

A GENETIC LINE OF NILE TILAPIA UNDERGOING SEVEN GENERATIONS OF SELECTION UNDER MODERATE SALINITY WATER ENVIRONMENT

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SUMMARY

To date, commercial strains of Nile tilapia (*Oreochromis niloticus*, L.) are not available to culture in brackish water systems. Our attempts were to develop a genetic line of Nile tilapia that can perform well not only under a moderate salinity water environment, but also have desired eating and marketing characteristics. The genetic line developed from our study showed a significant improvement in growth performance, with an average genetic gain for body weight of about 8% per generation (one year per generation). Selection for high growth did not have any adverse effects on survival or deformity. Under on-farm testing conditions, our selected line outperformed other strains especially in saline water environments. The overall eating acceptability of the improved genetic line was superior to other freshwater tilapia counterparts. It is concluded that the moderate salinity tolerant tilapia line developed from our selective breeding program can be cultured effectively under a diverse array of farming systems.

INTRODUCTION

Tilapia is the second most important commercial freshwater fish, after carp, for freshwater aquaculture around the world. The species are widely cultured in more than 100 countries (El-Sayed, 2006). Among over 100 tilapia species, about three major species are being used for aquaculture, Nile tilapia (*Oreochromis niloticus*, L.) contributes about 71% of the global tilapia production (4,207,900 metric tons with an estimated value of US\$ 6,923 million in 2012) (Fitzsimmons, 2013). Despite the significant role of tilapia in the fishery sector, there has been a lack of improved stocks that can produce high quality seed to supply fish producers and farmers. As a consequence, commercial production is not highly economically viable due to low productivity of existing stocks. A number of breeding programs have been initiated to develop improved lines of Nile tilapia (*O. niloticus*) such as the Genetically Improved Farmed Tilapia (GIFT) strain (Nguyen *et al.*, 2010; Hamzah *et al.*, 2014) or GIFT-derived strain called as NOVIT4 (Luan *et al.*, 2008). However, these strains are suitable for a freshwater culture environment only. To date there are no improved lines of Nile tilapia that can perform well in brackish water systems (> 10 parts per thousand; ppt). In this project, we aimed to develop a fast growing strain of Nile tilapia with high survival and good adaptation to a range of aquaculture production systems.

The specific objectives of our study were: (i) to improve growth performance of the genetic line under saline water environments (10 – 20 ppt), (ii) to explore possibilities to select for new traits such as early survival, delayed maturity or disease resistance, (iii) to examine the effect of genotype by environment interaction, (iv) to evaluate physiological stress response and flesh quality characteristics of the improved strain relative to tilapia counterparts currently available for freshwater culture systems, and (v) to understand osmoregulation of salinity tolerance in this improved strain. In this paper, we present the selection response achieved from the genetic improvement program, specifically selection response to growth rate after seven generations in moderately salinity water. In addition, we highlight some of the main findings obtained from this study in relation to the objectives (ii) to (v).

MATERIALS AND METHODS

Origin of the selection population. The selection population was established in 2007 at Research Institute for Aquaculture No.1 (RIA1), Vietnam, from a complete diallel cross involving three different strains: genetically improved farmed tilapia (GIFT), GIFT-derived strain named as NOVIT4 and Taiwanese Nile tilapia. A detailed description of the population is given in Ninh *et al.* (2014) and Thoa *et al.* (2015).

Family production and performance testing. In each generation from 2007 to 2014, between 66 and 108 full- and half-sib families were produced within a six week period. After hatching, each family was kept separately in hapas (net cages of 1m³) until the fish reached a fingerling size of 5-10 g for physical tagging. A random sample of 50-100 individuals were then identified using Passive Implant Transponder (PIT). The tagged fish from all families were communally grown out in a saline water pond of 15 – 20 ppt over a period of about 4 months for successive annual generations between 2007 and 2013. Representatives of each family produced in 2014 were also tested in a freshwater pond environment. At harvest, body measurements were made on all individual fish, including body weight, standard length, body depth and body width. In the latest generation (year 2014), fitness (early survival, sexual maturity) and disease related traits (gill condition, deformity) were also recorded.

Genetic evaluation and selection. Best linear unbiased prediction (BLUP) was applied to a multi-trait mixed model and used to estimate breeding values (EBV) for harvest body weight for all individuals in the pedigree. Based on EBV ranking for harvest body weight, a combined within- and between- family selection was applied to select the best (highest EBV) individuals to become parents of subsequent generations. Across generations, the proportion of females and males selected were about 4.5% and 3.5%, respectively. Selection was practised on body weight at harvest. Mating of closely related individuals was avoided and the number of individuals contributing to next generations was constrained to minimise inbreeding. The average inbreeding rate was less than 0.5% per generation.

Estimation of genetic parameters. Restricted maximum likelihood method (REML) was applied to estimate genetic parameters for traits studied. A linear mixed model was used to analyse continuous traits such as body weight or food conversion ratio. The random effects were the additive genetic effects of individual fish and full-sib family groups and the fixed effects were generation, sex, environment and their two-way interactions. Age from birth to harvest within sex and generation was fitted as a linear covariate for body weight traits. For binary characters including survival or sexual maturity, generalised threshold mixed models were applied as described by Thoa *et al.* (2015) and Nguyen *et al.* (2014).

RESULTS AND DISCUSSION

Response to selection. Genetic evaluation of 36,145 individual animals with performance records showed that direct genetic gain for body weight in the selection program was averaging 8% per generation or 0.20 to 2.84 genetic standard deviation units (Figure 1). Correlated changes in survival rate during grow-out were close to zero (Ninh *et al.* 2014). The moderate heritability for body weight ($h^2 = 0.53 \pm 0.12$) also shows that the present population will continue to respond to future selection.

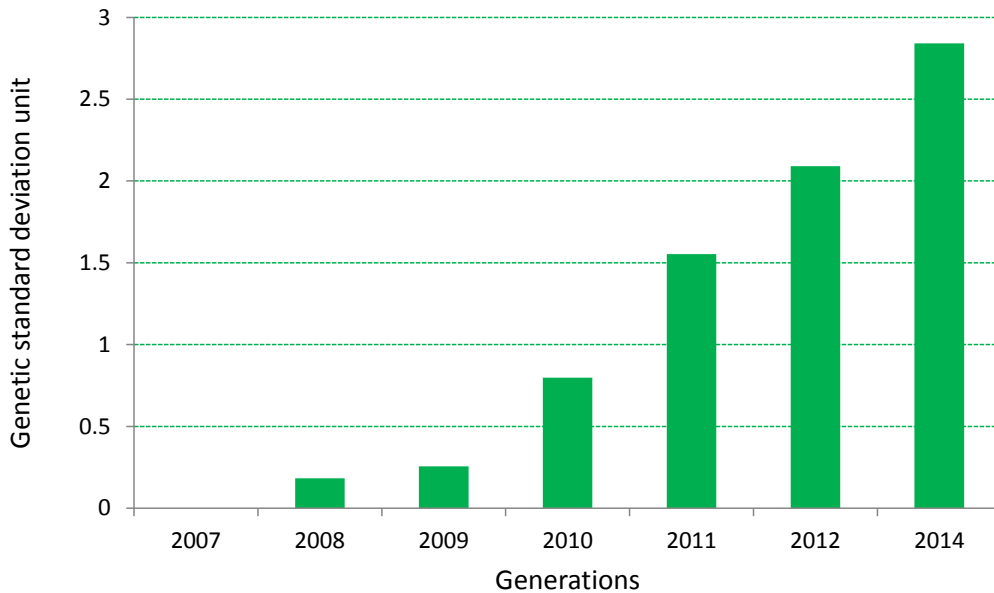


Figure 1. Genetic gain for body weight in standard deviation units achieved in the selection population of Nile tilapia under moderate salinity water environment (10 – 20 ppt) over seven generations including the base population in 2007.

Genetic parameters for new traits. To broaden the breeding objectives for this species, we examined the quantitative genetic basis of new traits collected in the latest generation (2014). REML analysis showed that there are additive genetic components for early survival rate, sexual maturity, gill condition and morphological deformity (heritability range from 0.05 to 0.29), suggesting potential to include these traits in a future breeding program for this population.

Offspring of the salinity tolerance line can perform well under freshwater ponds. We attempted to understand if the moderately salinity tolerant line can perform well in freshwater systems. The data, from performance testing under both salinity and freshwater environments, were combined with a full pedigree including a total of 36,145 individual animals recorded from 2007 to 2014. The estimates of genetic correlations for homologous trait expressions between salinity and freshwater environments were very high and close to one (0.78 – 0.99, s.e. 0.07 to 0.29). This result suggests that the genotype by environment interaction was not significant for growth and fitness related traits in this population. It is also suggested that the moderately salinity tolerant genetic line developed from this selective breeding program can be used in freshwater farming systems.

Physiological response. One indicator of physiological response measured in the selected line was Na⁺ and K⁺-ATPase activity. Under the same salinity culture conditions, the improved line showed an increase in Na⁺ and K⁺-ATPase activity relative to other ‘freshwater’ counterparts.

Flesh attributes and eating quality. Preliminary analyses show that in comparison with commercial ‘freshwater’ tilapia strains, our salinity tolerant line had better flesh quality attributes and overall eating quality.

Osmoregulation. Future studies will examine possible changes at the molecular and genomic levels as well as osmoregulatory adaptation that may have been accompanied by the selection program in the present population.

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