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**EVOLUTIONARY HISTORY OF THE NILE PERCH IN ITS NATIVE  
HABITAT - THE NILOTIC SYSTEM VERSUS ITS NEW HAVEN – THE  
LAKE VICTORIA REGION WATERS**

BY

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A THESIS SUBMITTED TO THE DIRECTORATE OF RESEARCH AND GRADUATE  
TRAINING FOR THE AWARD OF THE DEGREE OF DOCTOR OF PHILOSOPHY OF  
MAKERERE UNIVERSITY

OCTOBER 2013

## ABSTRACT

Nile perch is an important food fish species of the genus *Lates*, belonging to family Latidae. It widely occurs in the Afro-tropical region in Africa, and in East Africa it is native to Lakes Albert and Turkana and River Albert Nile. It was introduced to lakes Kyoga, Nabugabo and Victoria where it successfully established itself. Nile perch became the leading fishery, bolstering economies of Uganda, Kenya and Tanzania, countries that are engaged in Nile perch processing and export, to the value of US \$250m annually. But recently Nile perch stocks have been reported to be on the decline. Characterisation of Nile perch populations of E. Africa and understanding the species' evolutionary history are important for both capture fisheries management and culturing efforts of Nile perch. Earlier studies were mostly based on morphological characters and were all less or not definitive. This study combined morphological and molecular characterisation to establish the phylogenetics, genetics and evolutionary history of Nile perch sampled from lakes – Albert, Kyoga, Nabugabo, Victoria (Uganda), Turkana (Kenya) and Chamo (Ethiopia) and Senegal River (Senegal). The aims of this study were to determine phyletic and phylogeographic relationships among populations of Nile perch in its extant range in E. Africa and to establish the species evolutionary history on the African continent. Morphological phylogenetics of E. African Nile perch revealed existence 2 morphotypes. Analysis of genetic variation among populations in E. Africa, based on 9 polymorphic microsatellite loci and partial sequence (463bp) of mtDNA showed that introduced Nile perch had higher genetic diversity than populations from the putative native origins. In addition, findings revealed that all sampled water bodies had 2 underlying populations of Nile perch, which most probably represent 2 different subspecies. Evolutionary history studied using mtDNA CR partial sequence (476bp) revealed 37 distinct haplotypes in 124 samples. The haplotypes clustered into 2 major groups, one composed of individuals sampled from eastern and the other from western Africa. The 2 most probably belong to 2 different Nile perch lineages that may have developed in geographical isolation during the Pleistocene times and have remained largely allopatric. The 2 groupings should be considered as different ESUs since depletion of individuals from one lineage cannot easily be replenished by natural migration by the other. Therefore, the ESUs should be conserved as such and genetic exchange due to translocations should never be allowed

## DEDICATION

On his sick bed in hospital when we were little boys just 6 years old, our father while holding our hands firmly asked God to keep him alive to see his twin boys Wilson and Matthew through their education, which the Almighty granted, as 17 years later we graduated with bachelors. But he was not given the chance to see his twin doctoral graduands! For his love and commitment to our education and investment therein I dedicate this work to my parents – Isabirye ni Nabirye Mwanja and all Glory I give to God!