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Phenotypic and genetic parameters for body measurements, reproductive traits and gut length of Nile tilapia (*Oreochromis niloticus*) selected for growth in low-input earthen ponds

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Abstract

In this study we present estimates of phenotypic and genetic parameters for body size measurements, reproductive traits, and gut length for Nile tilapia (*Oreochromis niloticus*) selected for growth in fertilized earthen ponds for two generations. Throughout the experiment, ponds were fertilized daily with 50 kg dry matter, (dm)/ha chicken manure. No supplementary feeds were added. For the analysis, 6429 fully pedigreed experimental fish from G0, G1 and G2 were used. Generations were discrete and therefore parameters were estimated separately for each year. Heritability estimates for body measurements ranged from 0.4–0.6 for standard length to 0.69–0.79 for head length. Phenotypic correlations between body weight and body measurements ranged from 0.64 to 0.89. Genetic correlations were close to unity. The heritability estimate for maturity at harvest (corrected for sex) was 0.13. Heritabilities for carcass traits were estimated from G_1 only and were 0.16 for gutted weight and 0.06 for dressing percentage. Phenotypic correlation between body weight and gutted weight was 0.84 and the genetic correlation was 0.20. Heritability estimate for gut length was 0.22. We also estimated a high genetic correlation between gut length index and standard length (0.78) but a low genetic correlation between gut length index and body weight (0.22±0.28). These results suggest that selection for growth on an herbivorous diet could result in a correlated response in gut length.

Keywords: Nile tilapia; *Oreochromis niloticus*; Heritability; Phenotypic correlation; Genetic correlation; Reproduction; Low-input; Gut length

1. Introduction

The breeding objective of most fish selective breeding programs is enhanced growth rate which leads to more efficient fish production (Gjedrem, 1997). A number of selective breeding programs have been initiated to improve

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the growth of *O. niloticus* (Hulata et al., 1986; Eknath et al., 1998; Bentsen et al., 1998). These selection programs have typically been carried out in relatively favorable environments where fish were fed good quality pellets. However, there are reports that selection gains in Nile tilapia were lost when selected breeds were tested in less favourable, low-input environments (Macaranas et al., 1997). This could indicate that the expression of body weight in different environments, i.e. low and high-input culture conditions, is influenced partly by a different set of genes.

In an earlier paper (Charo-Karisa et al., 2006b), we reported phenotypic and genetic parameters for growth and survival from an experiment in which Nile tilapia had been selected for body weight during two generations in fertilized ponds with no supplementary feed. Heritabilities for body weight were between 0.4 and 0.6, and for survival between 0.03 and 0.14. We also observed a considerable selection response for growth. In the present study, we report on the analysis of body measurements, carcass traits and reproductive traits collected during this selection experiment for improved growth of *O. niloticus*. Knowledge of the correlated changes that occur in other traits due to selection for growth is important for the design of an efficient genetic improvement program (Falconer and Mackay, 1996). For Nile tilapia, phenotypic and genetic correlations have been estimated between body weight, body measurements and fillet weight (Rutten et al., 2004, 2005a) and between body weight and reproductive traits (Kronert et al., 1989). However, these authors carried out experiments in indoor recirculation systems, under high density conditions and feeding with high protein pellets, Phenotypic and genetic correlations between traits in Nile tilapia reared in low-input, fertilized ponds are lacking.

2. Materials and methods

2.1. Background information

The experiment was carried out at the Regional Center for Africa and West Asia of the World Fish Center, Abbassa, Egypt. Fish used for this study were the grandparental population (G_0) produced in 2002, the G_1 generation produced in 2003, and G_2 generation produced in 2004. G_1 and G_2 were the first and second generation of selection respectively.

2.2. The founder population and production of G_0

The founder population (i.e. parents of the G_0 population) was produced in spring of 2000 in a full diallel mating design among local Egyptian strains namely Maryout, Zawia, Abbasa and Aswan (Rezk et al., 2002, 2004). Eighty sires and 105 dams, selected at random from among the founder stock, were subsequently used to produce the G_0. Each sire was mated to two dams and each dam mated to only one sire, thus generating full and half sib groups. Fry were raised in 2 × 1 × 1m hapas suspended in concrete tanks and were fed twice daily with 40% protein supplements, initially in the form of powder and later as pellets. Initial feeding rate was 20% of body weight, which was gradually reduced to 5% body weight at tagging size (i.e. mean wet weight of 2 g).

2.3. Production of G_1 and G_2

The first and second generations of selection, G_1 and G_2, were produced in 2 × 3 × 1 m hapas suspended in fertilized ponds. Each sire was mated to two dams as in G_0. Fifty sires and 87 dams were used to produce generation G_1, while for generation G_2, 54 sires and 104 dams were used. At first, each sire was kept in a single hapa with two dams. Twice a week, hapas were checked for occurrence of spawning. Spawning was assumed to have occurred when the dam had eggs or yolk-sac fry in her mouth. The un-spawned dam and the sire were both transferred to an adjacent hapa thus producing the paternal half-sibs. To prevent multiple spawning, the male was removed immediately after spawning occurred. When swim-up fry were sighted in both hapas, the females were also removed. Two to three weeks later, the number of swim-up fry in each hapa was reduced to 80 individuals. In contrast to the G_0, the G_1 and G_2 fry were given no supplementary feeds and were reared in hapas suspended in the earthen ponds. To boost natural pond productivity, ponds with hapas containing fry were fertilized daily with chicken manure at the rate of 50 kg dry matter/ha.

2.4. Grow-out and pond management (G_0, G_1 and G_2)

As soon as a family reached suitable tagging size, 24 randomly chosen fry from each full-sib family were individually tagged with Floy® tags and returned into the hapas until stocking. Fry were between 31 and 96days old at stocking. Each family of fry was randomly divided into two groups which were then stocked in two 1000 m^2 fertilized earthen ponds for grow-out. Ponds were daily supplied with dry chicken manure from layer and broiler farms at the rate of 50-kg dry matter (dm)/ha. This fertilization rate corresponds to 0.3 kg nitrogen ha^{-1} day^{-1} which is enough to support yields of 4.3 kg fish BW ha^{-1} day^{-1} (calculated from Knud-Hansen et al., 1991). Fish that died within the first week of stocking were, when possible, replaced with individuals from the same family. After approximately 8 months of growth, which included 3–4 months of over-wintering, fish were harvested by seine netting.

2.5. Trait measurements

Before measurements were taken, fish were anaesthetized with MS222 (3-aminobenzoic acid ethyl ester) to avoid handling stress. Each fish was measured for body weight (BW). Breeding values were estimated from an animal model (Model 1 below). These estimates were used to select 100 males and 200 females as potential brooders for the next generation. After selection of