



Longitudinal genetic analyses of fillet traits in Nile tilapia *Oreochromis niloticus*

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ABSTRACT

There is little published information on genetic covariance estimates among meat yield traits in Nile tilapia. Longitudinal genetic analyses to evaluate patterns of environmental and genetic covariances among such traits during growth would help to establish selection criteria and predict direct and correlated response to selection. Accordingly, longitudinal genetic studies from 106 to 245 days of age were performed by random regression models for carcass and fillet weights and yields in Nile tilapia. For each analysis, the statistical model included random family common environmental and genetic effects and assuming heterogeneity of residual variances. For carcass and fillet yield, genetic correlations between closely paired ages (from 140 to 200 days) were higher (>0.80) than those separated by moderate (>0.40) or longer (approaching zero) intervals. For carcass and fillet weight, genetic correlations when both ages were greater than 125 days post-hatching were larger than 0.60, and those when both ages were greater than 149 days post-hatching were larger than 0.80. Heritability estimates for fillet and carcass yields ranged from moderate (0.12) to high (0.52), suggesting the likelihood that selection programs could improve these traits. The manner in which fillets were removed seems to influence the results. Heritability estimates for carcass and fillet weight ranged from high (0.52) to low (0.01). The family common environmental effect was important for reducing the heritability estimates of these two traits, probably due to high correlation of each trait to body weight at slaughter, which is substantially affected by the common family environmental effect. Accordingly, to increase the accuracy of predicted breeding values for these traits, it is important to reduce family effects by minimizing the duration during which families are reared separately, then tagging individual fish and initiating communal stocking at as early a life stage as possible. Based upon estimated genetic parameters among the traits, direct selection for body weight, carcass weight and fillet weight is not recommended if the breeding goal is to increase fillet yield as a correlated response. Contrarily, the high genetic correlations between body weight and fillet and carcass weights (>0.98) suggest that body weight could be used as a selection criterion to avoid slaughtering potential breeders to acquire data and to achieve higher selection intensity.

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1. Introduction

Most commercially farmed stocks of Nile tilapia (*Oreochromis niloticus*) are genetically similar to the wild stocks (Brummett et al., 2004; Eknath et al., 1991; Lymbery et al., 2000). Some designed breeding programs have been initiated for the species, and most breeding efforts have been limited to mass selection for improved growth rate. In many commercial production enterprises, fillet yield is also considered an important trait affecting the economic efficiency of production systems in Nile tilapia (Rutten et al., 2004).

There is little published information regarding genetic variance components for meat yield of Nile tilapia. Traits like meat, fillet and

carcass yields have great economic importance for the meat processing industry. Genetic improvement in such traits may reduce processing cost because fewer live fish would be necessary to produce the same amount of fillet or derived products for the market.

Low (Rutten et al., 2005b) to moderate (Nguyen et al., 2010) heritability estimates of fillet yield and no available estimates for carcass yield suggest the need for additional genetic studies involving these traits. Knowledge of genetic and environmental covariance structures from longitudinal analyses during the growing period could help to establish the best time to measure and select fish to obtain the maximum rate of selection response for these traits in Nile tilapia populations. It also would be useful to predict correlated response in each trait to direct selection for any other, body weight, for example, that would not require slaughtering to allow data collection.

Random regression models are well suited for analysis of longitudinal traits because they take into account the continuous change

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across time in phenotype and related genetic and environmental effects, facilitating analysis of all data, without pre-adjustment (Valente et al., 2008). Knowledge of the genetic and environmental covariance structures permits the estimation of variances and covariances of recorded traits for any combination of ages, as well as heritability estimates of traits at any age within the interval considered in the study. This methodology is expected to result in increased accuracy of predicted breeding values for the analyzed traits (Meyer, 2004).

In tilapia breeding programs, the age at which to practice selection frequently is arbitrarily chosen (i.e. 180 days of age, Nguyen et al., 2010). Alternatively, it might be directly related to age at market weight or to the weight that is optimal for reproduction. Longitudinal genetic studies can be beneficial at the beginning of any genetic improvement program, because they allow prediction of the best age for selection and estimation of all possible correlated responses.

Obviously, fillet and carcass weights and yields cannot be measured repeatedly in the same animal. However, random regression models provide functions of genetic covariances based on records of closely related fish throughout the growing period, which can then be used in the analyses of such traits. They have seldom, however, been used in fish. Only two such studies are published, one using rainbow trout *Oncorhynchus mykiss* (Mckay et al., 2002) and the other, Nile tilapia *O. niloticus* (Rutten et al., 2005a) both evaluating weight across a span of age. The present research was undertaken to investigate by random regression models the environmental and genetic covariance structures of fillet and carcass weights and yields of Nile tilapia of the Chitralada strain cultivated in a recirculating water system and to evaluate the correlated response in one trait (i.e. fillet weight) from direct selection on another (i.e. body weight).

2. Material and methods

2.1. The experiment

The experiment was conducted at the Aquaculture Laboratory of the Veterinary School of Federal University of Minas Gerais (UFMG), Brazil. The pedigreed population used in the study was the laboratory's Chitralada Nile tilapia strain. This strain was introduced from Thailand to Brazil in 1996 and has spread across the country. The UFMG stock came from a commercial hatchery in Minas Gerais State which conducts a breeding program based heavily on weight.

Seventy-two full-sib families were produced by mating 36 males and 72 females that were randomly sampled from 100 males and 300 females, each tagged with a unique passive integrated transponder device. One male and two females previously identified as "ready to spawn" were maintained in a 1 m³ fiberglass tank for 1 week. At the end of this period, fertilized females (those with eggs in their mouth) were transferred to individual 30 l bowls for a one-week incubation period, after which they were separated from their progenies.

To obtain the necessary number of full-sib families, non-reproducing females were replaced by new ones that were randomly sampled from among the "ready to spawn" females from the initial group. Males that did not produce a full-sib family during the two-week interval or that killed a female also were replaced.

Because the laboratory had only eight 1 m³ tanks for fish reproduction, only eight matings were possible each week. Consequently, full-sib families were produced over a 17-week period from July to November. During that time, the 1 m³ tanks were maintained in a recirculating water system, with quality control to provide comfort and promote reproductive success of the fish. The light program was similar for all of the tanks. For this reason, no effect of season was included in the subsequent model for statistical analysis.

Larvae from each dam were cultured in a 30 l bowl for 2 weeks and then transferred to a 75 l tank. At this point, family size was standardized to 100 larvae. Families were kept in these tanks for 6 weeks,

after which 50 fingerlings from each family were transferred to 100 l tanks where they were held for 8 weeks. All 30 l bowls and all 75 and 100 l tanks were maintained in a recirculating water system with temperature varying from 25.5 to 28.5 °C.

Between the 13th and 20th week of age post-hatching, groups of six tilapia families (those as close in age as possible) were combined and placed in 7 m³ tanks, 12 tanks for 72 full-sib families in all, with all tanks having the same culture conditions. In each of these tanks, 50% of the water volume was changed daily and the tanks were aerated by blowers and air diffusers and kept under electric thermostatic temperature control. Feeding management was the same for all tanks: fish were fed three times daily a commercial pellet containing 32% protein at a rate of 5% body weight and uneaten feed was collected. Chemical and physical water parameters were regularly monitored; oxygen was maintained above 4 mg/l, ammonium less than 0.5 mg/l, pH between 7.0 and 7.5 and temperature ranging from 25 to 26 °C.

At the time of communal stocking, all individuals were tagged by pit (passive integrated transponder) tags and sexed. Due to mortality prior to tagging, family sizes varied. Forty-eight families had 30–36 identified progeny (66.5% of total families), nine families had 22–29 progeny (12.5%), two families had 18–21 progeny (3%), and 13 families had 9–17 progeny (18.5%), totaling 2042 fish.

Unidentified fish previously removed to standardize family sizes were reallocated across tanks to guarantee homogeneity of stocking density.

2.2. Recordings

Each fish was individually weighed at most six times. The first weight was taken when fish were tagged, using an electronic balance with 5000 g capacity and 0.01 g precision. Time between subsequent measurements varied among tanks from 14 to 28 days. These variable and irregular intervals were chosen to obtain a distribution of weight observations throughout the entire range of ages.

At each time of measurement, randomly selected fish from each family were anesthetized by cryonarcosis to avoid handling stress and were slaughtered in order to record carcass and fillet weight and yield. Because family size varied, the number of slaughtered fish varied among families as well; but around ten fish per family generally were available for the last slaughtering date. From families having more than 30 initially identified fish, four tilapia were randomly selected in each of the five evaluation periods and were slaughtered. From families having more than 22 initially identified tilapia, three fish were randomly selected; from those having 18 to 22 fish, two were randomly selected; and from families having from 9 to 17 identified tilapia, one fish was randomly selected in each period, assuring at least 4 fish for the last measure. Thus fish records were distributed across the full range of the growth period from 106 to 245 days of age. A total of 2042 records for each trait were used in the analyses.

Carcass weight (CW) refers to fish weight without head, pectoral arch and pelvic bones and viscera but with scales. Fillet weight (FW) refers to a fillet from the left side with intact ribs and skin but without scales. The fillet was then cut through the ventral line, and its weight was multiplied by two. One person performed both procedures. Carcass and fillet yields (CY and FY, respectively) were expressed in relation to fish live weight. At the 6th recording, all the remaining fish of each family were measured and slaughtered to obtain meat yield (carcass and fillet). Earlier sex determination of each fish was confirmed during the evisceration process.

2.3. Statistical analysis

The model for the analyses of all traits considered heterogeneity of residual variance with ten classes of 14 days each and included the fixed effect of tank and sex and random effects for additive genetic

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