

Genetic Diversity of Wild Population of *Heterobranchus* Spp. Based on Mitochondria DNA Cytochrome C Oxidase Subunit I Gene Analysis

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Abstract : Catfish (*Heterobranchus* spp.) is a major freshwater fish that are widely distributed in Nigeria waters and are gaining rapid aquaculture expansion. However, indiscriminate artificial crossbreeding of the species with others poses a threat to their biodiversity. There is a paucity of information about the genetic variability, hence this insight on the genetic variability is badly needed, not only for the species conservation but for aquaculture expansion. In this study, we tested the level of Genetic diversity, population differentiation and phylogenetic relationship analysis on 35 individuals of two populations of *Heterobranchus bidorsalis* and 29 individuals of three populations of *Heterobranchus longifilis* using the mitochondrial cytochrome c oxidase subunit I (mtDNA COI) gene sequence. Nucleotide sequences of 650 bp fragment of the COI gene of the two species were compared. In the whole 4 and 5 haplotypes were distinguished in the populations of *H. bidorsalis* & *H. longifilis* with accession numbers (MG334168 - MG334171 & MG334172 to MG334176) respectively. Haplotypes diversity indices revealed a range of 0.59 ± 0.08 to 0.57 ± 0.09 in *H. bidorsalis* and 0.000 to 0.001051 ± 0.000945 in *H. longifilis* population, respectively. Analysis of molecular variance (AMOVA) revealed no significant variation among *H. bidorsalis* population of the Niger & Benue Rivers, detected significant genetic variation was between the Rivers of Niger, Kaduna and Benue population of *H. longifilis*. Two main clades were recovered, showing a clear separation between *H. bidorsalis* and *H. longifilis* in the phylogenetic tree. The mtDNA COI genes studied revealed high gene flow between populations with no distinct genetic differentiation between the populations as measured by the fixation index (FST) statistic. However, a proportion of population-specific haplotypes was observed in the two species studied, suggesting a substantial degree of genetic distinctiveness for each of the population investigated. These findings present the description of the species character and accessions of the fish's genetic resources, through gene sequence submitted in Genetic database. The data will help to protect their valuable wild resource and contribute to their recovery and selective breeding in Nigeria.

Keywords : AMOVA, genetic diversity, *Heterobranchus* spp., mtDNA COI, phylogenetic tree

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