Genetic variation and correlated changes in reproductive performance of a red tilapia line selected for improved growth over three generations

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ABSTRACT

The present study examines genetic variation and correlated changes in reproductive performance traits in a red tilapia (*Oreochromis* spp.) population selected over three generations for improved growth. A total of 328 breeding females (offspring of 111 sires and 118 dams) had measurements of body weight prior to spawning (WBS), number of fry at hatching (NFH), total fry weight (TFW) and number of dead fry (NDF) or mortality of fry including unhatched eggs at hatching (MFH). Restricted maximum likelihood (REML) analysis in a multi-trait model showed that there are heritable genetic components for all traits studied. The heritability for WBS was very high (0.80). The estimates for traits related to fecundity (NFH, TFW) and survival (NDF) were low and they were associated with high standard errors. Genetic correlations of WBS with other reproductive performance traits (NFH, TFW and NDF) were generally positive. However, NFH was negatively correlated genetically with TFW. As expected, body measurements during growth stage exhibited strong positive genetic correlations with WBS. The genetic correlations between body traits and reproductive performance (NFH, TFW, NDF) were not significant. Correlated responses in reproductive traits were measured as changes in least squares means between generations or spawning years. Except for WBS that increased with the selection programs, the phenotypic changes in other reproductive traits observed were not statistically significant (P > 0.05). It is concluded that the selection program for red tilapia has resulted in very little changes in reproductive performance of the animals after three generations. However, periodic monitoring of genetic changes in fecundity and fitness related traits such as NDF or MFH should be made in selective breeding programs for red tilapia.

1. Introduction

Body weight has been the sole selection criterion in majority of genetic improvement programs for farmed aquaculture species because it is the primary determinant of animal performance and market price (Nguyen, 2016). However, reproductive performance and fitness related traits are also important to hatcheries to maximize revenue and return per unit of production. It is, therefore, crucial to understand the consequences of selecting for increased body weight on other traits of commercial importance, including reproductive performance.

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Several studies in model species or farmed animals have shown that selection for high growth rate might not have negative effects on reproductive traits (Bünger et al., 2005), whereas breeding objectives placing emphasis on high efficiency of meat production might result in a reduction in fertility and litter size of the animals as well as increase the incidence of genetic defects (Rauw et al., 1998). In aquatic animal species, the genetic relationships between body traits and other economically important traits have been examined in unselected populations (Gall and Neira, 2004; Gjerde, 1986; Kristjánsson and Arnason, 2014; Su et al., 2002). Whereas the heritability and correlations have enabled the prediction of the consequences of selection for increased body weight on traits of economic importance, there have been limited selection experiments to measure the realised response in reproductive traits to selection for improved growth rate. To date, only one study was conducted to examine correlated responses in reproductive traits to the long term selection program for genetically improved farmed tilapia (GIFT) strain (Hamzah et al., 2016).

A selective breeding program for a red tilapia population was conducted since 2010 to improve production performance, survival and body colour in Malaysia. Substantial direct response was achieved for body weight (the main selection criterion) after three generations (years) of selection (one generation per year). Although selection was practised solely on growth, correlated responses in other dimensions of body measurements, body colour and survival were also achieved (Nguyen, unpublished results). Nevertheless, genetic changes in reproductive traits as an indirect consequence of short term selection for enhanced growth are still unknown. In this present paper, we hypothesise that there have been no significant impacts on reproductive performance traits of a red tilapia population which has underwent three generations of selection from 2008 to 2012. In addition, we examined quantitative genetic variation in reproductive characters and their relationships with growth performance. The results obtained from the present study are expected to assist with the review and monitoring of genetic progress achieved in the genetic programs. If unfavourable changes in reproductive traits occurred, the breeding objectives for red tilapia would need to be refined to sustain long term response to selection in a preferred direction.

2. Materials and methods

2.1. Origin of the red tilapia strain

Data were collected from three generations of selection for improved growth in a population of red tilapia (*Oreochromis* spp.) at Aquaculture Extension Centre of Department of Fisheries, Malaysia. A full detailed account of the population, family production, selection procedures and management of the animals are given in Nguyen et al. (2017). In brief, the base population (G0) was established in 2009 from a full 3×3 diallele cross involving three strains which originated from hatcheries in Malaysia, Taiwan and Thailand. The selected line was formed by within- family sampling from 103 families (four to 10 females and males per family). They came from 103 families produced from the full diallele cross in 2008. The line was selected for high breeding values for body weight at harvest. A combined between and within family selection was practised in the selected line. The average proportion of selected animals was about 3% in females and 2.3% in males. Note, however, that selection was on breeding values but not by truncation (due to the inability of some selected breeders to reproduce or due to mortality we had to resort to selecting lower ranking fish; also, the number of selected individuals contributed by each family was restricted to avoid later inbreeding). In generations G0 (year 2009), G1 (year 2010), G2 (year 2011) and G3 (year 2012) they were the progenies of 32–50 dams and 28–51 sires for the selected line. Matings were made among genetically unrelated broodstock based on their estimated breeding values (EBVs) and their relationship to other animals in the pedigree to produce full-sibs and (paternal) half-sibs families. Over three generations, a total of 328 breeding females (offspring of 111 sires and 116 dams) successfully produced progenies used for the analyses in this study (Table 1). The breeding scheme is given in Nguyen (2016).

2.2. Family production, rearing to harvest

Family (full- and half-sibs) production was normally completed within 30–45 days. Mating was conducted in hapas, following the mating design prepared from annual routine genetic evaluation and mate allocation analyses. After 7 days of mating, only fertilized eggs at eyed stage were collected from the mouth of the female and immediately transferred to hatching jars for artificial incubation. Fry often hatched after about 5–7 days. Soon after yolk-sac absorption, the hatched fry of each family were transferred from the incubators to the nursery hapas (1 m^3 with 2 mm mesh size), stocked at a density of 200 fry per m^3. At least three nursery hapa replicates for each family were maintained in the same pond to reduce environmental differences between families. When the fingerlings reached an average weight of 5–10 g, about 100–150 individuals per family were randomly sampled and physically

Table 1
Number of breeding female, sire and dam in the population.

Spawning years	Population	Breeding female	Sire	Dam
2009	Base	110		
2010	Selection	78	51	50
2011	Selection	65	28	32
2012	Selection	75	32	34
Total		**328**	**111**	**116**