

# Lack of Neutral Genetic Divergence in Tilapia of Lake Baringo, Kenya

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Tilapia fishing in Lake Baringo has been a major source of income for local fishermen until recently when fish numbers started to decrease due to overfishing and possibly changes in lake water quality. This has led to an increased interest in Tilapia fish farming by communities around the lake, as well as for countrywide fish farming under the Government of Kenya economic stimulus program. It is generally accepted that optimal production of offspring in fish farming is expected when fingerling used are genetically similar. This study aimed at determining the presence and pattern of genetic differences in Tilapia of Lake Baringo to enable selection of genetically pure fingerling for pond farming, with the goal of increasing the production of farm Tilapia from Lake Baringo. The amount and pattern of genetic variation within the lake was investigated to enable fish farmers to make an informed selection of fingerling for production of seed for fish farming. Fish samples were taken from two geographic extremes and were delineated at five microsatellite loci using an individual-based approach and Bayesian modeling that apportions individuals into putative ancestral populations on the basis of their multilocus genotypes. Genetic variation was found to be low, with observed heterozygosity ( $H_O = 0.70$ ) being considerably lower than those expected under Hardy-Weinberg law ( $H_E = 0.93$ ), both within individual subpopulations and overall ( $p > 0.05$ ). Hierarchical examination of homogeneous subsets in tilapia caught from the Northern and Southern ends of the lake was done using *STRUCTURE* which uses Bayesian modeling to apportion individuals into their source populations. This revealed no evidence for population differences, suggesting that they form a single gene pool at neutral genetic loci. These results indicated that selection of fingerlings can be done randomly within the lake, and vi

samples treated as panmictic in fish improvement programs. However, the results should be interpreted cautiously as differentiation could still exist at specific loci controlling certain quantitative traits. Results of this study suggest that introduction of this species into Lake Baringo could be too recent to accumulate detectable genetic variation at neutral loci but support observation that this population could be a good source of fingerling for commercial fish farming.