

Euro Biotechnology 2018: Single nucleotide polymorphisms and haplotype analyses in Tilapia fish inferred from mtDNA D-loop and Cyt-b regions- Ikpeme E V- Nigeria Federal University of Agriculture Abeokuta

Ikpeme E

Abstract

Tilapia fish is the most widely harvested and consumed fish after carp globally. Commercially, tilapia fish is highly consumed with a global harvest of approximately, 4,677,613 tonnes in 2013. For emphasis, China is the world's largest producer of tilapia with about 1,600,000 tonnes production, while in Africa; Egypt is the largest producer of about 800,000 ones. Nigeria has an estimated population of over 160 million with a coastline measuring approximately 853 kilometres. This vast coastline according to Osagie can be harnessed for tilapia fish farming, which might probably have the capacity to make a significant contribution to agriculture.

According to Oyakhilomen and Zibah, the demand-supply gap of fish is about 1.8million tones. This was premised upon the report that the annual demand for fish in Nigeria to be about 2.66million tones. Tilapia fish has received little or no research attention comparatively, its importance as rich protein, potassium, phosphorus, vitamin B12 as well as low-fat content notwithstanding. The other frightening important issue is the genetic erosion in this species of fish orchestrated by indiscriminate and over-exploitation from the wild by fishermen in the bid to bridging the demand supply gap. The implication, therefore, is that if efforts are not intensified, especially in research geared towards domesticating, conserving and integrating tilapia farming into the agricultural program in Nigeria, it might spell doom.

However, the complaint expressed by both breeders and farmers is poor growth, which affects market competition. To mitigate this shortcoming, a robust diversity analysis becomes imperative, which will be aimed at screening and selecting superior genotypes of tilapia fish for breeding and improvement. Undoubtedly, allelic differences between and among organisms of the same species have become an integrated part in agricultural/breeding programmers, which is aimed at selecting breeding stock and identifying extinct-threatened species for possible conservation measures .

Myriads of techniques and methods have been developed and adopted for genetic analysis such as morphometric-based technique. Unfortunately, though simple and direct for the identification and characterization of fish stock, its reliability has been marred by environmental factors.

The specificity and resolution power of other molecular markers such as RAPD, SSR, ISSR, AFLP, notwithstanding, DNA sequence data have been reported to be more informative in explaining genetic relatedness among species of organisms. Out of the two major genomic DNAs – nuclear and mitochondrial, mitochondrial DNA (mtDNA) have been used in studying stock structures invertebrates such as fish, birds, reptiles as well as mammals. Habib et al. reviewed that mtDNA variation is being adopted as a dependable tool for determining genetic diversity within and among species. The choice of mtDNA is hinged on the fact that vertebrates show more variations in mitochondrial genome than nuclear DNA due to rapid mutation rate and copy number per cell as well as being inherited maternally.

Two regions along the mtDNA have attracted research interest, especially in constructing phylogenetic relationship among or between species. These are cytochrome -b (cyt-b) and Dloop regions. Cyt-b region of mtDNA has been used widely in genetic diversity studies of many animal species widely fish. Similarly, the hyper-variable/control region (Dloop) of mtDNA flanked by tRNA_{pro} and tRNA_{phe} genes in the mitochondrial genome has been used for characterising tilapia species.

According to Chambers et al. phylogenetic analysis has been used in tracing the origin and evolution of species, prediction of physiological, biochemical and structural features of sequences. It is also used to assess ancestral history and relationships.

There are several landmarks on the DNA that can be utilised for the identification and characterisation of species of organisms, especially Single Nucleotide Polymorphisms (SNPs). SNP-based research is geared towards studying the genetic differences between species for the prediction of phenotypes and phylogeny. Giving that when SNPs occur inside a gene, they create different variants or alleles of that gene and the sequences tend to be transmitted unchanged across generation; in this present study, using SNPs markers on Dloop and cyt-b regions of mtDNA, genetic diversity, polymorphisms, and haplotype in tilapia fish sampled from two populations in Nigeria were investigated.

MATERIALS AND METHODS: Sample Collection, DNA Extraction from Fish Tissue, Polymerase Chain Reaction (PCR) Amplification, Sequencing of D-loop and Cytochrome Regions of mtDNA, Statistical Analyses. The results put together revealed higher nucleotide and haplotype diversity, more SNPs detected, positive selection and unshared haplotype in mtDNA D-loop when compared with mtDNA Cyt-b region of tilapia fish, giving rise to more polymorphism. By implication, tilapia fish within these populations could be employed in selective breeding and genetic improvement, especially from the south- south population.

ETHICAL APPROVAL: The research was performed on biological material derived from fish obtained from fish farms. After obtaining the tissue for analysis, the meat was standard for consumption. Therefore, our research did not require the approval of the Animal Experimentation committee.

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