeding, mass selection combined with genetic engineering, or mass selection combined with strain selection and hybridization than by any other genetic improvement program [61].

Research Gaps and Challenges

Studies on the genetic diversity and population structure of *C. gariepinus* species have advanced significantly, and these findings are valuable for long-term genetic improvement. However, there are still issues and gaps in our understanding that need to be resolved.

Conclusions and Recommendations

From this review we have investigated, African catfish, *C. garirpinus* fish genetic diversity and population structure assessments done by using molecular markers such as Microsatellites, SNPs, allozyme analysis, RAPD, mitochondrial DNA and SDS-PAGE markers as a useful tool to formulating meaningful conservation, and management strategies of commercially important fish species, which is African catfish. A key tool for selective breeding programmes that aim to provide economically significant genetic strains such as quickly increasing growth rate, disease resistance traits, improving meat quality, and so on is the study of genetic diversity and population structure. In order to maintain a diversified and representative brood stock population from multiple origins and geographical areas and retain genetic variety, an understanding of population structure and genetic diversity is essential. This indicates that regular monitoring and managing brood stock populations to minimize inbreeding depression and maintain genetic diversity. Employ advanced breeding strategies, including mate selection, genome-wide selection, and marker-assisted selection, to accelerate genetic improvement while maintaining genetic diversity.

Develop strategies for the conservation of genetically unique and endangered African catfish populations. Consider controlled hybridization between different populations, if appropriate, while ensuring genetic integrity and avoiding negative impacts on wild populations. Establish a system for continuous genetic monitoring of hatcheries, farms, and wild stocks to ensure the preservation and improvement of genetic diversity. Regularly report these findings to relevant stakeholders, including researchers, breeders, and policymakers. Foster collaboration between researchers, breeders, and stakeholders to share knowledge, exchange genetic resources, and implement sustainable breeding practices. Invest in capacity building programs to train professionals involved in genetic improvement activities.

References

1. FAO. The State of World Fisheries and Aquacultur: Towards Blue Transformation, Rome. FAO. 2022.

2. Chandra ST, Azra MN, Piah RM, Lananan F, Téllez-Isaías G, Gao H, et al. Catfishes: A

Table 3: Throughout this review, the main identified knowledge gaps and challenges on the studied genetic diversity and population structures of African catfish, *C. gariepinus* species.

Identified knowledge gaps	Identified challenges
Lack of comprehensive genetic data on African catfish species.	Research efforts have been limited, information related to their genetic diversity and population structure is still scarce.
Genetic composition and how African catfish species interact with each other are not well understood.	Taxonomic uncertainties, clear taxonomic boundaries and genetic differentiation among species are essential for understanding their genetic diversity and population structure accurately.
For conservation and sustainable management initiatives, it is essential to ascertain how aquaculture methods affect genetic diversity. Therefore, there are considerable gaps in our understanding of how aquaculture techniques affect the genetic diversity of the *C. gariepinus* species.	The genetic diversity and population structure of African catfish species can be greatly impacted by human activities such habitat degradation, overfishing, and the introduction of non-native species. Therefore, determining the full scope of these effects and creating sensible conservation plans are significant tasks.
Small sample numbers and a lack of representation over larger geographic regions are problems that plague many studies. Hence, in order to accurately reflect the genetic diversity and population structure of the *C. gariepinus* species, investigations should strive to incorporate a greater number of individuals from diverse geographic regions.	High-throughput sequencing and genome-wide markers are examples of sophisticated molecular methods that can be used to gain more precise insights on the genetic diversity and population structure of African catfish species. But putting these strategies into practice and deciphering the massive amounts of data they produce can be difficult technically.

global review of the literature. Heliyon. 2023;9(9):e20081.

3. Nwafili S, Gao T. Is the Dutch domesticated strain of C. gariepinus (Burchell, 1822) a hybrid? Afri J Biotech. 2007;6(8):6.

4. Hanssens M. A review of the clarias species (Pisces; Siluriformes) from the lower congo and the pool Malebo. J Afrotrop Zool. 2009;5:27-40.

5. Ouma DF, Barasa JE. Perspective chapter: species diversity and distribution of catfishes and their current contribution to global food security. Catfish-advances, technology, and experiments. 2022. IntechOpen.

6. Barasa JE, Mdyogolo S, Abila R, Grobler JP, Skilton RA, Bindeman H, et al. Genetic diversity and population structure of the African catfish, C. gariepinus (Burchell, 1822) in Kenya: implication for conservation and aquaculture - Corrigendum. Belgian J Zoology. 2017;147(2):9.

7. Dauda AB, Natrah I, Karim M, Kamarudin MS, Bichi A. African catfish aquaculture in Malaysia and Nigeria: Status, trends and prospects. Fish Aqua J. 2018;9(1):1-5.

8. Suleiman IO, Moruf RO, Usman BI. Population Genetic Structure of Feral and Cultured African catfish (C. gariepinus) inferred from Random Amplified Polymorphic DNA in Kano, Nigeria. Tropic J Nat Pro Res. 2023;7(3):2650-4.

9. Suleiman SB, Diyaware MY, Aliyu M, Mohammed ZB. Genetic Characterization of farmed and wild populations of African catfish (C. gariepinus burchell, 1822) using the random amplified polymorphic marker. J Agri Sci Belgrade. 2020;65(4):375-89.

10. Popoola OM. Genetic Differentiation and Molecular Phylogenetics of North African Catfish from Three Distinct Waterbodies. Croatian J Fish. 2022;80(3):123-32.

11. Bassey H. Phenotypic and Genetic Evaluation of Farmed and Wild Claria s gariepinus Broodstocks in Nigeria. UNESCO GRÓ Fish. Train Program Iceland Final Proj. 2020.

12. Ikpeme E, Udensi O, Okolo M, Ogban F, Ufford N, Odo E, et al. Genetic relatedness of C. gariepinus (L.) from cultured and wild populations using multivariate analyses. Asian J Animal Sci. 2016;10(2):131-8.

13. Ola-Oladimeji FA, Awodiran MO, Olaleye VF, Awopetu JI. Genetic Characterization Based on RAPD-PCR in Cultured Strains of C. gariepinus (Siluriformes: Clariidae). Gene Aqua Organisms. 2020;4(2):81-8.

14. Okumuş İ, Çiftci Y. Fish population genetics and molecular markers: II-molecular markers and their applications in fisheries and aquaculture. Turk J Fish Aqua Sci. 2003;3(1):51-79.

15. Nguyen NTTN, Duong TY. High Genetic Diversity and Gene Flow among Cultured and Wild Populations of Bighead Catfish (Clarias macrocephalus) in the Mekong Delta of Viet Nam Inferred from ISSR Markers. J Fish Environ. 2022;46(2):67-76.

16. Wachirachaikarn A, Na-Nakorn U. Genetic diversity of the North African catfish, C. gariepinus (Burchell, 1822) hatchery stocks in Thailand. Sci Asia. 2019;45(4):301-8.

17. Awodiran MO, Afolabi O. Genetic diversity in cultured and wild population of C. gariepinus (Burchell, 1822) in Nigeria Using Random Amplified Polymorphic DNA (RAPD) and Microsatellite DNA. Fish Aquac J. 2018:9(2):247.

18. Ezilrani P, Christopher JG. Genetic variation and differentiation in African catfish, C. gariepinus, assessed by heterologous microsatellite DNA. Indian J Biotech. 2015;14:388-93.

19. Agbebi O, Ilaboya D, Adebambo A. Preliminary characterization of genetic strains in clariid species, C. gariepinus and Heterobranchus bidorsalis using microsatellite markers. Afr J Biotech. 2013;12(4):364-9.

20. Ali MF, Salam MA, Sarder M, Rahman M, Mollah M. Genetic diversity and population structure of endangered catfish Rita rita (Hamilton, 1822) Revealed by Heterologous DNA Microsatellite Markers. Asian Fish Sci. 2021;34(2):181-94.

21. Kánainé SD, Bakos K, Ősz Á, Hegyi Á, Müller T, Urbányi B, et al. Development and characterization of 49 novel microsatellite markers in the African catfish, Clarias gariepinus (Burchell, 1822). Mol Biol Rep. 2019;46(6):6599-608.

22. Wachirachaikarn A, Rungsin W, Srisapoome P, Na-Nakorn U. Crossing of African catfish, C. gariepinus (Burchell, 1822), strains based on strain selection using genetic diversity data. Aquaculture. 2009;290(1-2):53-60.

23. Isa SI. Development of Genetic Improvement in the African Catfish (C. gariepinus, Burchell, 1822). FAO. 2019.

24. Echessa JB. Genetic Diversity, Population Structure and Influence on life-history traits of the African catfish, C. gariepinus (burchell 1822), in Kenya. University of Eldoret. 2018.

25. Uruku MN, Adikwu IA, Oyebola OO, Akombo PM. Genetic diagnosis on strains of the African Catfish, C. gariepinus (Burchell 1822) in River Benue and a Tributary in North East Nigeria. Int J Fish Aqua Studies. 2021;9(3):91-7.

26. Lal K, Singh R, Mohindra V, Singh B, Ponniah AG. Genetic make-up of exotic catfish Clarias gariepinus in India. 2003;16(3-4):229-34.

27. Nyunja C, Maina J, Amimo J, Kibegwa F, Harper D, Junga J. Stock structure delineation of the African Catfish (C. gariepinus) in selected populations in Kenya using mitochondrial DNA (Dloop) variability. J Aqua Res Dev. 2017;8(5):485.

28. Hvilsom C, Segelbacher G, Ekblom R, Fischer MC, Laikre L, Leus K, et al. Selecting species and populations for monitoring of genetic diversity. IUCN Publication. 2022.

29. Sjöqvist CO, Kremp A. Genetic diversity affects ecological performance and stress response of marine diatom populations. ISME J. 2016;10(11):2755-66.

30. Aliyu M, Diyaware MY, Aliyu J, Suleiman SB, Suleiman SB. Genetic diversity of African Catfish (C. gariepinus Burchell, 1822) from lakes alau and maladumba using sodium dodecyl sulfate polyacrylamide gel electrophoresis (SdsPage). Nig Ani Sci Techno. 2019;2(2):46-55.

31. Kim JE, Hwang JA, Kim HS, Lee JH. Genetic variability comparison of wild and cultured far eastern catfish (Silurus asotus) of korea using microsatellite marker. Dev Reprod. 2020;24(4):317-26.

32. Ma Q, Wu B, Jiang J, Song Z. Genetic characterization of selected domestic populations of channel catfish (Ictalurus punctatus) using microsatellites. Pakistan J Zool. 2020;52(5):1683-9.

33. Nazia AK, Tam BM, Jamaluddin JAF, Nor SAM. High genetic structure between natural populations of bighead catfish, Clarias macrocephalus (Günther, 1864) from the Mekong Delta and Peninsular Malaysia. Fish Res. 2021;241:105993.

34. Zhong L, Wang M, Pan J, Li D, Tang S, Bian W, et al. Evaluation of genetic diversity and population structure of five yellow catfish populations by microsatellite markers. Oceanolo Hydrobio Studies. 2018;47(2):99-106.

35. Neff BD, Garner SR, Pitcher TE. Conservation and enhancement of wild fish populations: preserving genetic quality versus genetic diversity. Canadian J Fish Aqua Sci. 2011;68(6):1139-54.

36. Sahoo L, Barat A, Sahoo SK, Sahoo B, Das G, Das P, et al. Genetic diversity and population structure of endangered Indian catfish, Clarias magur as revealed by mtDNA D-loop marker. Turk J Fish Aquat Sci. 2020;21(1):9-18.

37. Tan MTC, Jumawan JC, Quilang JP. Low genetic diversity in Clarias macrocephalus, 1864 (Siluriformes: Clariidae) populations in the Philippines and its implications for conservation and management. J Threatened Taxa. 2016;8(6):8849-59.

38. Manel S, Guerin PE, Mouillot D, Blanchet S, Velez L, Albouy C, et al. Global determinants of freshwater and marine fish genetic diversity. Nature Comm. 2020;11(1): 692.

39. Alal GW, Barasa JE, Chemoiwa EJ, Kaunda-Arara B, Akoll P, Masembe C. Genetic diversity and population structure of selected lacustrine and riverine populations of African catfish, C. gariepinus (Burchell, 1822), in Kenya. J Applied Ichthyo. 2021;37(3):427-38.

40. Pechsiri J, Vanichanon A. Genetic diversity in slender walking catfish (Clarias nieuhofii) populations: Implications for population management. Walailak J Sci Techno. 2016;13(7):511-19.

41. Holsinger KE, Weir BS. Genetics in geographically structured populations: defining, estimating and interpreting F(ST). Nat Rev Genet. 2009;10(9):639-50.

42. Wei H, Geng L, Shang X, Li L, Ma B, Zhang Y, Li W, et al. Comparison genetic diversity and population structure of four Pseudaspius leptocephalus populations in Heilongjiang River Basin based on mitochondrial COI gene. Front Mar Sci. 202310:1158845.

43. Guo XZ, Chen HM, Wang AB, Qian XQ. Population genetic structure of the yellow catfish (Pelteobagrus fulvidraco) in China inferred from microsatellite analyses: Implications for fisheries management and breeding. J World Aqua Soc. 2022;53(1):174-91.

44. Na-Nakorn U, Moeikum T. Genetic diversity of domesticated stocks of striped catfish, Pangasianodon hypophthalmus (Sauvage 1878), in Thailand: relevance to brood stock management regimes. Aquaculture. 2009;297(1-4):70-7.

45. Awodiran M, Adeniran F, Akinwale R, Akinwande A. Microsatellite variability of two populations of C. gariepinus (siluriformes, Clariidae) in Nigeria. Vestnik Zoologii. 2019;53(3):195-208.

46. Rodrigues KF, Biun H, Yong WTL, Chin GJWL, Ching FF, Othman R. The Application of Molecular Markers in Fish Breeding and Aquaculture. Marine Biotechnology: Applications in Food, Drugs and Energy". Springer. 2023. p. 73-101.

47. Daniel O. Population genetics structure of wild and domesticated African catfish (C. gariepinus) in Victoria and Albertine Drainage Basins in Kenya. 2015.

48. Martinez V, Guimarães E, Ruane J, Scherf B, Sonnino A, Dargie J. Marker-assisted selection in fish and shellfish breeding schemes. Marker-Assisted selection-Current status and future perspectives in crops, livestock, forestry and fish. 2007:329-62.

49. Haldar C. Importance of marker assisted selection in fish breeding in India: Challenges and opportunities. Ann Aquac Res. 2018;5(1):1047.

50. Eze F. Marker-assisted selection in fish: A review. Asian J Fisheries Aquatic Res. 2019;3(4):1-11.

51. Imron I, Iswanto B, Suparapto R, Marnis H. Development of genetically improved farmed African Catfish, C. gariepinus; a review and lessons learned from indonesian fish breeding program. In IOP Conference Series: Earth and Environmental Science. 2020;593(1):012032.

52. Sae-Lim P, Kause A, Mulder HA, Olesen I. Selective breeding in aquaculture for future environments under climate change. Internal project View project Or Aqua View project. 2016.

53. Oldenbroek K, van der Waaij L. Textbook animal breeding: animal breeding and genetics for BSc students. 2014.

54. Gjedrem T, Robinson N, Rye M. The importance of selective breeding in aquaculture to meet future demands for animal protein: a review. Aquaculture. 2012;350-353:117-29.

55. Hallerman E. Genome editing in cultured fishes. CABI Agriculture and Bioscience. 2021;2(1):1-19.

56. Gratacap RL, Wargelius A, Edvardsen RB, Houston RD. Potential of genome editing to improve aquaculture breeding and production. Trends in Genetics, 2019;35(9):672-84.

57. Gaj T, Sirk SJ, Shui SL, Liu J. Genome-editing technologies: principles and applications. Cold Spring Harb Perspect Biol. 2016;8(12):a023754.

58. Lisachov A, Nguyen DHM, Panthum T, Ahmad SF, Singchat W, Ponjarat J, et al. Emerging importance of bighead catfish (Clarias macrocephalus) and north African catfish (C. gariepinus) as a bioresource and their genomic perspective. Aquaculture. 2023;573:739585.

59. Qin G, Qin Z, Lu C, Ye Z, Elaswad A, Bangs M, et al. Gene Editing of the Catfish Gonadotropin-Releasing Hormone Gene and Hormone Therapy to Control the Reproduction in Channel Catfish, Ictalurus punctatus. Biology (Basel). 2022;11(5):649.

60. Houston RD, Kriaridou C, Robledo D. Animal board invited review: Widespread adoption of genetic technologies is key to sustainable expansion of global aquaculture. Animal. 2022;16(10):100642.

61. Dunham RA, Liu Z. Gene mapping, isolation and genetic improvement in catfish. Aquatic genomics: Steps Toward a Great Future. 2003. p. 45-60.