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The Threat of Foreign Tilapia Species to the Ghanaian Aquaculture Industry

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Simple Summary: Aquaculture in Ghana is a multi-million-dollar industry with great potential in boosting the country's GDP and food security goals. Presently, such a fast-growing industry is challenged with the inflow of illegal tilapia strains and along with them, many fish pathogens due to porous trade boarders. The major fish disease outbreaks recently reported in Ghana were speculated to be linked with importation of foreign fish species. In this report, we provide evidence of the presence of a foreign red tilapia strain in Lake Volta, where intensive cage fish farming is practiced and addresses threats that such strains may pose to the Ghanaian aquaculture sector. Different management options that could be considered to curb infiltration and spread of exotic fish species within the country is highlighted.

Abstract: The Akosombo Nile tilapia is the only approved local strain for aquaculture production in Ghana. In this study, an exotic red tilapia sample suspected to be cultured in a fish farm within the Lower Volta River Basin of the Lake Volta was collected for species identification. A molecular screening using DNA barcoding sequencing was performed on the samples targeting the cytochrome C oxidase subunit 1 mitochondrial gene (*COX*1). We confirmed the identity of the red tilapia fish to be a non-native *Oreochromis* sp. recently introduced into the country. The data obtained clearly demonstrates a breach of biosecurity that potentially threatens Ghana's native tilapia genetic resources and aquaculture development.

Keywords: biosecurity; non-native; GIFT; aquaculture; tilapia

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1. Introduction

Aquaculture is a key player for securing and sustaining food fish production in Ghana. The past two decades has seen expansion in the aquaculture sector, especially for Nile tilapia, with production rising from barely 2,000 MT in 2006 to 57,000 MT in 2017 [1]. This success story has partly been attributed to the improved local Akosombo Nile tilapia strain developed and released in 2005 [2]. Although the sector has shown great potential it has not yet met the high food protein demand within the country [3]. Currently, the performance of the Akosombo strain is perceived as non-optimal [4]. Studies comparing the farmed Akosombo strain, and the GIFT strain has shown a remarkable evidence of better growth performance for the latter [4]. The GIFT strain was genetically developed from a combination of four wild African strains which included a Ghanaian strain and four farmed Asian strains, three of which originated from Ghana [5,6]. Although this strain has demonstrated remarkable gains in growth rate and socioeconomic benefits and has out-performed other strains, the importation and commercial farming of the GIFT strain is prohibited in Ghana [7,8]. Permit to import the GIFT strain is only available for selected governmental institutions solely for research purposes [8]. Currently, there is a complete ban on importation of alien tilapias for commercial food production in Ghana. Nevertheless, transboundary movement of aquatic animals continues to operate, albeit illegally. Suspicion of Chinese tilapia strains and GIFT or its derivatives infiltrating Ghana's aquaculture production systems has previously been noted by some investigators [9]. This may not only allow the introduction of non-native species into new geographical areas, but also a major pathway for pathogen transfer [10–13]. Pathogens may inadvertently be carried along with live fish in different life stages. Infected ova, larvae, juveniles and adult fish can all spread disease. The situation is further complicated by sub-clinical infections where fish shows no sign of disease at the time of transport [12]. Evidently, Ghana has in recent times experienced major *Streptococcus agalactiae* and Infectious Spleen and Kidney Necrosis Virus (ISKNV) disease outbreaks causing serious mortalities and huge revenue losses, which is speculated to have been introduced through illegal importation of fish [12,14]. In both outbreak cases, a molecular based DNA sequencing approach was used in the initial investigations to accurately define their genetic relatedness compared to other strains globally [4,6]. Through genomic surveillance studies, other variants of ISKNV have recently been reported, which also suggests their likely introduction through fish importation [12,15]. It was within this context that we sought to further investigate the genetic background of tilapia species farmed especially in and around Lake Volta, a major hub of intensive commercial tilapia cage farming in the country. This hub also happens to be where most fish disease outbreaks occur.

2. Materials and Methods

Based on a report received by the Fisheries Commission, Ghana, of the presence of exotic tilapia species on fish farms within the lower Volta River Basin, we collected a red tilapia sample from a fish farm in the area. Three sub-samples from the fish specimen were used in the investigation; V01 – frozen flesh, V02 – dried anal fin clip, and V03 – caudal fin clip fixed in 70% ethanol. Total DNA was extracted using the DNeasy Blood and Tissue Kit (Qiagen) according to the manufacturer's protocol with a slight modification incorporating both mechanical and enzymatic disruption of tissues. The samples were characterized using a DNA barcoding approach by sequencing the cytochrome C oxidase subunit 1 (*COX1*) mitochondrial gene [16]. PCR amplification was carried out at the following cycling conditions: initial denaturation at 94 °C for 3 min followed by 35 cycles of 94 °C for 40 s, 52 °C for 30 s, 72 °C for 1 min, and a final extension at 72 °C for 5 min. Upon sequencing of the DNA amplicons (~ 650 bp fragment sizes), a phylogenetic analysis was performed to establish their genetic relationships with other known existing sequences from GenBank using Mega 11 [17]. Two farmed tilapia samples previously identified as native Ghanaian haplotypes (ARDEC1 and VCA1 were included in the analyses.

3. Results and Discussion

Our initial BLAST analysis revealed that our sequences were 100% identical. These sequences matched *Oreochromis aureus* with 100% identity to strains reported from Philippines (KU565851) and Nigeria (MK130703.1), respectively (Figure 1). It also matched closely with enhanced strains of *O. niloticus* reported from Philippines and China. On the contrary, the sequences were distinct and separated from the Ghanaian farmed tilapia (*O. niloticus*) strain (ARDEC1 and VCA1) reported in 2017 (Figure 1) [9]. The data suggest that the investigated strain is an *Oreochromis* sp., likely developed through an initial crossing of Blue tilapia (*O. aureus*) with Mozambique tilapia (*O. mossambicus*) to produce the distinct observed red phenotype; and further crosses involving the offsprings with both *O. niloticus* and *O. aureus* [18,19]. This probably explains why the test strain (V02) did not group with the other strains of red tilapia reference samples, which were closely related to *O. mossambicus* (Figure 1). Both *O. aureus* and *O. mossambicus* historically do not naturally occur in Ghanaian waters and were likely imported.

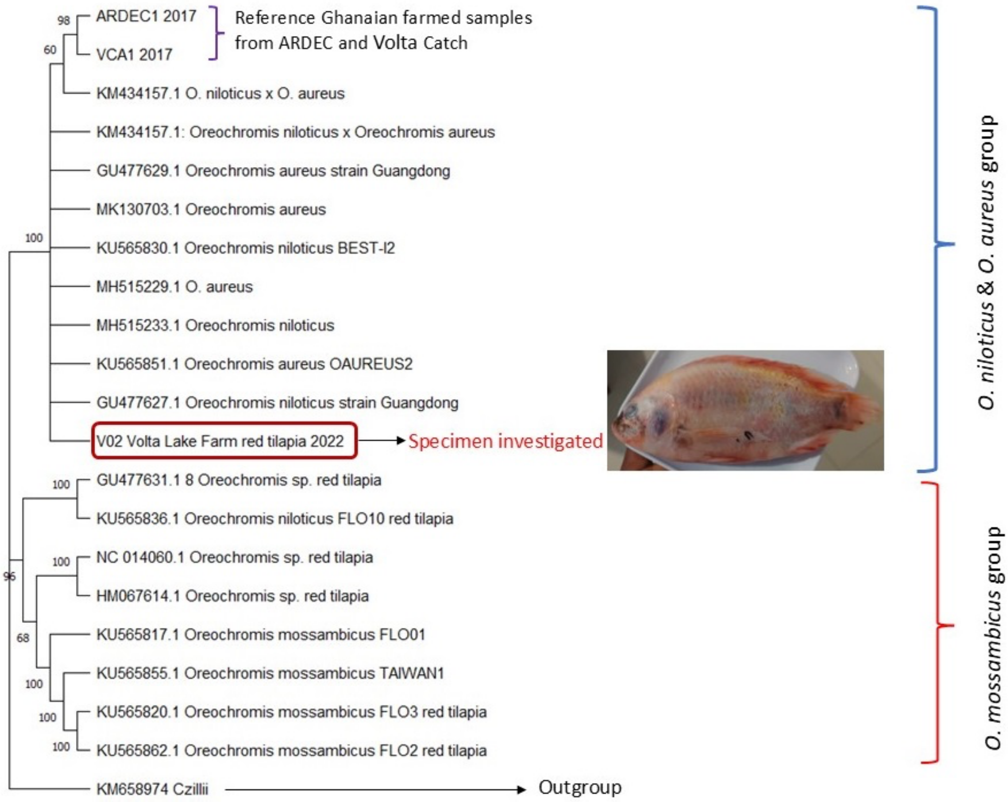

Figure 1. Phylogenetic tree showing the relationship between V02 red tilapia and Ghanaian farmed Nile tilapia from ARDEC and Volta Catch. The tree was constructed from 632-bp cytochrome C oxidase subunit 1 (COX1) consensus sequence of *Oreochromis* sp. using the Neighbor-Joining method.

Ghana recently experienced an overflow of the Lake Volta due to spillage of the Akosombo Dam, the main source of hydroelectric generating power for the country. The spillage unleashed untold devastation on aquaculture activities both upstream and downstream of the Lake, which dislodged and destroyed most communities along the lower Volta Basin (GhanaWeb, September 15, 2023) including large-scale tilapia cage farms and a research facility that houses the GIFT strain. Although, farming has recommenced and production is on-going in most sites, the evidence of non-native *Oreochromis* sp. in Ghana waters and potential release of the GIFT strain into the environment should be a worry to the aquaculture sector. There is the threat of pure local strains becoming less fit with possible extinction due to uncontrolled breeding and hybridization in the lake. Knowing the potential of the Ghanaian aquaculture and the quest to increase its annual production cycles and make more profits [20,21], the inflow of illegal tilapia strains will always be a challenge. Regulation of illegal importation of fish will also be rendered baseless as the lines between already imported and recently imported strains blurs. Remapping of the species diversity through baseline studies and possibly revisiting the conversation on the need to regularize importation of foreign species into the country through better control and monitoring is imminent. Whereas some may advocate for better control and stringent regulation to allow importation of foreign species, this may be a challenge due to porous trade borders confounded by the lack of quarantine facilities. Taking stock of existing foreign infiltrations and intensifying surveillance and regulatory systems, especially on the Lake Volta for easy detection of new species and emerging pathogens using rapid genomic tools may be a better alternative solution to protect the aquaculture sector. We also recommend the introduction of programs to safeguard local strains for future reference and studies.

4. Conclusions

This is the first molecular evidence of the presence of exotic farmed red tilapia species in Ghanaian waters. This is a serious breach of biosecurity that potentially threatens Ghana's native tilapia genetic resources and aquaculture development. It is necessary to place institutional management measures to prevent its spread within wild tilapia populations.

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Institutional Review Board Statement: No ethical approval was required for this work, as samples were collected as part of the oversight responsibility of the Fisheries Commission, Accra, Ghana

Informed Consent Statement: Not applicable

Data Availability Statement: The sequences generated during the current study have been submitted to GenBank and are available from the corresponding author on reasonable request.

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Conflicts of Interest: The authors declare no conflicts of interest.

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