

Abstract

The African catfish *Clarias gariepinus* is an important species in the rapidly expanding aquaculture industry in East Africa. Most Kenyan catfish farmers use stocks with unknown genetic characteristics, with uncertified seeds and inter-basin exchange of brood stocks threatening the genetic distinctness of wild populations. Using 346 base pairs of D-loop sequence variation, genetic diversity and gene flow between *C. gariepinus* populations from Lake Victoria and its satellite, Lake Kanyaboli, were explored. A total of 17 haplotypes were identified in 52 individuals sampled, with the two populations sharing four haplotypes, and one haplotype being the most frequent (50%) in both populations. Catfish from Lake Victoria showed marginally higher genetic variation compared to those from Lake Kanyaboli, reflected in the higher number of haplotypes, singletons, polymorphic sites and haplotype and nucleotide diversities. Yet neither population showed signs of significant loss of diversity compared to other wild populations of the species. *Clarias gariepinus* from Lakes Victoria and Kanyaboli clustered into one clade, showing low population structuring and with a between-population F_{ST} value of 0.026, which was not indicative of significant ($p \geq 0.05$) differentiation between the two lakes. Nevertheless, each population contained 60–64% of unique haplotypes. Inter-basin transfer of *Clarias* populations and human impact on Lake Kanyaboli should be controlled to conserve the unique *Clarias* genetic resources in the lake basin of Kenya.