Twenty-five traditional land-races, gynogenetic lines and two-line hybrids of common carp, *Cyprinus carpio*, have been collected in Hungary. Nearly 600 hybrids could be produced from these. Performance tests for such a high number of hybrid would be impractical. Distributions of the body weights of fish in simple crosses (1x1) and in a group created by using sperm and eggs of all available parents (kxk) were compared to predict the efficiency of a large scale hybridization program. According to our model, the distribution in the (kxk) group can be computed as the sum of the distributions in the (1x1) groups. We estimated the probabilities of finding hybrids, that perform 5, 10, 20, 30, ...etc. % better than the average, when randomly choosing 1, 2, ..., 20 crossings. The probability for genetic improvement of carp through hybridization is high.

**INTRODUCTION**

More than 20 years ago collection of domestic and foreign land races of common carp had been started in Hungary (Bakos, 1965). This collection has been significantly expanded by production of gynogenetic and semigynogenetic lines (Nagy et al. 1978, 1984) and now consists of about 25 land-races, gynogenetic lines, semigynogenetic lines and hybrids. Mass selection for growth in these common carp has been ineffective (Bercsenyi and Bakos, 1983). Moav and Wohlfarth (1976) obtained similar results, however significant heterosis can be expected in some traditional and gynogenetic common carp hybrids (Nagy et al. 1984). Hybridization appears to be the most promising breeding program for common carp.

More than 600 hybrids could be produced from the 25 genetic groups available at the Fish Culture Research Institute, Hungary. Although impossible to evaluate all possible hybrids, rough estimates of the expected success were necessary. An experiment designed to estimate the probabilities of the success of hybridization, utilizing two-thirds of the available parental groups was carried out.

**MATERIALS AND METHODS**

**Experimental populations.**

Seven female and 14 male breeders were chosen from the carp race collection, each of them representing a genetic group. Breeders were artificially spawned to produce 6 progeny groups. One group (kxk) type, was produced by mixing sperm and eggs of all breeders of equal rates. The other 5 groups were produced by using eggs and sperm of only one female and one male.
Conditions of raising

After hatching fry were stocked into aquaria, with flowing water. The initial number of fish in each aquarium was 200. The groups were grown in 2-5 replicate aquaria and each group had a reserve aquarium. In the case of death, individual experimental fish were replaced by a similar sized fish from the group's reserve. As the fish grew, the number per aquarium was reduced. At age of 60 days fish were individually measured, thereafter marked according to their genetic group, but not to their replicate. From that time all fish were grown in a common nursing tank. At age of 105 days individual body weights were determined again.

Fish were fed ad libitum with brine shrimp, tubifex and crumbled fish feed.

Model for calculations

The distribution of distributions. The $(1 \times 1)$ group is the sum of the all possible $(1 \times l)$ groups. The theoretical number of these $(1 \times l)$ groups would be $98$, $70 \times 140 = 98$. The distributions of the body weights in the $(1 \times 1)$ group could be reproduced by the sum of the distributions of all $(1 \times l)$ groups. The means of the $(1 \times l)$ groups are distributed around the mean of the $(1 \times 1)$ group. This is the distribution of distributions $DiDi$(Fig.1).

If the $(1 \times 1)$ distribution is normal, and the $(1 \times l)$ distributions are normal distributions, the $DiDi$ must be normal distribution too. If the mean and the variance of the $(1 \times 1)$ distribution, and the average of the variances of the $(1 \times l)$ distributions are known, the parameters of the $DiDi$ can be calculated. The computation is based on the supposition, that locating the $(1 \times l)$ distributions according to the correct $DiDi$, their sum and the original $(1 \times 1)$ distribution give a minimum Chi2 value in their Chi2 test.

Probabilities. The probability that the mean of a randomly chosen $(1 \times l)$ cross is over a $xl$ limit is:

$$P = \frac{\int_{X_1}^{+\infty} f(x)dx}{\int_{-\infty}^{+\infty} f(x)dx}$$

where $P$=the probability, $f(x)$= the function of the $DiDi$ distribution

When randomly choosing more than one cross, the probability to find at least one cross with its mean over the limit is given by:

$$R = 1 - \frac{\binom{z}{k}}{\binom{n}{k}}$$

where $R$= the probability, $z$= the number of crosses with their means below the limit, $n$= the number of all possible crosses (here 98), and $k$= the number of cross chosen.

Data adjustment. Due to competition of the fish, the body weights showed a log-normal distribution (Nakamura and Kasahara 1961, Chevassus 1982). Computations were simplified by ln transformation of the rough data.
Because of individual differences between aquaria, mean body weights and variances varied within replicates. There was very high correlation between means and variances, but there was no significant correlation between means and C.V.%-s even at $P=10\%$. Therefore when computing parameters of the different genetic groups, individual weights were adjusted as follows:

$$x'_{ijk} = \frac{M_i - m_{ij}}{m_{ij}} x_{ijk}$$

(c)

where, $x'_{ijk}$ = the adjusted weight, $M_i$ = the mean weight of the $i$-th genetic group $m_{ij}$ = the mean weight of the $j$-th replicate in the $i$-th group, and $x_{ijk}$ = the measured weight of the $k$-th individual in the $j$-th replicate of the $i$-th group.

**RESULTS**

The growth of the fish was similar to the growth of fingerling at an average Hungarian fishfarm. The means and C.V.%-s of the body weights within replicate at age 60 days, and within genetic group are given in Table 1 and 2.

Table 1. The mean weights (gramm, up) and C.V.%-s (down) of fish at age 60 days

<table>
<thead>
<tr>
<th>Genetic groups</th>
<th>(x$x$)</th>
<th>(lx1)A</th>
<th>(lx1)B</th>
<th>(lx1)C</th>
<th>(lx1)D</th>
<th>(lx1)E</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>10.03</td>
<td>9.14</td>
<td>8.50</td>
<td>10.88</td>
<td>7.66</td>
<td>9.06</td>
</tr>
<tr>
<td></td>
<td>47.70</td>
<td>46.19</td>
<td>56.33</td>
<td>42.58</td>
<td>37.44</td>
<td>32.29</td>
</tr>
<tr>
<td>B</td>
<td>10.14</td>
<td>8.95</td>
<td>8.61</td>
<td>10.04</td>
<td>7.98</td>
<td>9.12</td>
</tr>
<tr>
<td></td>
<td>52.95</td>
<td>46.31</td>
<td>48.95</td>
<td>43.65</td>
<td>46.30</td>
<td>39.14</td>
</tr>
<tr>
<td>C</td>
<td>10.00</td>
<td>7.99</td>
<td>6.93</td>
<td>8.97</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>47.16</td>
<td>45.21</td>
<td>46.30</td>
<td>37.12</td>
<td></td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>8.39</td>
<td>8.80</td>
<td></td>
<td>8.69</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>55.28</td>
<td>40.01</td>
<td></td>
<td>41.97</td>
<td></td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>9.77</td>
<td>7.09</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>50.52</td>
<td>37.21</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

(group means)

|                |       |        |        |        |        |        |
|                | 9.69  | 8.40   | 8.01   | 9.65   | 7.82   | 9.09   |
|                | 50.72 | 42.99  | 50.53  | 41.33  | 41.87  | 35.72  |

Table 2. The mean weights (gramm, up) and C.V.% (down) of fish at age 105 days.

<table>
<thead>
<tr>
<th></th>
<th>(x$x$)</th>
<th>(lx1)A</th>
<th>(lx1)B</th>
<th>(lx1)C</th>
<th>(lx1)D</th>
<th>(lx1)E</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>22.26</td>
<td>17.69</td>
<td>15.82</td>
<td>26.34</td>
<td>16.43</td>
<td>22.26</td>
</tr>
<tr>
<td></td>
<td>62.79</td>
<td>50.57</td>
<td>64.60</td>
<td>52.97</td>
<td>49.28</td>
<td>40.36</td>
</tr>
</tbody>
</table>
When using ln transformed data, the functions of the DiDi distributions were as follows:

\[ f(x) = \frac{1}{0.281\sqrt{2\pi}} e^{-\frac{(x-2.158)^2}{2\cdot0.281^2}} \text{ at age 60 days} \]

\[ f(x) = \frac{1}{0.376\sqrt{2\pi}} e^{-\frac{(x-2.94)^2}{2\cdot0.376^2}} \text{ at age 105 days} \]

According to the scheme described in the Materials and methods, using the above equations we calculated the probabilities of randomly choosing a cross which has its mean over a given limit. The probabilities to different limits at age 60 and 105 days are given in Table 3 and Table 4.

**Table 3. Probabilities for choosing 1 cross with its mean over a limit (age 60 days)**

<table>
<thead>
<tr>
<th>Limit (g)</th>
<th>9.69</th>
<th>10.12</th>
<th>10.57</th>
<th>11.51</th>
<th>12.56</th>
<th>13.69</th>
<th>14.92</th>
<th>15.58</th>
<th>16.27</th>
</tr>
</thead>
<tbody>
<tr>
<td>% difference from the (x) mean</td>
<td>0.00</td>
<td>4.41</td>
<td>9.01</td>
<td>18.84</td>
<td>29.56</td>
<td>41.25</td>
<td>53.98</td>
<td>60.07</td>
<td>67.87</td>
</tr>
<tr>
<td>Probability</td>
<td>0.50</td>
<td>0.44</td>
<td>0.38</td>
<td>0.27</td>
<td>0.18</td>
<td>0.11</td>
<td>0.07</td>
<td>0.05</td>
<td>0.04</td>
</tr>
</tbody>
</table>

**Table 4. Probabilities for choosing 1 cross with its mean over a limit (age 105 d)**

<table>
<thead>
<tr>
<th>Limit (g)</th>
<th>22.2</th>
<th>23.2</th>
<th>24.41</th>
<th>26.62</th>
<th>28.84</th>
<th>31.06</th>
<th>32.29</th>
<th>35.50</th>
<th>37.72</th>
</tr>
</thead>
<tbody>
<tr>
<td>% difference from the (xx) mean</td>
<td>0.00</td>
<td>5.0</td>
<td>10.0</td>
<td>20.0</td>
<td>30.0</td>
<td>40.0</td>
<td>50.0</td>
<td>60.0</td>
<td>70.0</td>
</tr>
<tr>
<td>Probability</td>
<td>0.50</td>
<td>0.45</td>
<td>0.40</td>
<td>0.31</td>
<td>0.24</td>
<td>0.18</td>
<td>0.14</td>
<td>0.10</td>
<td>0.08</td>
</tr>
</tbody>
</table>

With the help of the probabilities in Tables 3 and 4, we calculated the \( z \) values for the (b) equation. The probabilities to find at least one cross with its mean over the limit, when randomly choosing more than one cross are shown on Figures 2 and 3.

**DISCUSSION**

At present circumstances, there is opportunity to test 5-6 carp hybrids yearly at the Fish Culture Research Institute, Hungary. In order to estimate
Figure 1.
Location of the (zxz), (lxl) and DiDi distributions

Figure 2.
Probabilities to find at least one cross with its mean over the limit, when choosing 1, 5, 10, 20 crosses. Age 60 days.
P= probability
l= limit, % over the (zxz) mean

Figure 3.
Probabilities to find at least one cross with its mean over the limit, when choosing 1, 5, 10, 20 crosses. Age 105 days
P= probability
l= limit, % over the (zxz) mean
the success of a large scale carp hybridization program, a model was set up. Six different genetic group of common carp were raised up to 20-25 g size. Data of these fish were used for basic parameters in our model.

Although the fish were raised in aquariums, and the experiment did not consider the whole production cycle, the results indicate, that a large-scale (30-40 hybrid) hybridization program of the common carp would be successful. For example by testing 20 hybrids, there is over 90% chance to find at least one performing 50% over the average. This hybrid would 25-30 percent surpass the presently best ones.

The model, with minor modifications would be suitable for prediction of the potential success of hybridization programs for other fish species.

ACKNOWLEDGEMENT

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