LIVE WEIGHT GENETIC PARAMETERS IN TWO PRODUCTION ENVIRONMENTS IN
THE GIFT STRAIN OF NILE TILAPIA (OREOCHROMIS NILOTICUS)

R. W. Ponzoni¹, A. Hamzah², N. Kamaruzzaman¹ and Hooi Ling Khaw¹
¹WorldFish Center, Batu Maung, Penang, Malaysia
²National Prawn Fry Production and Research Center, Kedah, Malaysia

SUMMARY
A pedigreed population based on the sixth generation of GIFT (Genetically Improved Farmed
Tilapia) was established in Malaysia. Progeny were generated in two spawning seasons, 2002 and
2003, a Selection and a Control line were created, and two production environments (cages and
ponds) were used to grow them out. Live weight in cages and in ponds was treated as two different
traits (LWC and LWP, respectively). The heritabilities were 0.38 (s.e. 0.083) and 0.45 (s.e. 0.103),
whereas the maternal and common environment effects estimated from the dam variance component
were 0.17 (s.e. 0.038) and 0.22 (s.e. 0.047), for LWC and LWP, respectively. The genetic correlation
between LWC and LWP was 0.58 (s.e. 0.135). It was concluded that although the genetic correlation
between LWC and LWP was less than 1.0, there was not enough evidence to justify the conduct of
separate genetic improvement programs for cage and pond environments.

Key words: Nile Tilapia; Heritability; Genetic correlation.

INTRODUCTION
In Tilapia the focus of selection programs has been almost exclusively restricted to growth rate.
Some estimates of phenotypic and genetic parameters are available, but in a strict sense these are only
applicable to the population and the environment where they were obtained. Furthermore, individual
estimates are subject to sampling problems and the parameters can change over time, particularly in
relatively small populations undergoing selection. Hence, the desirability of having parameter
estimates that are directly relevant to the population one is working with. Tilapia farming in
Malaysia is conducted in two main production systems, namely, cage and pond (Annual Fisheries
Statistics 1996). In this paper we present estimates of genetic parameters for harvest weight
expressed in cage and pond environments in the GIFT (Genetically Improved Farmed Tilapia) strain
(Bentsen et al. 1998).

MATERIALS AND METHODS
The environment and the fish. The work was conducted at the Aquaculture Extension Center,
Department of Fisheries, Jitra, Kedah State, Malaysia (latitude 6° N, longitude 100° E, altitude 23 m).
The daily average temperature is 27° C, with little variation throughout the year. The fish belonged
to the sixth generation of selection of GIFT, and were received at Jitra during the end of 2000 and the
beginning of 2001. They were mated and produced a seventh generation in the spawning season of
2002, which in turn produced an eighth generation in 2003. No selection took place among the fish
transferred from the GIFT Foundation. Animal model breeding values were calculated for all
individuals, and two lines were created with the 2002 progeny, one selected on high breeding value
for live weight (Selection line), and another one selected for average breeding values (Control line).
The number of sires and dams from which progeny was harvested in both spawning seasons and
lines, as well as the number of progeny, are shown in Table 1. All the sires and dams were represented in both cage and pond environments except in the Selection line in the spawning season 2003, where one sire and four dams that were represented in pond were not represented in cage environment. None of the parents used in the 2002 spawning season were used in 2003 (i.e. generations were discrete). We consider the progeny produced in the 2002 spawning season our Base Population, and in our analyses we treat it as part of the established Control line. One male was mated to two females, but not always successfully, with the result that fewer females than planned left progeny (see detailed methodology in WorldFish Center (2004) and Ponzoni et al. 2005). Full sib groups remained together in hapas until they were individually tagged, at approximately two months of age. After tagging the fish were communally grown out either in cages or in earthen ponds.

Table 1 Number of sires, dams and progeny, by spawning season and line

<table>
<thead>
<tr>
<th>Spawning season</th>
<th>Line</th>
<th>Environment</th>
<th>Sires</th>
<th>Dams</th>
<th>Progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td>2002</td>
<td>Base</td>
<td>Cage</td>
<td>52</td>
<td>54</td>
<td>978</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pond</td>
<td>52</td>
<td>54</td>
<td>706</td>
</tr>
<tr>
<td>2003</td>
<td>Selection</td>
<td>Cage</td>
<td>34</td>
<td>61</td>
<td>1524</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pond</td>
<td>35</td>
<td>65</td>
<td>1036</td>
</tr>
<tr>
<td></td>
<td>Control</td>
<td>Cage</td>
<td>19</td>
<td>19</td>
<td>695</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pond</td>
<td>19</td>
<td>19</td>
<td>455</td>
</tr>
<tr>
<td></td>
<td>Total</td>
<td></td>
<td>106</td>
<td>138</td>
<td>5394</td>
</tr>
</tbody>
</table>

Records and data analysis. Data recording of all the tagged fish was done at harvest, when individual live weight (LW) was measured. Sex of the fish was also recorded. From the harvesting and spawning dates we are able to compute the age (in days) of each individual fish. The computer program ASReml was used (Gilmour et al. 2002) to analyse the data. Treating LW in cages and ponds as a single trait (Ponzoni et al. 2005), and fitting all fixed effects (spawning season, selection line, environment, sex) and random effects (sire, dam nested within sire and sire by environment interaction) using PROC MIXED in SAS (1997), we found a statistically significant sire by environment interaction. It is known that a trait (LW in this case) expressed in two environments may be regarded as two different traits (Falconer 1952). Live weight in the cage environment (LWC) and live weight in the pond environment (LWP) were treated as two traits in a bivariate analysis. The models fitted included the fixed effects of spawning season (2002 and 2003), selection line (S and C) and sex. Because in the preliminary analyses interactions among fixed effects were either statistically non-significant or deemed unimportant (due to scale and not to reversal of rankings), for variance component estimation we fitted ‘spawning season, line, sex’ classes. Age at harvest was used as a covariate within those classes, with the ‘spline’ option available in ASReml. The availability of a complete pedigree in the population enabled fitting an animal (random) model. Dam was fitted as another random effect, but solely accounting for the environmental effect on the progeny, without a genetic structure. For both LWC and LWP the dam variance component ($\sigma^2_D$) was in this case a combination of the maternal effect and the common environment (so $\sigma^2_D = \sigma^2_{M_E}$) to which full sibs are exposed early in life (i.e. while being hatched and while in the nursing and rearing hapas).
animal variance component provided the estimate of the additive genetic variance ($\sigma^2_A$), whereas the phenotypic variance ($\sigma^2_P$) was estimated from the sum of all variance components. The maternal and common environmental effect ($\sigma^2_D$) was calculated as the ratio between the dam variance component and the phenotypic variance. The square root transformation of LWC and LWP improved the distribution of residuals and was used in all analyses.

**RESULTS**

Table 2 shows the number of observations, simple mean, and coefficient of variation values for body weight in both environments, and for age at harvest.

<table>
<thead>
<tr>
<th>Environment</th>
<th>Variable</th>
<th>N</th>
<th>Mean</th>
<th>CV(%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cages</td>
<td>Live weight</td>
<td>166</td>
<td>48</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Harvesting age</td>
<td>3197</td>
<td>232</td>
<td>12</td>
</tr>
<tr>
<td>Pond</td>
<td>Live weight</td>
<td>192</td>
<td>60</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Harvesting age</td>
<td>2197</td>
<td>220</td>
<td>14</td>
</tr>
</tbody>
</table>

The REML estimates of variance components, heritabilities, maternal common environmental effect and the genetic correlation between LWC and LWP are shown in Table 3.

**DISCUSSION**

The heritability estimates for LWC and LWP were high. It was greatest for the latter trait (Table 3). They were greater than when, for the same data set, the expression in cages and pond was treated as a single trait (Ponzoni et al. 2005). For both traits the estimates were greater than that of Gall and
Bakar (2002) but they were in good agreement with those reported by Kronert et al. (1989), and with the ‘field environment’ estimates of Oldorf et al. (1989). They were slightly lower than the ‘laboratory environment’ estimates of the latter authors, and than those of Bolivar and Newkirk (2002).

The genetic correlation between LWC and LWP estimates the degree to which the same genes are involved in the expression of weight in cages and ponds. The genetic correlation was positive and in the moderate to high range (Table 3). This result indicates that if selection were conducted in one environment (say, cages), but progeny were to perform in another environment (say, ponds), assuming equal heritability in both environments, selection in cages would capture 60 per cent of the gain that could be achieved if it were carried out in ponds. Our estimate of the genetic correlation had a relatively large standard error, resulting in 95 per cent confident limits ranging from 0.32 to 0.84. We will again estimate this genetic correlation after adding the data of another generation. We tentatively concluded that there was not enough evidence to justify the conduct of separate genetic improvement programs for cage and pond environments in Tilapia.

REFERENCES