MODELING FILLET WEIGHT IN NILE TILAPIA (OREOCHROMIS NILOTICUS)

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INTRODUCTION

The focus in genetic improvement of tilapia has been limited to growth for years (Tave and Smitherman, 1980; Teichert-Coddington and Smitherman, 1988; Bentsen et al., 1998). Fillet yield of fish however, can be regarded as an increasingly important trait (Kause et al., in press). Since measurement of fillet yield implies killing of animals, this compromises phenotypic selection for the trait.

Allometric models have been frequently used to relate multidimensional body measurements e.g. body weight or body surface, to linear body measurements e.g. length or height (Huxley, 1924). Body measurements can be taken easily without harming fish, and would thus provide a possibility to model fillet weight of fish. Nowadays, it is possible to take body measurements automatically via e.g. image analysis (Zion et al., 1999). Lines et al. (2001) were even able to determine body measurements of swimming fish.

The aim of this paper was to develop an allometric model to predict fillet weight, based on linear body measurements, for future use in breeding programs based on mass selection.

MATERIAL AND METHODS

Data. Tilapias were collected which originated from three strains: the Chitralada strain (AIT), the IDRC strain and the GIFT strain (5th gen.). The fish were grown to an average weight of 784 gr (n=430), 715 gr (n=414) and 705 gr (n=371) for the AIT, IDRC and GIFT strain respectively. Strains were reared in separate tanks, in the same recirculation system at equal densities up to 200 kg/m³, feeding was ad lib. Random samples of fish were taken for each strain, and measured for the following traits: total weight (TW) in grams, standard length (L), height (H) and width (W) all in cm. Scales of the fish were removed, and the fish were filleted by one of five persons (P). Fillet weight (FW, with skin and ribs) in grams was recorded. Gonads were examined to record sex (S), and fillet percentage was calculated as: 

\[ F\% = \left( \frac{FW}{TW} \right) \times 100 \]

Statistical analysis. The presence of possible systematic effects of person or biological effects of strain and sex on fillet percentage, was studied with an ANOVA model (proc GLM, SAS, 1990):

\[ Y_{ijkl} = \mu + P_i + ST_j + S_k + e_{ijkl} \]

where, \( Y \) is an observation of fillet percentage, \( \mu \) is the overall mean, \( P \) is a fixed effect of persons (i=1,5), \( ST \) is a fixed effect of strains (j=1,3), \( S \) is a fixed effect of sex (k=1,2), \( e \) is a random residual term. Least square means (LSM) were calculated to quantify the model effects.
Allometry. Since fillet weight is directly related to body measurements (contrary to fillet percentage), fillet weight was modeled with an allometric model. Observations of fillet weight were corrected for effects of person first, using LSMeans of the ANOVA model: 

\[ FW^* = \frac{F\%}{100} \times TW \]

(\* indicates a corrected value).

The standard allometric relationship 

\[ Y = a \times X^b \times \epsilon \]

was extended to enable use of multiple body measurements:

\[ FW^*_i = a \times \prod_{n} X_i^{b_n} \times \epsilon_i \]

where, \( FW^*_i \) is an observation of corrected fillet weight, \( a \) is a constant, \( b_n \) is a proportionality constant, \( n \) is the number of body measurements used in the model, \( X \) is an observation of a body measurement and \( \epsilon \) is a random residual term. Note that the allometric model is intrinsically linear due to the multiplication of the error term (e.g. Neter and Wasserman, 1974) and can thus be expressed as a linear model, when applying a logarithmic transformation:

\[ \ln(FW^*_i) = \ln(a) + \sum_{n} b_n \ln(X_i) + \ln(\epsilon_i) \]

where, \( \ln(a) \) is the intercept, \( b_n \) is a regression coefficient and \( \ln(\epsilon) \) is a random residual term.

A full model including L, H and W as independent variables was fitted to the full data set. Later other combinations of body measurements were used to study their explanatory value. Goodness of fit was calculated as indicator for the model performance.

RESULTS AND DISCUSSION

Statistical analysis. The effects of person, strain and sex on fillet percentage were highly significant (p<0.001, not shown). Large differences in LSMeans were found for different strains of tilapia (Table 1). Fish from the GIFT strain yielded almost 3.6% higher fillet percentage than fish from the AIT strain. Since environmental factors were held constant during the growth period of the different strains, the differences in fillet percentage are thought to originate from genetic differences. Fish from the GIFT strain were selected for growth for a number of generations (Bentsen et al., 1998) and therefore we hypothesize that higher fillet percentage in the GIFT strain originated as correlated response from selection on weight, and this would imply a positive genetic correlation between growth and fillet percentage. In rainbow trout a genetic correlation between growth and fillet percentage of 0.29 was found, which supports this hypothesis (Kause et al., in press).

<table>
<thead>
<tr>
<th>Strain</th>
<th>M</th>
<th>F</th>
<th>M + F</th>
</tr>
</thead>
<tbody>
<tr>
<td>AIT</td>
<td>34.70</td>
<td>34.06</td>
<td>34.40</td>
</tr>
<tr>
<td>IDRC</td>
<td>35.08</td>
<td>35.00</td>
<td>35.10</td>
</tr>
<tr>
<td>GIFT</td>
<td>38.23</td>
<td>37.75</td>
<td>37.99</td>
</tr>
<tr>
<td>Overall</td>
<td>36.04</td>
<td>35.62</td>
<td>35.73</td>
</tr>
</tbody>
</table>

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A linear regression of fillet percentage on total weight (Figure 1a) shows that the two traits are not related, the differences found between strains could thus not be attributed to differences in average weight of the strains, which is suggested often.

A difference of 0.4 % in fillet percentage between male and female fish was found (Table 1). This can be of particular interest for e.g. producers who work with all male populations, since these populations not only benefit from faster growth (Mair et al., 1995), but could also benefit from higher fillet percentages.

**Allometry.** Parameter estimates and goodness of fit of the allometric model are presented in table 2. It shows that the full model explained 91.0% of the observed variance, which is illustrated by a scatter plot of observed values and corresponding model predictions in figure 1b.

**Table 2. Parameter estimates and goodness of fit (R²) of the allometric model using different combinations of body measurements**

<table>
<thead>
<tr>
<th>Ln(a)</th>
<th>b_L</th>
<th>b_H</th>
<th>b_W</th>
<th>R²</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2.54065</td>
<td>1.47635</td>
<td>0.89048</td>
<td>0.71001</td>
<td>0.910</td>
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<tr>
<td>-2.60493</td>
<td>1.60951</td>
<td>1.20325</td>
<td>0.95221</td>
<td>0.887</td>
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<tr>
<td>-3.43507</td>
<td>2.29414</td>
<td>0.83027</td>
<td>0.863</td>
<td></td>
</tr>
<tr>
<td>-0.23223</td>
<td>1.84428</td>
<td>1.20325</td>
<td>0.887</td>
<td></td>
</tr>
<tr>
<td>-4.01169</td>
<td>2.93468</td>
<td>0.83027</td>
<td>0.863</td>
<td></td>
</tr>
<tr>
<td>-0.06132</td>
<td>2.31785</td>
<td>0.83027</td>
<td>0.863</td>
<td></td>
</tr>
<tr>
<td>1.72466</td>
<td>2.40295</td>
<td>0.83027</td>
<td>0.863</td>
<td></td>
</tr>
</tbody>
</table>

1b. Variance of body measurements is often heteroscedastic i.e. error variance is not constant over all observations. The logarithmic transformation, however, stabilizes error variance and overcomes otherwise violated model assumptions (Neter and Wasserman, 1974).

**Figure 1. a) Scatter plot of observed total weight and observed fillet percentage; b) model predictions of fillet weight and observed values of fillet weight (full allometric model)**
This study shows that the performance of the allometric model enables mass selection for fillet weight, contrary to e.g. findings of Bosworth et al. (1998) in a similar study with bass. However, the extent to what fillet weight in tilapia can be improved by artificial selection is unknown, because genetic parameters of fillet weight are lacking for tilapia. Moderate heritabilities for fillet weight and fillet percentage (0.22 and 0.33 respectively) were reported in rainbow trout (Kause et al., in press), indicating possible prospects for genetic improvement of fillet weight in tilapia. If mass selection for fillet weight would be practiced, genetic improvement can be expected in both total weight and fillet percentage, because both traits are combined in the trait fillet weight. The extent to what both traits would be improved depends largely on their genetic (co)-variances.

Selection differentials of predicted and observed fillet weight, calculated for the 10% highest scoring males and females based on predicted fillet weight (all on normal scale) show that the performance of the model is good also among the highest fillet weight values. Only small differences between predicted and observed selection differentials were found: for males \( S_{p} = 177.4 \text{ gr.} \) vs. \( S_{o} = 174.3 \text{ gr.} \), and for females \( S_{p} = 117.6 \text{ gr.} \) vs. \( S_{o} = 122.2 \text{ gr.} \). Using the heritability for fillet weight in rainbow trout of 0.22 (Kause et al., in press) and selecting the 10% best scoring male and females for fillet weight, mass selection can result in a genetic gain of: \( A = h^2 \times S = 0.22 \times 177.4 = 39.0 \text{ gr.} \) per generation for males, and: \( A = h^2 \times S = 0.22 \times 117.6 = 25.9 \text{ gr.} \) per generation.

Reduction of the number of body measurements in the allometric model, results in a small reduction of fit (Table 2). Using a combination of 2 body measurements, goodness of fit varied between 0.887 for a combination of length and width, and 0.863 for a combination of height and width. For models using single body measurements, goodness of fit differed little between the use of length or height (0.833 and 0.827), but was lower for the use of width only (0.594). These results provide prospects for the use of e.g. image analysis, since image analysis provides measurements of length and width (flank of the animal; e.g. Cibert et al., 1999). Use of this technique would enable mass selection for fillet weight in large numbers of fish.

REFERENCES