Longitudinal genetic analysis of Nile tilapia (*Oreochromis niloticus* L.) body weight using a random regression model

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Abstract

Genetic parameters for body weight at ages over approximately 120 days are scarce in Nile tilapia. In this study, genetic parameters for body weight in Nile tilapia were estimated for ages ranging from 100 to 326 days. To this end, five repeated observations of body weight were collected on 2483 pedigreed fish. The fish originated from a population descending from four different genetic backgrounds. Genetic parameters were estimated using a random regression model with covariance functions. The heritability of body weight was fairly constant around 0.2, which offers good prospects for selection on body weight. Genetic correlations were estimated between all ages (100–326 days). At higher ages, genetic correlations were clearly more stable: for example genetic correlations were over 0.9 between the age of 100 days and all ages up to 115 days of age; at higher ages genetic correlations were over 0.9 between the age of 223 days and all ages up to 326 days of age. The estimated genetic parameters showed that early selection results in higher selection response than direct selection, when the target trait is body weight at the age of 326 days. This is due to somewhat higher heritabilities at lower age and a shortened generation interval. Furthermore, evidence was found for genetic differences in growth patterns of fish of different strains. This means that the possibility to change the shape of body weight curves by selection exists and that the choice of strains should depend on the target market weight of the production chain. From the raw data we concluded that differences in body weight between male and female fish were significant already at early ages (100 days). Results from a bivariate genetic analysis, where body weight of male and female fish are treated as separate traits, suggest that body weight in male and female fish is most likely controlled by the same genes. Prospects to

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decrease the difference between mature male and female body weight by selection are therefore unfavorable in Nile tilapia.

1. Introduction

Interest in genetic improvement of Nile tilapia is increasing rapidly. In the Netherlands, a new synthetic population was created based on four strains of Nile tilapia previously described (Rutten et al., 2004b). This population is kept in a closed recirculation system and is subjected to a breeding program for mature body weight. To facilitate the design and evaluation of breeding programs, genetic parameters are required. When genetic parameters are available, not only the amount of response from selection can be predicted, but also the effectiveness of alternative information sources and the increase of a populations inbreeding coefficient due to a systematic breeding program can be evaluated (Bijma et al., 2000; Rutten et al., 2002). Genetic parameters for body weight of this population are lacking, however, and have to be estimated to serve this purpose.

Several studies have reported genetic parameters (mostly heritabilities) for body weight in Nile tilapia in the past (Tave and Smitherman, 1980; Lester et al., 1988; Teichert-Coddington and Smitherman, 1988; Kronert et al., 1989; Oldorf et al., 1989; Brzeski and Doyle, 1995; Eknath et al., 1998; Bolivar and New-kirk, 2002; Gall and Bakar, 2002). These parameters were estimated for body weight at ages less than 200 days and often in small data sets. Tilapia production for the European market, however, targets body weights over 600 g, for which at least 300 days are needed. To our knowledge, genetic parameters (her-itabilities) for the age of 360 days have been published only by Langholz (1987). Genetic correlations for body weight at different ages have not been published before in Nile tilapia whereas these can provide valuable information for possibilities of early selection.

The aim of this study was, therefore, to estimate genetic parameters of body weight of Nile tilapia up to the age of at least 300 days. For this purpose, a random regression model was used which allows estimation of genetic variances for all ages, and genetic covariances between all ages present in the data.

2. Materials and methods

2.1. Experiment

Parents originating from four different strains of Nile tilapia (AIT, GIFT, IDRC and Göttingen; Rutten et al., 2004a,b) were randomly mated to produce progeny in 73 full-sib families. All matings were performed in vitro, after hand-stripping females for eggs and males for sperm. Transport of fish from the production to the breeding facilities probably caused fertility problems of female fish. Since parents originated from four different strains, an attempt was made to maximize the contribution of parents to the next generation. Therefore, each female was crossed with 2 males. Eventually, 40 dams and 56 sires contributed and paternal as well as maternal half-sib families were present.

After incubation of eggs, 150 fry of each full-sib family were raised in separate tanks of approximately 25 l, all attached to the same recirculation system. Due to the fact that spawning of females was not synchronized, all families were produced over a period of 12 weeks. When the fry reached an average weight of approximately 5 g, 100 fry per family were individually tagged using Floy® fingerling tags. First, 17 families were tagged and then combined into one tank (4500 l). One week later the next 18 families were tagged and combined together with the first 17 families. These 35 families will be referred to as group one (GR1). At the moment of combining, 1500 untagged fish randomly chosen from the 73 families were added to the tank, to increase the stocking density to commercial levels (3500+1500=5000 fish in total). For families 36–73 the scenario was similar, except that they were tagged in three batches. This