Genetic Parameters for Within-family Variance of Harvest Weight in Nile tilapia (Oreochromis niloticus)

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ABSTRACT: Relaying on traditional selection, animal breeders were successful in improving mean levels of trait values, but have struggled to make the same progress in reducing variability of trait values among individuals. Large size differences can be observed in domestic Nile tilapia, but the genetic background of this variability is almost entirely unknown. In this study, we estimated genetic variance in within-family variance for harvest weight in Nile tilapia using a bivariate model. Data consisted of 6,330 fish with phenotypic observations on harvest weight and 882 observations for within-family variance of harvest weight. Additive genetic variance in within-family variance was 0.279 indicating that the within-family variance could be reduced by 53% when changed by one genetic standard deviation. Genetic correlation between harvest weight and within-family variance was 0.66. Results indicate very good opportunities to genetically improve uniformity and robustness in aquaculture.

Key words: Harvest weight; Uniformity; Within-family variance; Nile tilapia

Introduction

Aquaculture is an area of continuing growth that offers vast opportunities for genetic improvement, however these remain mostly unexploited. Focusing on traditional selection, animal breeders were successful in improving mean levels of trait values, but little progress has been made in reducing variability of trait values among individuals. The latter one may be significant from economical point of view, and is especially interesting in situations where mean trait values in a population are near an intermediate optimum (Mulder et al. 2008). Although genetic improvement of uniformity is desirable, the complexity inherent in the estimation of genetic differences in variability prevents its implementation in breeding programs (SanCristobal-Gaudy et al. 2001; Sorensen and Waagepetersen 2003).

Pronounced variability in values of a trait, such as harvest weight can be observed in domestic Nile tilapia (Oreochromis niloticus), which is regarded as one of the main freshwater cultured species in the world (FAO 2012; Khaw et al. 2014). In GIFT (Genetically Improved Farmed Tilapia) strain of WorldFish, coefficient of variation (CV) for harvest weight has a value of 40-60%, which is considered to be high (Khaw et al. 2010) and much higher than in livestock species for body weight. Genetic background of this variability is almost entirely unknown.

Reducing variability by means of selective breeding can be realized if there are genetical differences in residual variance among genotypes (Mulder et al. 2008). Empirical evidence of substantial genetic variation in residual variance comes from the analysis of litter size in sheep, litter size in pigs and body weight in broiler chickens (Hill and Mulder 2010). In aquaculture, it seems that there is also considerable genetic variation in residual variance, as Sonesson et al. (2013) found large genetic variance in residual variance when studying within-family variance of body weight in Atlantic salmon. Exploring the heterogeneity of variance and utilization of this genetic variation, may be a promising route to produce more homogeneous stocks in commercial fish farming (Sonesson et al. 2013).

The aim of this study was to estimate genetic variance in within-family variance of harvest weight in Nile tilapia. In addition, the genetic correlation between harvest weight and within-family variance was estimated.

Material and methods

Environment. A large scale experiment with aim to provide records on body weight in groups of full sibs, was conducted at Jitra Research Station of WorldFish, located in Kedah State of Malaysia. Data were collected in four batches using GIFT strain of WorldFish, with each batch named after year when the fish was stocked in experimental ponds (Khaw et al. 2014).

Experimental design. This experiment was specifically designed to estimate social genetic effects on growth rate. In this design, groups were formed using fish from two different families, with each family contributing by 8 randomly selected individuals (Bijma 2010). Since GIFT breeding program is based on one male to two females mating scheme, data has a strong half-sib structure that also allows the estimation of genetic variance in within-family variance. Total number of 237 families was used to form 701 groups (Khaw et al. 2014). Unique combinations of families were created using block design composed of 11 full-sib families, where each family combined only once with other 10 families (Khaw et al. 2014). The groups were stocked in netcages and placed in earth ponds of size 0.1 ha. For each batch two earth ponds were used, except...
for batch 2010, where due to high mortality of fry, only one pond could have been stocked.

**Records.** Harvesting of the fish was done after five to eight months of grow-out period, when the individuals had reached weight of 200-250 grams on average (Khaw et al. 2014). During this process, live weight, body length, body depth and body width were collected, as well as sex of the fish. The age at harvest of each fish was computed using documented spawning and harvesting dates (Khaw et al. 2014). As a consequence of unexpected weather conditions, batch 2012 had high level of mortality and was excluded from further study. Eventually, 6,330 fish with phenotypic observations on body weight at harvest were available for analysis. For analysis of within-family variance, net cages containing insufficient number of individuals (less than 8 out of 16 in a group) or expressed significant discrepancy in contribution of two families at the end of the experiment (less than 3 individuals per family) were discarded from data set. At the end, the analysis of within-family variance of harvest weight was restricted to 441 groups, formed by 108 different families. With 2 families in each group there were 882 observations for within-family variance. The pedigree used in both analyses consisted of 34,517 records, tracing back seven generations.

**Data analysis.** Genetic parameters for harvest weight and within-family variance of harvest weight were estimated using a bivariate model. Response variables were log transformed in order to improve the distribution of their estimated using restricted maximum likelihood (REML) methods implemented in ASReml software (Gilmour et al. 2009). For the bivariate analysis, the following sire-dam model was used:

\[
\begin{align*}
\mathbf{y}_1 &= \mathbf{Xb}_1 + (\mathbf{Z}_p + \mathbf{Z}_m)\mathbf{u}_1 + \mathbf{Vc}_1 + \mathbf{e}_2 \\
\mathbf{y}_2 &= \mathbf{Xb}_2 + (\mathbf{Z}_p + \mathbf{Z}_m)\mathbf{u}_2 + \mathbf{Vc}_2 + \mathbf{e}_2
\end{align*}
\]

where, \(\mathbf{y}_1\) and \(\mathbf{y}_2\) are the vectors of observed log-transformed harvest weight and log-transformed phenotypic variance of harvest weight, respectively; \(\mathbf{b}_1\) and \(\mathbf{b}_2\) are the vectors of fixed effects; \(\mathbf{u}_1\) and \(\mathbf{u}_2\) are the vectors of additive genetic sire and dam effect with distribution \(\begin{pmatrix} \mathbf{u}_1 \\ \mathbf{u}_2 \end{pmatrix} \sim N \left( \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \mathbf{A} \otimes \mathbf{G} \right)\) where \(\mathbf{A} = \frac{1}{4} \mathbf{G}_{\mathbf{a}}\) (Sonesson et al. 2013); \(\mathbf{c}_1\) and \(\mathbf{c}_2\) are the vectors of random group effect, \(\begin{pmatrix} \mathbf{c}_1 \\ \mathbf{c}_2 \end{pmatrix} \sim N \left( \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \mathbf{I} \otimes \mathbf{C} \right)\) and \(\mathbf{e}_1\) and \(\mathbf{e}_2\) are the vectors of random residuals with distribution \(\begin{pmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{pmatrix} \sim N \left( \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \mathbf{I} \otimes \mathbf{R} \right)\). The \(\mathbf{X}, \mathbf{Z}_p, \mathbf{Z}_m\) and \(\mathbf{V}\) are known design matrices assigning observations to the level of fixed, sire, dam and group effects and \(\mathbf{I}\) is the identity matrix. The fixed effects included for harvest weight were batch (2009, 2010, 2011), sex (male, female), pond (1, 2) and their interaction with age at harvest (Khaw et al. 2014). The same fixed effects were fitted for variance of harvest weight, except sex subclass, which in this case was expressed as \(p_m p_r\), where \(p_m\) is proportion of males, and \(p_r\) proportion of females in each family in the group. Prior to bivariate analysis both response traits were analyzed separately in univariate sire-dam model with fitted fixed and random effects as described above.

**Results and Discussion**

Variance components estimated based on univariate and bivariate analysis for harvest weight and within-family variance of harvest weight, are presented in Table 1.

**Harvest weight.** The estimated \(h^2\) for harvest weight in univariate analysis had value of 0.4676 that remained almost the same in bivariate analysis. This result is in agreement with heritability of harvest weight in Nile tilapia reported in the literature (Khaw et al. 2009; Ponzoni et al. 2005). Other genetic parameters also showed insignificant change in values obtained from two approaches. The group effect gave important contribution of 26.2% to phenotypic variance of harvest weight.

**Within-family variance.** Genetic variance of within-family variance increased in the bivariate analysis compared to the univariate. This can be especially observed in heritability that changed from 0.333 to 0.489 in bivariate analysis. The heritability is really high, but should be interpreted with caution as it depends on the group size. The differences in variance components between the bivariate and univariate analysis are likely due to different disentangling of fixed and random effects, indicating some confounding between families and environmental effects. Here we also notice substantial residual variance of 0.4649 and 0.4606 from univariate and bivariate model, respectively. The high residual variance is partly due to that the residual variance contains Mendelian sampling genetic variance (Sonesson et al. 2013). Bivariate analysis of within-family variance revealed significant level of additive genetic variance of 0.279, higher than estimates of Sonesson et al. (2013) for harvest weight in Atlantic salmon. This result implies that there is considerable amount of variation between families that offers the opportunity to genetically improve uniformity and robustness in aquaculture. The additive genetic variance in within-family variance would indicate that the within-family variance could be reduced by 53% when changing it by one genetic standard deviation. In this case, group effect accounted for only 5.2% (univariate model) and 6.9% (bivariate model) of phenotypic variance.

Genetic correlation between harvest weight and within-family variance has found to be 0.66. This magnitude of genetic correlation is defined as high and it suggests that selection for higher mean value in harvest weight also leads to increase of variation in trait values among individuals. Therefore, index selection to simultaneously increase harvest weight and reduce variation is required.
Conclusion

Substantial amount of additive genetic variance in within-family variance for harvest weight in Nile tilapia was found in our study. This finding opens the possibilities to reduce variability among individuals within family in aquaculture and increase robustness of fish. High genetic correlation of 0.66 between harvest weight and within-family variance suggests necessity for index selection in order to increase harvest weight and reduce variation at the same time.

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Literature Cited


Table 1. Estimates of variance components for harvest weight (HW) and within-family variance (Var(PHW)), obtained by univariate (U) and bivariate (B) analysis.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>HW</th>
<th>Var(PHW)</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>U</td>
<td>B</td>
</tr>
<tr>
<td>(\sigma_A^2)</td>
<td>0.0458 (0.0069)</td>
<td>0.0469 (0.0070)</td>
</tr>
<tr>
<td>(\sigma_g^2)</td>
<td>0.0257 (0.0021)</td>
<td>0.0258 (0.0021)</td>
</tr>
<tr>
<td>(\sigma_e^2)</td>
<td>0.0608 (0.0011)</td>
<td>0.0607 (0.0011)</td>
</tr>
<tr>
<td>(\sigma_P^2)</td>
<td>0.0979 (0.0029)</td>
<td>0.0982 (0.0029)</td>
</tr>
<tr>
<td>(h^2)</td>
<td>0.4676 (0.0636)</td>
<td>0.4782 (0.0644)</td>
</tr>
<tr>
<td>(g^2)</td>
<td>0.2622 (0.0171)</td>
<td>0.2622 (0.0170)</td>
</tr>
</tbody>
</table>