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[THE UGANDAN VERSION]

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CHAPTER 13B

Characterization of Genetic Biodiversity of Nile perch, *Lates niloticus*, Tilapiines, Haplochromine flock and *Ningu (Labeo victorianus)* in the Victoria Lake Basin: an overview

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Introduction

Genetic biodiversity is the variation among individuals within and between units of interbreeding individuals (populations) of a species. It includes inheritable and transmittable differences that occur between individuals and/or of a given species through reproductive interaction. There exists enormous variability among individuals and/or populations of a species for most living organisms, and most of this variation is inheritable. Differences among individuals arise through mutation and via recombination of genes during meiosis. These differences are then transmitted to successive generations through sexual reproduction and maintained in the populations through processes such as natural selection and genetic drift. Unfortunately much of this variation is normally threatened and often in danger of extinction because most focus in conservation of natural resources is put at saving species or habitats than varieties or strains of a species.

Evolutionary forces such as natural selection and genetic drift act on individual level rather than at species level. It is now increasingly understood and agreed upon by most natural scientists that conservation efforts should be targeted at protecting as much variation as possible at population level rather than only at maintenance or protection of a species because protection of individual variation (genetic biodiversity) ensures evolutionary continuity of the species. For survival of a species is measure of conservation efforts at the individual or population level. Maintenance of genetic biodiversity though is normally constrained by resources, and most times conservation efforts are started only after remnant populations of a species are noticed to be in danger rather than dealing with the status of individual populations.

There is need to genetically identify and characterize all extant variation for all flora and fauna. This guards against loss of strains or variation without knowledge. It also boosts the genetic bank from which genetic improvements are sought and can be made for the economically important strains or species. The inventory of genetics biodiversity assists in protection of vital habitats that contain key strains. The inventory helps in allocation of resources to the protection of a species which may be geographically widely distributed. In case of mitigation efforts understanding of genetic relationship between populations is essential for protection of locally adapted variation or restoration of endangered taxa.

Below are evaluations of preliminary studies of genetic biodiversity of key taxa in the Lake Victoria Region (LVR). These species or groups of species are singled out because

of their economical and/or ecological roles in the system. The list includes the introduced Nile perch, exotic and native tilapiine species, the Ningu and the haplochromine flock.

Nile perch (*Lates niloticus*)

Although the introduction of Nile perch, *Lates niloticus*, to lake Victoria has received intense global attention, especially in relation to its impact upon endemic cichlid species and the yields from its fishery, fundamental information on its taxonomy and population genetics is lacking. Most importantly, the introduced fish originated from two lakes (Lakes Albert and Turkana) containing three *Lates* species, and it has never been entirely clear which of these became established in Lake Victoria, or indeed whether the Lake Victoria population is derived from hybridization between *Lates* species. In addition, genetic drift caused by the relatively small founder population (approx. 400), the initially slow population increase followed by a period of explosive growth and selection pressures in the new environment may have resulted in substantial genetic changes.

In this study, allozyme electrophoresis has been used to assess taxonomic affinities of Lake Victoria *Lates* to possible source populations. Results suggest strongly that the survivors of the introduced fish were indeed *L. niloticus* from Lake Albert. In contrast, none of the other species appears to have become established in Lake Victoria. Introduced populations in lakes Kyoga and Nabugabo were likely derived from Lake Albert *L. niloticus* as well.

Our results indicate a loss of genetic variability both during and after the introductions of Nile perch to Victoria and Kyoga. In addition, introduced Nile perch from these two lakes were genetically differentiated, suggesting genetic drift following each of the introductions. The reduction in genetic variability and subsequent genetic differentiation, may affect the adaptability and thus the persistence of the introduced population in the rapidly changing environment of Lake Victoria, and may, therefore have implications for the management of the fishery as well as for the conservation of endangered cichlids.

Ningu (*Labeo victorianus*)

Ningu, *Labeo victorianus*, is an endemic cyprinid fish cherished as a delicacy by the peoples of the Lake Victoria and Lake Kyoga basins. Ningu was heavily sought prior to the 1960s, but subsequently has become commercially extinct. The population declined drastically in size, due to the combined effects of the introduction of modern nylon fiber nets, the practice of drift netting at the river mouths during upstream migration, and the introduction of competing non-indigenous fishes in the two basins and degradation of its habitat. It is now extant only as small, isolated populations of little commercial value. The genetic characterization of the remaining natural population of ningu was examined. The method of randomly amplified polymorphic DNA (RAPD) was used to identify molecular markers in order to characterize three of the remnant populations of ningu, and to compare these populations with samples from two allopatric congeners, *L. horie* and *L.*

coubie from Lake Albert. The ningu populations were found to be markedly differentiated by locality. Genetic differences between populations account for 64.4% of the total genetic variation within ningu. Comparisons of genetic variability between the three species shows that the ningu retains slightly more variation per population than is seen in the other forms. For each of the three species of *Labeo*, gene diversity within population measured by RAPDs was relatively low. *Labeo* populations had lower levels of genetic variation than was observed in samples from Lake Albert of the cyprinid *Barbus bynii*, and the characid species *H baremose*, or than had been previously observed in several tilapiine cichlids from the Lake Victoria basin. Natal stream fidelity would seem to play an important role in leading to genetic differences between local populations of the ningu, since it can lead to population isolation. Given the recent severe decline in population size, and the evidence for significant isolation and differentiation between populations, further studies are urgently needed to evaluate the genetic constitution of ningu populations and develop a plan to conserve genetic resources of the species to increase the potential for long term survival.

Tilapiines (*Oreochromis* species)

Four microsatellite marker loci were used to estimate genetic diversity and degree of genetic differentiation among populations within the species of the principal tilapiine genus, *Oreochromis niloticus*, of the Lake Victoria Region (LVR). The tilapiine fauna of the LVR includes a number of forms: two native species, *Oreochromis esculentus* and *O. variabilis*, and several non-indigenous species. The Nile tilapia, *O. niloticus*, which is an introduced species in LVR, is currently the most abundant tilapiine. Microsatellite analysis of *Oreochromis* populations showed clear differentiation among populations. The microsatellite technique revealed sufficient molecular variation to differentiate among populations and species. The Nile tilapia was the least differentiated among populations, while *O. esculentus* exhibited the highest level of population subdivision. Among Nile tilapia populations, the Nabugabo population was closest to the Lake Edward population while Napoleon Gulf, Lake Kyoga, and Namasagali (Victoria Nile) populations clustered with Lake Albert and George populations. All trees generated indicate *O. esculentus* as being closer to *O. leucostictus* and *O. variabilis*, than to *O. niloticus*, the supposed sister species.

The Nile tilapia (*Oreochromis niloticus*)

Molecular genetic methods have been used to investigate the historical population patterns resulting from introduction of the Nile tilapia into the lakes of Uganda. Genetic polymorphisms were studied in populations of *Oreochromis niloticus* from the Lake Victoria basin and the Lake Kyoga basin, in both of which it is not native. Genetic variations was also studied in populations from Lake Albert and the Lake Edward-George system, from which transplanted Nile tilapia populations of lakes Victoria and Kyoga are thought to have originated. Genetic variation was determined using the method of Randomly Amplified Polymorphic DNA (RAPD). Genetic differences between populations have been determined by measuring RAPD band sharing and calculating genetic similarity from the percent of band sharing. Populations within a lake basin (i.e.

Lake Victoria or Lake Kyoga) were more similar to each other than to populations from other basins. Populations from the Lake Victoria basin were more similar to the putative source population of Lake Edward than to other possible sources, while the populations from Lake Kyoga were more similar to the putative source population sampled from Lake Albert. Populations from the Lake Kyoga basin were less diverse than those from the Lake Victoria basin, consistent with the hypothesis that introductions into Lake Kyoga are more recent and that a more diverse set of introductions may have contributed to the older populations of Lake Victoria.

Haplochromine species

Most genetics studies of haplochromine species of the LVR prior to studies by Fuerst at Ohio State University and Kaufman at Boston University have been focussed on species radiation, phylogenetics and loss of species. Our studies have been broadened to include detailed studies of individual key haplochromine species. In our on going studies we have selected several key species (Wu et al. 1999) representative of extant genera as defined by Greenwood (1981). Among the reasons for lack of studies on the population genetics of haplochromine species was the depauperate nature of genetic variation of haplochromine species as revealed by the conventional molecular markers' such as allozyme (Sage et al. 1984) and mitochondrial DNA sequencing (Meyer et al. 1990). The evolutionary younger nature of haplochromine species and their history of recent divergence made such molecular tools useless in differentiating individuals and/or populations within species. But with the recent advancement in molecular technology, development of techniques such as RAPDs and microsatellites has enabled us to generate genetic markers which have revealed a high level of genetic diversity within and among populations of key representative species of the haplochromine flock of the LVR. This studies have greatly improved the ability to discern relationships among individuals within a population and between populations of haplochromine species as well as allow us to detail phyletic relationships among species.