GENETIC AND PHENOTYPIC DIFFERENTIATION OF NILE TILAPIA REVEALED BY MOLECULAR MARKERS

By

AHMED SALEM ABDEL AZIZ DORGHAM
B.Sc. Agric. Sci. (Fish production), Fac. Agric., Al-Azhar Univ., 2006

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APPROVAL SHEET

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ABSTRACT

Morphometric, growth, random amplified polymorphism DNA (RAPD) and microsatellites variation of one wild population and two cultured stocks of *Oreochromis niloticus* has been studied. Five characters were selected by step-wise discriminant function analysis (DFA) on morphometric data for separating the three Nile tilapia male populations. In the bivariate plot of the first two canonical functions, the first function separated Kafr-Elshekh male population from both Fayiuom and wild male populations. The second discriminant function scores were used to separate Fayiuom and wild male populations. Six characters were selected by step-wise discriminant function analysis (DFA) on morphometric data for the separated three Nile tilapia female populations. In the bivariate plot of the two canonical functions, the first function separated Kafr-Elshekh female population from Fayiuom and wild female populations. The second discriminant function scores were used to separate Fayiuom and wild female populations. Examination of discriminant function coefficients indicated that harvest weight, head length and body depth were important characters for separating males and females within Kafr-Elshekh population. Results revealed that Kafr-ELshekh strain had the highest mean final weight (50.82 g/fish) with a corresponding daily weight gain of 0.53 g/fish/day. Following Kafr-Elshekh strain, were Fayiuom and wild strains with mean harvest weights of 42.28 and 42.26 grams/fish and daily growth rates of 0.44 and 0.43 g/fish/day, respectively In RAPD, of twenty five primers, 11 primers produced monomorphic RAPD fragment patterns, while 14 primers produced polymorphic RAPD fragment patterns. A total of 134, 139 and 129 amplified bands were produced from Kafr-Elshekh, Fayiuom and wild populations, of which 55, 48 and 58 bands were polymorphic (41.04%, 34.53% and 44.96%, respectively). Average heterozygosities were 0.113, 0.108 and 0.102 for wild, Kafr-Elshekh and Fayiuom tilapia stocks, respectively. In microsatellites, All the five loci were found to be polymorphic among all populations. Microsatellite variation at five loci was more informative in characterizing stock differences than the RAPD (DNA) markers. All loci showed some heterozygote deficiencies, when tested for deviation from Hardy-Weinberg expectations. The Overall mean, within population observed heterozygosity was 0.689. Populations ranged in heterozygosity from a low in Fayiuom sample (H_0= 0.652), to a high in the wild population (H_0= 0.711). According to the results, unselected wild population was more genetically diverse than Fayiuom farmed population. The Kafr-ELshekh population was also more genetically diverse, suggesting that the founder stocks used in developing most of the genetically improved stocks were well managed. The heterozygosity levels of the farmed Kafr-ELshekh population and the wild population were moderately high (H_0= 0.709 and H_0= 0.711, respectively) based on microsatellite data.

Key words: Genetic, phenotypic, molecular marker, Nile tilapia.

DEDICATION

To my family

For their support

Encouragement

Patience

and unconditional love

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INTRODUCTION

Tilapia is the second most cultivated fish in the world, only surpassed by carp, with almost 100 countries as producers (FAO, 2002). The worldwide use of Nile tilapia (*Oreochromis niloticus Linnaeus,* 1758) in aquaculture represents a somewhat unique scenario. According to recent statistics of the Egyptian General Authority for Fish Resources Development (GAFRD, 2009), tilapia comprise 68.82% (477.458 tones) of the Egyptian production from fish culture sector (693.815 tones) in 2008. Also, Egypt produces 22.5% of the world farmed tilapia (2.121.009 tones) (FAO, 2007). Moreover, Egypt by far produces 92.2% of tilapia production in the Middle East and North Africa (MENA) region (Feidi, 2010). In Egypt, most of the aquaculture production of tilapia is derived from semi-intensive fish farms in earthen ponds, intensive systems, integrated intensive fish farms and cages (GAFRD, 2006).

Management of aquatic genetic resources should ideally involve a continuum of activities: documentation of genetic resources and the variety of ecosystems in which there are functional components, including the status of potential threats to these resources; characterization to determine the genetic structure and conservation value of the resource; and utilization in sustainable genetic improvement schemes, with due regard to the emerging codes of practices of access to and benefit sharing of the genetic resources.

Tilapia hatcheries use only few individuals as broodstock for natural or artificial propagation, which have been taken from other commercial farms or natural resources. Consequently, this may lead to