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Genetic and Haplotype Diversity of *Clarias gariepinus* (Burchell 1822) Based on *Cytochrome c Oxidase I* (COI) Gene

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Abstract: The evaluation of mitochondrial DNA and genetic analysis is helpful for economically significant species. *Clarias gariepinus* is a critical species in aquaculture. This study investigates the genetic diversity and population differentiation of *C. gariepinus* from 19 countries using 164 sequences of the mitochondrial DNA's *Cytochrome c oxidase I* (COI) gene. The haplotype analysis revealed a total of 17 haplotypes, with a nucleotide diversity (π) of 0.012 and a haplotype diversity (Hd) of 0.87. The results of an AMOVA and fixation index indicated significant genetic variation and structure among the populations. Additionally, neutrality tests and mismatch distribution analysis supported the hypothesis of under-purifying selection in *C. gariepinus*. The findings suggested that the population did not experience expansion. In conclusion, the genetic analysis highlighted substantial variation among *C. gariepinus* populations from different locations, providing valuable insights for the global management of this species.

Keywords: African catfish; *Cytochrome c oxidase I*; neutrality tests; AMOVA

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1. Introduction

The African catfish (*Clarias gariepinus*) is a well-known freshwater fish found in the African savannah woodland [1]. It can survive in low-oxygen environments and tolerate poor water quality due to its accessory air-breathing organs. However, this fish has a wide range of temperatures [2]. Catfish are hardy and can withstand various environmental fluctuations [3]. The African catfish is one of the most widely cultured fish globally, accounting for 0.33% of total aquaculture production in Nigeria, Uganda, and Egypt [4]. This species is extensively used in aquaculture in South and Southeast Asian countries such as Bangladesh, China, India, Indonesia, Malaysia, Myanmar, North Korea, the Philippines, and Thailand [5].

Recently, farmers have observed a decline in the performance of African catfish, including reduced growth, sperm quality, disease resistance, and an increased occurrence of abnormal body and testes development [6]. While environmental factors may contribute to these changes, genetic deterioration is a likely explanation [7].

Understanding the genetic diversity of organisms is crucial for examining and preserving their ecosystems. Genetic diversity plays a pivotal role in the conservation of species within their natural habitats [8]. Several factors, such as pollution, unfavorable habitat, and the environment, may cause a substantial change in population allele frequency [9]. The *cytochrome c oxidase I* (COI) gene was proven reliable for genetic diversity and geographical distribution studies in various fish species [10]. Studies showed that the COI gene's slow evolution makes it a suitable DNA marker for genetic studies [10]. Several studies reported that the genetic variability of *C. gariepinus* is moderately high [11,12]. Barasa et al. [8] reported high genetic diversity and population differentiation of *C. gariepinus* from Kenya. However, Kundu et al. [13] revealed that the genetic diversity of *C. gariepinus* from Cameroon was reduced across its native and introduced range, which inbreeding might have induced.

Studying the global population genetic structure of *C. gariepinus* is essential due to its significance in worldwide aquaculture and regional fisheries. This research aimed to determine the haplotype diversity and genetic structure of *C. gariepinus* worldwide using the COI marker. Therefore, a worldwide survey of the genetic diversity, haplotype diversity, and population differentiation of *C. gariepinus* could provide recommendations for managing this species in aquaculture and suggest conservation plans.

2. Materials and Methods

2.1. Genetic Diversity, Phylogenetic Analysis, and Genetic Structure

To assess the genetic diversity of *C. gariepinus* globally, based on all available sequences on the GenBank, we collected 164 COI sequences of *C. gariepinus* from NCBI (GenBank; Table S1). We used BioEdit [14] to analyze the quality of the COI sequences. Sequences were aligned using the ClustalW [15] method in the MEGA X software [16], and all COI gene sequences were standardized to 580 bp to eliminate any missing data through the FaBox online toolbox [17].

Genetic diversity was determined by evaluating the number of haplotypes (H), segregating sites (S), haplotype diversity (h), and nucleotide diversity (π) across all populations and regions using DnaSP version 6 [18]. To explore the relationship among the haplotypes of COI loci in the *C. gariepinus* population, we exported the sequence data for the Median-joining haplotype Network from DnaSP v6.12.03 and conducted a haplotype network analysis in the PopART program [19]. Phylogenetic trees were generated using the Bayesian inference method implemented in the program Mr. Bayes 3.1.2 [20]. The GTR+I+G model was selected using jModeltest 2.1.10 [21]. Then, the chosen model was initiated with a random starting tree and was run with the Markov chain Monte Carlo (MCMC) for 10^6 generations. *Clarias macrocephalus* (MG407382) was selected as an outgroup to root the phylogenetic tree. The trees were visualized using FigTree v1.4.4 [22].

An AMOVA was performed to estimate genetic diversity within and among populations. Furthermore, we calculated the fixation index (Fst) with 10,000 permutations using Arlequin version 3.5 [23] to determine the genetic differentiation between populations. We evaluated the degree of population differentiation using pairwise Fst values in Arlequin 3.5 ($p < 0.05$), treating all populations as a single group. The genetic relationships between populations were visualized using the pairwise Fst matrix.

2.2. Neutrality and Population Size Change Test

The statistical tests Tajima's D [24] and Fu's Fs [25] are commonly used to distinguish between sequences evolving neutrally under mutation–drift equilibrium and those evolving non-neutrally due to balancing or directional selection processes. These tests help determine whether mutations are selectively neutral or not. The analyses were performed using Arlequin version 3.5 [23] by running 1000 simulations under a selective neutrality model. The program DnaSP v6.12.03 was used to analyze the population size change.

3. Results

3.1. Haplotype Network and Genetic Diversity

The haplotype diversity (Hd) varied from 0.0 (China, Turkey, Algeria, Malaysia, and Brazil) to 0.66 (Bangladesh) among populations. The average Hd was 0.87, and the average nucleotide diversity (π) was 0.012 (Table 1). Additionally, among all populations analyzed, Indonesia and Bangladesh showed the highest nucleotide diversity (0.01), while China, Turkey, Algeria, Malaysia, and Brazil showed the lowest (0.00) (Table 1).

The median-joining (MJ) network comprised 17 haplotypes (Table S2), which indicates the distribution of haplotypes across different populations in various countries (Figure 1). Haplotype 1 was the core haplotype and was present in *C. gariepinus* populations from Egypt, Nigeria, Zimbabwe, Ethiopia, Sudan, Syria, India, Bangladesh, Indonesia, Thailand, and China. Haplotype 4 was found in Malaysia, the Philippines, Bangladesh, Thailand, and India.

Table 1. Genetic diversity values for the 161 sequences of *Clarias gariepinus* of mtDNA *Cytochrome c oxidase I* sequences. n: Sample size; S: Number of segregating sites; h: Number of haplotypes; Hd: haplotype diversity; π: Nucleotide diversity. Syria, Ethiopia, and Sudan had only one sequence, which was removed automatically by the software.

Country	Genetic Diversity					Neutrality Test	
	n	S	h	Hd	π	Tajima (D)	Fu's Fs
Egypt	7	2	3	0.52	0.0016	−1.35 NS	−1.79 NS
Nigeria	21	2	3	0.4	0.0015	−0.48 NS	−0.14 NS
Indonesia	6	6	2	0.6	0.01	2.25 NS	6.77 NS
Bangladesh	3	6	2	0.66	0.01	NA	NA
Thailand	13	8	3	0.41	0.007	0.06 NS	3.04 NS
India	20	9	3	0.46	0.0075	0.18 NS	4.34 NS
Zimbabwe	4	7	2	0.5	0.0098	−0.84 NS	4.6 NS
China	2	0	1	0	0	NA	NA
Turkey	21	0	1	0	0	NA	NA
Cameroon	13	7	2	0.5	0.0065	−0.43 NS	2.87 NS
Algeria	4	0	1	0	0	NA	NA
Malaysia	2	0	1	0	0	NA	NA
Philippines	5	2	2	0.4	0.0022	−1.12 NS	0.64 NS
Congo	10	1	2	0.5	0.0015	−0.35 NS	0.39 NS
Brazil	5	0	1	0	0	NA	NA
Uganda	25	4	5	0.65	0.0026	−0.77 NS	−3.2 NS
Total	161	22	17	0.87	0.012	0.31	−0.31

NS = not significant ($p > 0{\cdot}05$); NA = not applicable.

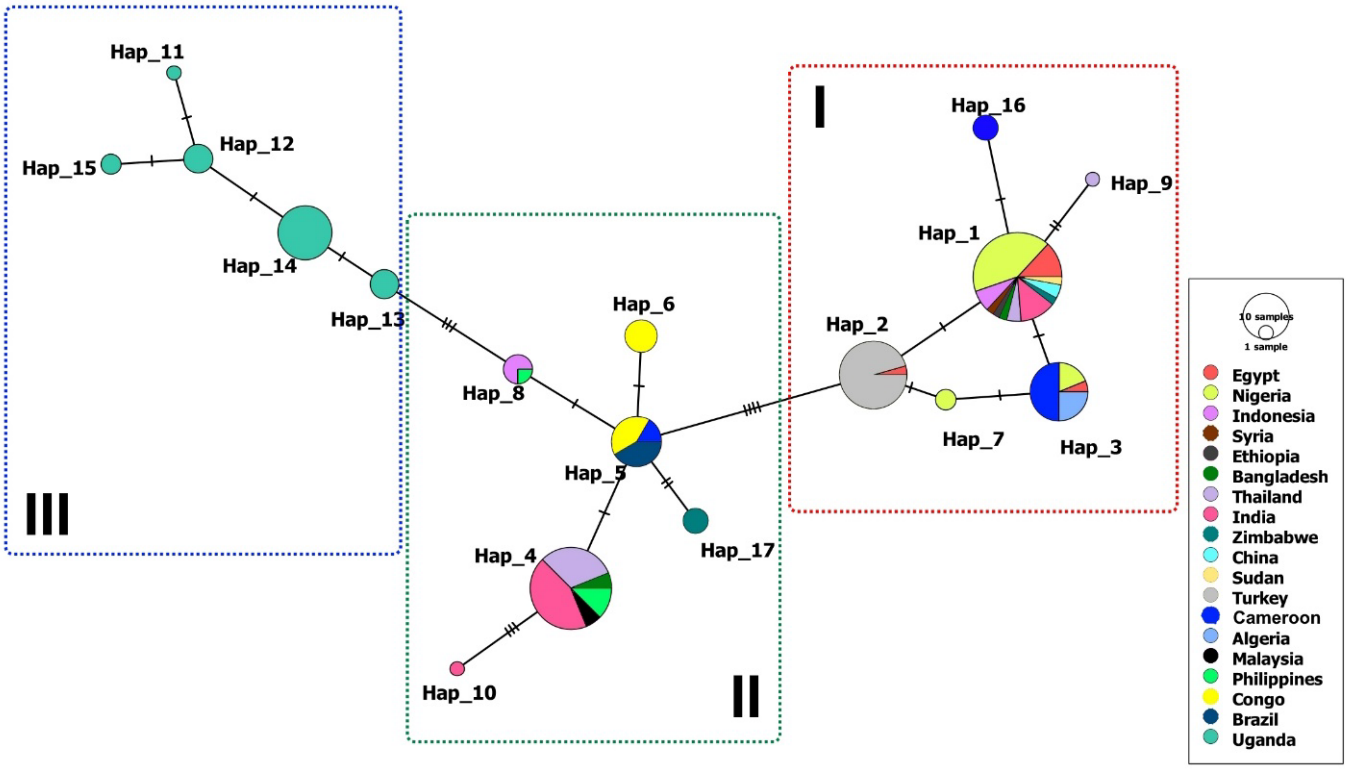

Figure 1. A median-joining network of *Clarias gariepinus* haplotypes. The size of the circle indicates the relative frequency of the corresponding haplotype, and the colors represent the corresponding population/country. The branches' black lines point to the mutational changes between two haplotypes. Cluster I indicates different haplotypes from India, Thailand, Indonesia, Bangladesh, Cameroon, China, Turkey, Syria, Algeria, Zimbabwe, Ethiopia, Sudan, Nigeria, Uganda, and Egypt.

Cluster II indicates different haplotypes from India, Cameroon, Philippines, Indonesia, Bangladesh, Malaysia, Zimbabwe, DR Congo, and Brazil. Cluster III indicates different haplotypes from Uganda.

Figure 2 illustrates the distribution of COI haplotypes in the *C. gariepinus* population across different countries. The African populations exhibited the highest variation with 12 distinct haplotypes, followed by India, Thailand, the Philippines, and Indonesia.

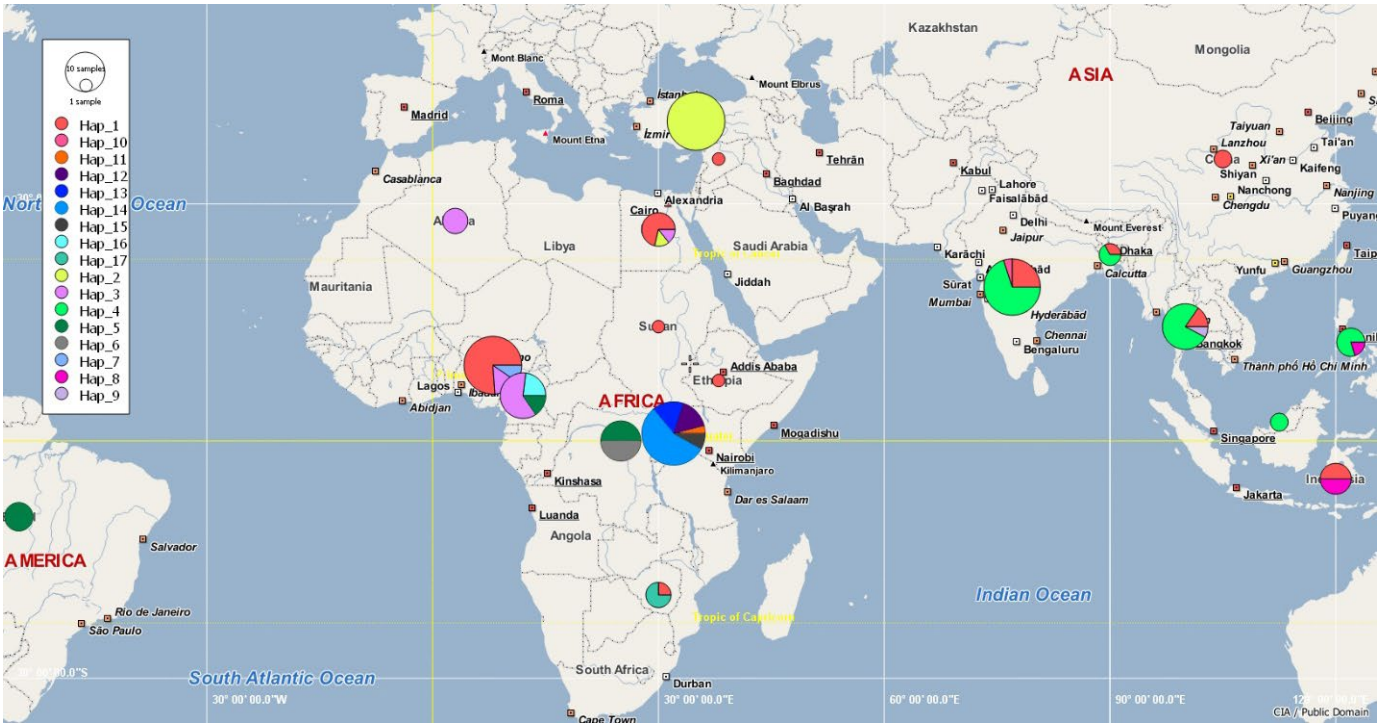

Figure 2. Frequency of haplotypes in different countries. Colors show various haplotypes of COI in the *Clarias gariepinus* population. The size of the circle is proportional to the number of specimens in different geographic regions.

3.2. Phylogenetic Analysis

The result of phylogenetic analysis indicated that three major clades, including Clade I, represented haplotypes belonging to populations of Africa and Asia (Egypt, Nigeria, Zimbabwe, Algeria, Ethiopia, Sudan, Uganda, Syria, Turkey, India, Bangladesh, Indonesia, Thailand, China, Cameroon); Clade II represented haplotypes from India, Bangladesh, Thailand, Malaysia, Philippines, Indonesia, Cameroon, DR Congo, Brazil; and Clade III represented haplotypes from Uganda, which showed a high posterior probability value (Figure 3). The phylogenetic tree revealed that the haplotype variation in Uganda is high, which confirmed the results for the median-joining haplotype network (Figure 1). The population of Uganda with five different haplotypes (Hap 11, 12, 13, 14, 15) is distributed into Clade III of the phylogenetic tree (Figure 3).

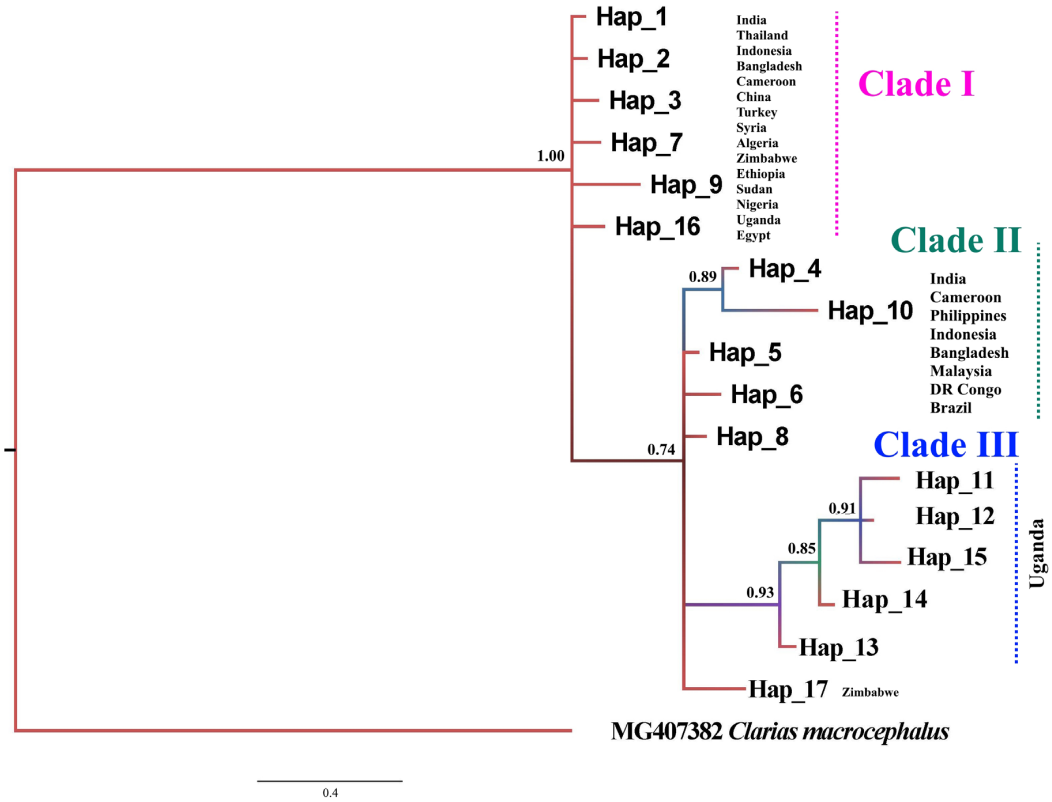

Figure 3. The Bayesian tree inferred for *Clarias gariepinus* using haplotypes. Clade I indicates different haplotypes from India, Thailand, Indonesia, Bangladesh, Cameroon, China, Turkey, Syria, Algeria, Zimbabwe, Ethiopia, Sudan, Nigeria, Uganda, and Egypt. Clade II indicates different haplotypes from India, Cameroon, Philippines, Indonesia, Bangladesh, Malaysia, DR Congo, and Brazil. Clade III indicates different haplotypes from Uganda.

3.3. Molecular Variance Analysis

An analysis of molecular variance (AMOVA) was conducted on populations of *C. gariepinus* in various countries to assess their genetic structure. The findings revealed that 76% of the genetic variation existed among populations, while 23.9% was within populations, with significant differences among populations at $p < 0.001$.

The F_{ST} value of 0.75 for each pair of populations significantly differed from zero ($p < 0.001$), indicating a substantial genetic structure among the populations (refer to Table 2). Additionally, Table 3 displays the degree of population differentiation. The pairwise F_{ST} values demonstrated noteworthy distinctions between all populations from different countries. The genetic structure of Uganda populations displayed a highly significant difference ($p > 0.05$) from the other populations, except for populations from India and Thailand ($p < 0.05$).

Table 2. AMOVA analysis was carried out using the Arlequin program for 164 sequences of *Clarias gariepinus* based on COI.

Source of Variance	df	Sum of Squares	Variance Component	% Total of Variance	Significance
Among populations	18	1766.958	10.414	76.03	$p < 0.001$
Within populations	145	476.085	3.283	23.97	$p < 0.001$
Total	163	2243.043	13.697	100	$p < 0.001$

Table 3. Heatmap of pairwise F_{ST} values estimated from mitochondrial DNA sequence data. The significant *p*-values are present in the upper diagonal; F_{ST} values are in the lower diagonal.

	Egypt	Congo	Nigeria	Ethiopia	Uganda	Cameron	Algeria	Zimbabwe	Sudan	Malaysia	Indonesia	Syria	Philippines	Turkey	Bangladesh	Thailand	India	China	Brazil
Egypt	0	*			*		*	*		*			*	*	*	*	*		*
Congo	0.99369	0	*	*	*	*	*	*	*	*	*	*	*	*				*	
Nigeria	−0.03424	0.87068	0		*			*		*			*		*	*	*		*
Ethiopia	−0.83333	0.99535	−0.88707	0	*		*			*			*	*		*			*
Uganda	0.98645	0.81673	0.90522	0.98523	0	*	*	*	*	*	*	*	*	*	*			*	*
Cameron	0.20429	0.65997	0.13968	−0.38625	0.76875	0							*						*
Algeria	0.61763	0.99652	−0.03011	1	0.98693	0.11628	0	*	*	*		*	*	*	*	*		*	*
Zimbabwe	0.75296	0.85974	0.69942	0.33333	0.92261	0.45197	0.66839	0		*			*	*		*		*	*
Sudan	−0.83333	0.99535	−0.88707	0	0.98523	−0.38625	1	0.33333	0	*			*	*		*			*
Malaysia	0.99245	0.80769	0.82461	1	0.77335	0.49473	1	0.63977	1	0		*		*				*	*
Indonesia	0.42429	0.50665	0.35525	−0.2	0.69402	0.00512	0.32458	0.38803	−0.2	0.15493	0			*					
Syria	−0.83333	0.99535	−0.88707	0	0.98523	−0.38625	1	0.33333	0	1	−0.2	0	*	*		*			*
Philippines	0.99068	0.65901	0.84572	0.98993	0.76146	0.5835	0.99425	0.77465	0.98993	−0.29032	0.3609	0.98993	0	*				*	*
Turkey	0.83709	0.99853	0.15808	1	0.99182	0.38071	1	0.89312	1	1	0.664	1	0.99829	0	*	*	*	*	*
Bangladesh	0.69744	0.4377	0.57085	0	0.68054	0.11114	0.58264	0.39575	0	−0.2	−0.23918	0	0.17909	0.87578	0				
Thailand	0.70883	0.14103	0.66687	0.54345	0.35719	0.38266	0.66734	0.60324	0.54345	−0.20999	0.10486	0.54345	0.00253	0.81736	−0.17659	0		*	
India	0.52531	0.1565	0.51258	0.2865	0.31308	0.24204	0.48252	0.45213	0.2865	−0.13015	−0.00514	0.2865	0.05509	0.64584	−0.22063	−0.03022	0		
China	−0.22709	0.99582	−0.27778	0	0.98587	−0.00703	1	0.52941	0	1	0.14286	0	0.99196	1	0.36842	0.61306	0.41187	0	
Brazil	0.99471	0.33333	0.84762	1	0.80016	0.5857	1	0.7797	1	1	0.3617	1	0.66667	1	0.22103	0.04619	0.07859	1	0

* indicates significant difference ($p < 0.05$). Red and green cells represent the level of significant and non-significant pairwise FST values, respectively.

3.4. Demographic History and Neutrality

The analysis of the combined COI sequences revealed that Tajima's D and Fu's Fs were not statistically significant. Specifically, the values for Tajima's D and Fu's Fs were 0.31 ($p > 0.05$) and −0.13 ($p > 0.05$), respectively, as indicated in Table 1. Tajima (D) values for Zimbabwe, Cameroon, Philippines, Congo, Egypt, Nigeria, and Uganda were negative, whereas Tajima (D) for Indonesia, Thailand, and India populations were positive. However, Fu's Fs in all populations were positive except for the populations of Egypt, Nigeria, and Uganda.

Pairwise and mismatch comparisons are shown in Figure 4 for all sequences. The raggedness index was 0.038, and there was no significant difference from zero for entire populations ($p > 0.05$). The results revealed a multimodal mismatch distribution graph, indicating an equilibrium in the population structure. Additionally, the results showed that the population did not experience expansion.

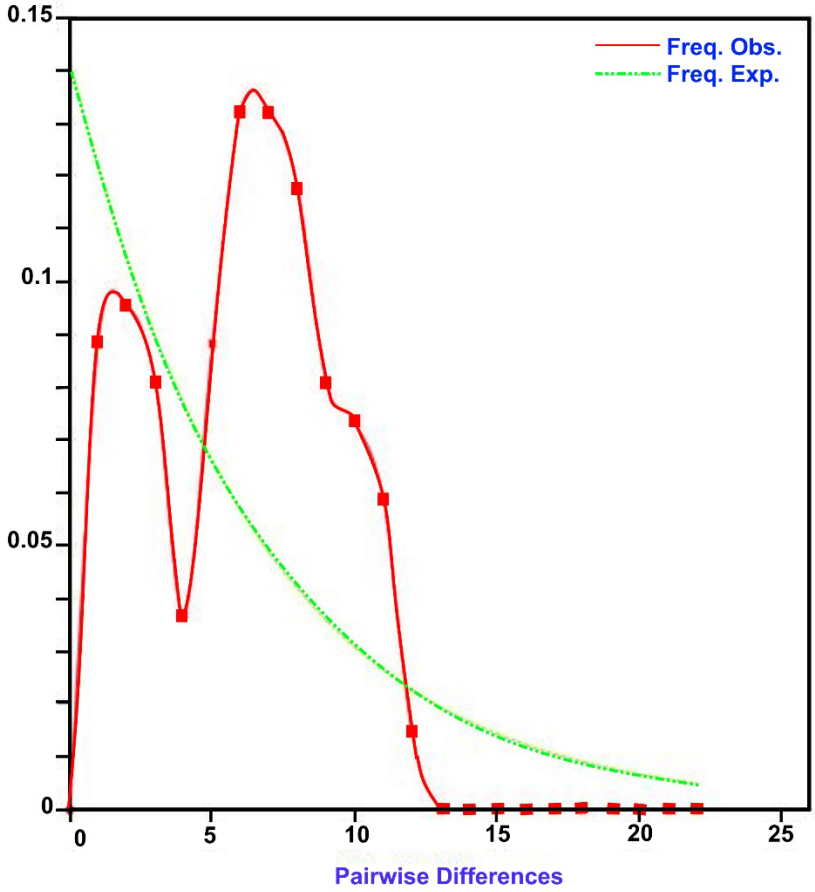

Figure 4. Frequencies of the observed and expected pairwise nucleotide differences (mismatch distributions) from COI sequences of all *Clarias gariepinus* populations. X-axis (x): number of pairwise differences; Y-axis (y): frequency of mismatches; Freq. Exp.: frequency expected (green dashed line); and Freq. Obs: frequency observed (red solid line).

4. Discussion

The present study was based on comparing the genetic diversity of *C. gariepinus* in different locations in the world using an mtDNA marker. This study analyzed 17 haplotypes that existed in the population of *C. gariepinus*, six of which were detected similarly. The presence of shared haplotypes (Hap_1, Hap_2, Hap_3, Hap_4, Hap_5, Hap_8) across various countries suggests a common ancestral lineage. This observation highlights that individuals from geographically distant countries and continents possess these haplotypes, indicating a shared origin associated with introducing fish for aquaculture purposes. As

a result, *C. gariepinus* has been widely introduced to other parts of the world for fish farming. In 1975, *C. gariepinus* was introduced from the Central African Republic to Côte d'Ivoire, Vietnam, Congo, and Laos [26]. In 1987, *C. gariepinus* was introduced from Laos to Thailand [27], and then from Thailand, it was introduced to the Philippines (1985), Malaysia (1986), and Bangladesh (1989) [28]. African catfish was introduced to India from Bangladesh [29].

In this study, 11 haplotypes were singleton haplotypes, especially for African continent populations. As a result, *C. gariepinus* has been widely distributed across different geographical locations because this fish has biological fecundity and ecological tolerance. Therefore, the current genetic structure is due to the geographical isolation of populations. Similar genetic differentiation patterns were observed in *C. gariepinus* populations in Kenya [12]. In contrast, Van Steenberge et al. [30] found that colonization, rather than extinction, has shaped the distribution patterns of *C. gariepinus*, distinguishing it from other common African freshwater fish and highlighting its connection to the evolution of African drainage basins. Kundu et al. [13] also identified distinct separations between populations of *C. gariepinus* and noted high genetic diversity across various African regions. Furthermore, Weyl et al. [31] and Parvez et al. [28] discussed the widespread use of *C. gariepinus* in aquaculture and its introduction into multiple African riverine systems. Human activities, particularly in the case of Clarias, involve frequent movement of fish populations across drainage basins [32]. Additionally, Barasa et al. [12] reported the extraction of pituitary hormones and milt for artificial propagation in hatcheries, involving the removal of males from natural populations of Clarias. Lastly, Barasa et al. [33] emphasized the potential for increased genetic variation in farmed *C. gariepinus* through the combination of genetically distinct stocks.

The African catfish populations showed high nucleotide diversity ($\pi > 0.005$) and high haplotype diversity (Hd > 0.5) due to the high mutation rate of the COI region [34]. The study also found that the populations from Indonesia and Bangladesh displayed high nucleotide diversity ($\pi > 0.005$) and high haplotype diversity (Hd > 0.5) attributed to a high mutation rate of the COI region, likely due to inbreeding or hybridization for aquaculture purposes [33]. Comparing populations with high haplotype diversity to those with low nucleotide diversity (e.g., Uganda, Congo, Egypt) suggests a recent divergence in *C. gariepinus* [35], leading to the establishment of independent lineages from ancestral populations with a small effective population size [36]. In this study, according to the low number of sequences (N = 2), some populations, such as China and Malaysia, showed low haplotype diversity. However, the results for the Bangladesh population (N = 3) showed high haplotype diversity. Fatsi et al. [37] found that the level of genetic diversity depends on species-specific molecular markers. Therefore, it can be inferred that the genetic structure of the populations is a result of disturbances in the genetic structure of *C. gariepinus*. The present study's haplotype network demonstrated a mutational topology, with several mutations separating branches between haplotypes, resulting in high haplotype variation. The high number of unique variations in the mitochondrial DNA of populations may be due to its rapid evolution rate for genetic structures [34]. The mitochondrial region serves as an effective indicator of genome changes due to its population size being four times smaller than that of the nuclear genome [38]. Consequently, this discrepancy results in the manifestation of private haplotypes within populations [8]. The results were in agreement with several studies. Giddelo et al. [1] reported a high variation in haplotypes with a low number of mutations in *C. gariepinus* in Eastern Africa. Barasa et al. [8] found thirty-one haplotypes in *C. gariepinus* from mtDNA sequences in the Kenya population, in which a few mutations separated haplotypes.

The phylogenetic analysis (Figure 3) showed that the population from cluster III in Uganda, represented by Hap 11, 12, 13, 14, and 15, is distinct from other groups on the phylogenetic tree. This group displayed significant demographic differences. Additionally, the haplotype network analysis revealed that most haplotypes are specific to only one population and unique [39]. The result of the phylogenetic analysis indicated that Clade I

includes all the countries (Asian countries) where this fish was introduced for aquaculture purposes. On the other hand, Southeast Asian countries (e.g., the Philippines and Thailand) have the same climate [40]. Therefore, a low number of mutations happened in the COI gene (Hap_2, 3, 7, 9,16).

Population genetic structures undergo dynamic changes through historical and ongoing evolutionary processes [41]. Identifying these structures is important for understanding biological processes that have shaped contemporary species' evolution from past to present species [42]. The AMOVA analysis of *C. gariepinus* populations revealed that the greatest proportion of variation exists among populations, indicating substantial distinctions between them, as shown in Table 2. This outcome implies that *C. gariepinus* exhibits a varied distribution pattern across all populations. The 17 haplotypes displayed strong genetic structuring, which could be due to asymmetric introgression. It seems that younger populations resulting from uneven breeding exhibit more hybrid vigor in certain areas and have not yet reached a genetic equilibrium, suggesting that these populations are relatively new and active. The haplotype network, which aligns with the AMOVA, separates genetic clusters among populations by 76.03% genetic variance and differentiated genetic clusters among populations. The genetic ancestry for all populations and locations in our dataset is clearly displayed in Table 3.

Genetic distance is a measure of the genetic divergence between species or between populations within a species, whether the distance measures the time from a common ancestor or the degree of differentiation [43]. Hence, genetic distance also showed significant genetic differentiation within and among groups of catfish populations and determined the population structure. Genetic distance between catfish populations (Table 3) indicated no significant genetic distance exists in all the countries (e.g., Bangladesh, Thailand, India, and Philippines) where this fish was introduced for aquaculture purposes. However, the African populations had a significant genetic distance (e.g., Uganda, Cameron, Algeria, Zimbabwe, and Congo). We can observe this significant difference in distribution patterns of *C. gariepinus* for African populations. The previous study indicated that colonization, rather than extinction, shaped the distribution patterns of *C. gariepinus* [30]. These patterns indicate that catfish populations with many similar alleles have small genetic distances. Meanwhile, catfish populations with different alleles may have high genetic distances.

Negative Tajima's D values and positive or negative Fu's Fs values for Zimbabwe, Cameroon, Philippines, Congo, Egypt, Nigeria, and Uganda suggest that the observed frequency of polymorphism is lower than expected. The lower frequency is because the average heterozygosity was lower than the number of polymorphic sites, indicating that these populations were significantly influenced by either a purifying selection or population expansion. On the other hand, the combination of positive Tajima's D and Fu's Fs values for Indonesia, Thailand, and India populations indicates a population contraction following the deficiency of rare alleles. This contraction results in an increase in the number of haplotypes due to the average heterozygosity being greater than the number of segregating sites. Our study found that the values for Tajima's D and Fu's Fs were not statistically significant.

Furthermore, the potential hybrids of this fish with *C. jaensis* (Cameroon), *C. macrocephalus* (Thailand), *C. batrachus* (Bangladesh), and *C. microstomus* (Malaysia) [44–47] suggest that a purifying selection is likely to be the driving force influencing the demography of the *C. gariepinus* population rather than a demographic expansion. Purifying selection increases mutations at silent sites without significantly expanding the heterozygosity. Similar results were reported by Barasa et al. [8] and Modeel et al. [48] for *C. gariepinus* and *Labeo rohita*, respectively.

The mismatch was used to show the mutation through the pairwise distances of the sequence [49]. The analysis revealed that the *C. gariepinus* population exhibited a distribution with multiple peaks, indicating a stable population size. Additionally, the nonsignificant raggedness index value further supported this finding. Several studies reported a multimodal distribution in fish taxa, including *C. gariepinus* [8,12], *Schilbe intermedius* [49], and *L. rohita* [48].

Effective conservation and resource management rely on monitoring natural population genetics. It is essential to evaluate genetic diversity and population structure in samples and populations [50]. Genetic diversity is critical for individual fitness, ecosystem function, and ecological and evolutionary processes [51]. Loss of genetic diversity in cultured populations may result from strict breeding practices that isolate the stock from other populations (e.g., Turkey, Algeria), while in wild populations, it may be due to overfishing, poaching, population division, genetic drift, and natural selection (e.g., Nigeria) [52].

Understanding genetic diversity greatly informs the development of conservation and management plans for wild fish populations. This knowledge also influences fish species selection and long-term genetic improvement. In this study, the haplotype diversity of *C. gariepinus* populations from Uganda and Bangladesh was found to be the highest, indicating the presence of genetically diverse populations of *C. gariepinus*. This underscores the need for spatially explicit management measures, including reducing pollution, minimizing habitat degradation and fragmentation, and decreasing fishing pressure to ensure sustainable stock utilization.

5. Conclusions

In conclusion, the current study provides information on the global haplotype diversity of *C. gariepinus*. The results show that haplotype diversity was high in the population of the African continent. Additionally, the genetically distinct populations of *C. gariepinus* are important for conserving biodiversity and genetic diversity. Examining genetic diversity and population structure can aid in devising strategies for preserving the genetically unique and endangered African catfish populations. This study found that mtDNA (COI) is a useful marker for assessing genetic diversity in these populations. However, all these sequences from COI were obtained in different periods, quality, extraction, purification, and amplification, which can be limitations of this kind of study.

Supplementary Materials: The following supporting information can be downloaded at the following website: https://www.mdpi.com/article/10.3390/hydrobiology3040021/s1, Figure S1: Nucleotide sites indicate each haplotype (17 haplotypes) in *Clarias gariepinus*; Table S1: List of Countries, Number of Sequences (NS), and their accession numbers of GenBank; Table S2: Nucleotide sites indicate each haplotype (17 haplotypes) in *Clarias gariepinus*. References [1–14] are cited in Supplementary file.

Author Contributions: Conceptualization, methodology, software, validation, formal analysis, investigation, resources, data curation, writing—original draft preparation, writing—review and editing, visualization, supervision, project administration, funding acquisition, M.A. and N.A.G.M. All authors have read and agreed to the published version of the manuscript.

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Informed Consent Statement: Not applicable.

Data Availability Statement: All data for the present work were downloaded from GenBank (https://www.ncbi.nlm.nih.gov) (accessed on 1 November 2023). The accession IDs for 164 species are listed in Table S1.

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