Aquaculture 442 (2015) 112–118

Contents lists available at ScienceDirect

Aquaculture

journal homepage: www.elsevier.com/locate/aqua-online

Genetic variation in survival of tilapia (*Oreochromis niloticus*, Linnaeus, 1758) fry during the early phase of rearing in brackish water environment (5–10 ppt)

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ARTICLE INFO

Article history:
Received 27 September 2014
Received in revised form 27 November 2014
Accepted 26 February 2015
Available online 6 March 2015

Keywords:
Heritability
Genetic correlation
Survival
Brackish water and tilapia

ABSTRACT

Tilapia fry viability is one of the important traits because it affects number of seed produced and marketed and, therefore, yield and economic return for hatcheries and the aquaculture industry. In the present study, we examined the effect of female body weight prior to spawning and fry birth weight on survival rates at 20 days of nursing (D20) and at 62 days (D62) (when tagged). Genetic parameters for D20 and D62 were estimated from 86,609 individual fry which were offspring of 63 sires and 77 dams in the sixth generation of a Nile tilapia (*Oreochromis niloticus*) population undergoing selection for high growth in brackish water environment. Both linear and threshold models were used to estimate genetic parameters for these two traits. The estimates of heritability for D20 after hatching were low and not significantly different from zero across the models studied. By contrast, D62 showed a large heritable additive genetic component on both the liability and observed scales ($h^2 = 0.24$–0.79). The maternal and common environmental effects were 6–12% for survival at 20 days (D20), whereas they were small for survival from 21 days to tagging, D62 (1–5%). Genetic correlation between D20 and D62 was high and positive (0.72 ± 0.06). However, the estimate was significantly different from one, which suggests that D20 and D62 are under different genetic control and should be treated as different traits in selective breeding programs for tilapia. The results from the present study indicate for the first time that there is potential for simultaneous improvement of both survival rates at 20 days of nursing and at tagging in the future genetic improvement program for this tilapia population.

1. Introduction

Survival during the early phase of rearing is one of the important traits affecting overall productivity of hatcheries and fish farms. This character is influenced by various genetic and environmental factors such as age or body weight of females, egg size, fry weight, strains (lines), sire and dam effects (Rana, 1988). In the aquaculture sector, the survival rate of fish and shrimps until they reach an appropriate size for market can be as low as 30–66% under commercial production (Chou and Lee, 1997; Gitterle et al., 2005). Although survival figures vary between species and farming systems, they all show that mortality during the growth phase can be a major source of economic loss across the aquaculture sector (Andersen et al., 2008). For instance, by using the bio-economic model developed by Kankainen et al. (2012), an improvement of survival rate by 10% would earn an extra of about 70,500 USD for an aquaculture enterprise producing 1,000 tonnes of tilapia per year.

While systematic environmental effects and management options, such as water quality parameters (temperature, salinity levels) (Boucher et al., 2014), stocking density (DiMaggio et al., 2014) and diets (Santos et al., 2014; Takeuchi, 2014), have been extensively investigated to improve survival rate, genetic studies have focussed on factors that determine survival during the grow-out phase (Ponzoni et al., 2011). Additive genetic components for grow-out phase survival have been reported in salmonids (Standal and Gjerde, 1987), shrimp (Gitterle et al., 2005; Kenway et al., 2006) and mollusks (Dégremont et al., 2005, 2007), suggesting that these species will respond to selection for traits associated with survival. Only a few studies have reported heritabilities for early rearing survival and these involved Atlantic salmon and rainbow trout (Rye et al., 1990; Vehviläinen et al., 2008, 2010). For tilapia, studies have also focussed on survival during grow-out phase, predominantly in freshwater environments (Charo-Karisa et al., 2006). One exception is a study by Ninh et al. (2014) that was

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http://dx.doi.org/10.1016/j.aquaculture.2015.02.040
0044-8486/

conducted in brackish water (15–20 ppt). There are however no genetic parameter estimates for survival traits in the early phase of rearing tilapia, either in fresh or brackish water.

It is crucial to have information on genetic parameters for survival during the early phase of rearing in order to understand the genetic control of this trait and to formulate future plans for the improvement of the species. The objectives of our study were (a) to estimate heritability for survival at 20 days of nursing (D20) and at tagging (averaging 62 days, D62), (b) to examine the effect of dam weight and fry birth weight on survival and to (c) estimate the genetic correlations between survival traits (D20 and D62). The data were collected from the 6th generation of a Nile tilapia population that has been undergoing family based selection for high growth in brackish water environment.

2. Materials and methods

2.1. Location and pond preparation

The experiment was conducted in brackish water in earthen ponds of 800 m^2 (40 m × 20 m × 1.5 m) in Quy Kim Research Station under Research Institute for Aquaculture No. 1 (RIA1). The station is located in Hai Phong city, 120 km East of Hanoi. During the experimental period, the water temperature ranged from 25°C to 30°C and salinity from 5 to 10 ppt. The experimental ponds were prepared following a standard procedure, as follows. First, the mating and nursing ponds were drained and allowed to dry for 2 weeks before liming (100 g/m^2) and refilling with water to a depth of 1.2 m. So lime was scattered over the dry bed before filling with water and then stirring to dissolve. A fine mesh (1mm) screen net was used to cover the pond inlet to prevent the entry of predators (e.g., snakehead *Channa channa*, barramundi *Lates calcarifer*). In addition, 10 days before the nursing period, the pond was fertilized with an inorganic fertilizer (triple superphosphate) at a rate of 50 kg per hectare to stimulate the production of natural food.

2.2. Experimental animal and families production

A detailed description of the origin of the brackish water tilapia population and selection approach is given in Ninh et al. (2014). In brief, the genetic line was established in 2007 at the Research Institute for Aquaculture No. 1, Vietnam, from a complete diallel cross involving three strains (Genetically Improved Farmed Tilapia (GIFT strain), GIFT-derived strain named as NOVIT4 and a Taiwanese strain). Single pair mating was practiced with a total number of 397 sires (47–87 sires/generation) and 525 dams (66–104 dams/generation) in order to produce progeny during six yearly generations of selection from 2008 to 2014. In each generation, combined between- and within-family selection was practiced. Parents were selected for high breeding values of body weight at harvest. The average proportion of selected animals was 4.43% in females and 3.48% in males. Matings were made among genetically unrelated broodstock based on their estimated breeding values and their relationship to other animals in the pedigree to maintain genetic variability in the population for future selection. These breeding protocols and selection procedures were used in all generations.

The female and male breeders were conditioned in separate hapas (20 × 5 × 2 m) suspended in brackish water ponds (8–10 ppt) for 60 days before mating. In April 2014, a total of 103 breeding hapas (2 × 1 × 1.5 m) were assembled in the breeding pond in rows with enough space among them (1 m apart) to enable water circulation. The female was transferred to the breeding hapa for 2–3 days prior to transfer of the male (1 male with 2 females per hapa). The body weights of female and male brooders prior to mating were 437 ± 11 g and 629 ± 13 g, respectively. After 7–10 days of mating, fertilized eggs were collected from the mouth of the female and immediately transferred to hatching trays (40 × 20 × 10 cm) for artificial incubation. Each family was incubated in separate hatching tray. Water conditions during incubation were 25°C–30°C; pH 7.5–8.2; salinity, 3–5 ppt; and water flow, 0.2–0.3 l/s. The date of egg collection for each of the 77 families, which were produced from 63 male and 77 female brooders, was recorded.

2.3. Fry nursing and rearing to tagging

Fry were often hatched after about 5–7 days. Immediately after yolk sac absorption, the hatched fry of each family were transferred from the incubators to the nursery hapas (3 × 1.2 × 1.5 m with 2 mm mesh size) at a stocking density of 200 fry per square meter of surface water. At least three nursery hapa replicates for each family were maintained in the same pond to reduce environmental differences between families. The salinity level in nursing ponds fluctuated from 5 to 10 ppt. The number of fry and the hatching date of each family were recorded. During the first 20 days of nursing in hapas, the fry were fed four times per day with a commercial powder feed (AQUAXCEL®, Cargill Company) that had a dietary protein level of 45%, at the rate of 10% of their body weight. In the next period of nursing (day 21th to tagging period - day 62), the fry were transferred to a larger size hapa (3 × 2 × 1.5 m) until they reached a suitable size (5–8 g) to be physically tagged. During this second rearing period, the fry were given 35% protein feed twice a day at 8 am and 4 pm at a rate of 5% of the estimated total body weight.

2.4. Measurements

Body weight of all individually tagged female brooders was recorded (to nearest 0.1 g) using a digital scale before introducing them into the mating hapas and after fertilized egg collection. Immediately after yolk sac absorption, the number and the total weight of hatched fry of each family were measured and fry were transferred from the incubators to the nursery hapas. Total fry weight was measured (to nearest 0.01 g) using a digital scale. At 20th day of nursing (D20) and at tagging (averaging 62 days after hatching, D62), total numbers of fry were counted for each family. Individuals alive at the time of counting were coded as 1 otherwise as 0 for the fish that were absent. The survival data included two different measurement periods: (1) from hatching to 20 days of nursing (D20) and (2) from 21 days to tagging (averaging 62 days, D62). At tagging, one hundred fish from each family were randomly sampled to measure body weight (BW) using a digital scale (to nearest 0.1 g) and total length (L) using a ruler (with precision of 0.1 cm).

2.5. Statistical analyses

2.5.1. Exploratory and regression analyses

Preliminary analyses were performed to examine the distribution of the data and to identify possible systematic factors for consideration in the full statistical models for each trait. The effects of female body weight prior to spawning and fry birth weight were tested using logistic regression analysis available from PROC LOGISTIC in SAS 9.3 (SAS Institute Inc., 2011).

2.5.2. Estimation of genetic parameters

Genetic parameters for survival traits were analyzed using linear general mixed models (LMM) and threshold generalized mixed models (TGMM) in ASReml 3.0 (Gilmour et al., 2009). For the LMM, two models were used. The first model included only the additive genetic effect of individual fish (model 1), whereas in the second model, the effect of dam (i.e., full-sib groups) was also included (model 2). The general form of the LMM model written in mathematical notations is as follows:

$$y_{ijklm} = \mu + \mathrm{AGE}_i + \mathrm{DW}_j + \mathrm{FW}_k + a_l + e_{ijklm} \quad \text{[Model 1]}$$

$$y_{ijklm} = \mu + \mathrm{AGE}_i + \mathrm{DW}_j + \mathrm{FW}_k + a_l + d_m + e_{ijklm} \quad \text{[Model 2]}$$