GENETIC CORRELATIONS BETWEEN TEST STATION AND ON-FARM PERFORMANCE FOR GROWTH RATE AND BACKFAT IN PIGS

T. A. Van Diepen and B. W. Kennedy
University of Guelph, Guelph, Ontario, Canada N1G 2W1

ABSTRACT

Record of performance data taken on Yorkshire pigs on-farm in 123 breeder herds and at a central test station were used to estimate genetic correlations between measures of backfat depth and days to 90 kg on boars at the test station and boars and gilts on-farm. The data involved records on 3,513 station-tested boars, 13,760 farm-tested boars and 28,203 farm-tested gilts from 838, 2,098 and 2,339 sires, respectively. For backfat depth, estimates of genetic correlations were .85 for test station and on-farm boars and 1.04 for test station boars and on-farm gilts. Estimates of genetic correlations between test station and on-farm measures of days to 90 kg were .80 for boars and .74 for boars and gilts. Based on these results, selection of boars on the basis of test station performance for backfat and growth rate would be expected to result in genetic improvement on-farm in both sexes under North American testing and management conditions.

(Key Words: Genetic Correlation, Station Tests, Farm Tests, Backfat, Growth Rate, Pigs.)

Introduction

The use of central stations for performance testing potential breeding animals from different herds in a uniform environment is common. However, test station environments may differ from farm environments with respect to type of housing, number of pigs per pen, floor space per pig, level of nutrition, health programs and other management practices. Genotype × environment interactions have been found to be important in pig breeding (Webb and Curran, 1986). European work, recently reviewed by Webb and Curran (1986) and Merks (1988), indicates that genetic correlations between the same or similar traits measured at test stations and on the farm generally are low, particularly for growth and feed efficiency traits. If this is the case, selection on test station performance for genetic improvement under farm conditions may be ineffective.

There are differences between Europe and North America in the management and environments provided to pigs both at the test station and on the farm. For example, in North America pigs usually have ad libitum access to feed, whereas in Europe restricted or scale feeding frequently is practiced. It would be of use to know whether genetic correlations between test station and on-farm performance under North American testing and management conditions are similar to those found in Europe. This study measured genetic correlation for growth rate and backfat depth between boars tested at a central station and boars and gilts tested on-farm.
Materials and Methods

Source of Data

Record of performance data on Yorkshire pigs in Ontario, Canada taken on-farm in 123 breeder herds and at the New Hamburg test station between 1977 and 1985 were used. Eighty-seven of the herds had pigs tested at the central station. Traits were days of age and backfat thickness adjusted to 90 kg live weight. Backfat thickness was measured ultrasonically and was the average of probes taken above the outside curve of the last rib and anterior to the aitch bone on each side of the pig approximately 5 cm off mid-line.

Only boars were tested at the station. The test station consisted of four wings, one of which was filled each month. Each wing held up to 128 boars of various breeds, about 40% of which were Yorkshire. Only Yorkshire data were used in this study. Boars were delivered to the test station in littermate pairs between 20 and 29 kg live weight. After an adjustment period, the boars were weighed on test at an average weight of 29 kg and littermates were housed together in pens of two until completion of the test at approximately 90 kg (minimum of 75 kg and maximum of 105 kg). During the test period all boars had ad libitum access to a corn-based ration of at least 16% crude protein.

Both boars and gilts were tested on-farm. On-farm management and environmental conditions were more variable, but all herds had intensive management with pigs raised in indoor facilities. All herds were on a herd health program, but herds differed in health status (see Kennedy and Quinton [1987] for additional details). The usual feeding practice was to provide test pigs with ad libitum access to a corn-based ration of at least 16% crude protein. However, pigs tested on-farm usually were group-housed. Numbers of pigs per pen and pen sizes varied from farm to farm. All pigs were weighed off-test and probed for backfat thickness ultrasonically by provincial government technicians. Probe sites and end-of-test weights on the farm were the same as at the test station.

The data were edited to restrict the data to one litter per dam. The first available litter was used. This provided a hierarchical structure to the data with dams (litters) nested within sires. Further, if pigs of a litter were split between station test and on-farm test, the on-farm data were removed. This created on-farm and test station data sets that were independent with respect to dams but connected with respect to sires. Three data sets were created for analysis: test station boars, on-farm boars and on-farm gilts. Within each data set, further edits were made to restrict the data such that at least two pigs were represented in each herd-year-season for test station data and at least six pigs per herd-year-season for both the boar and gilt on-farm data sets. Seasons were 6-mo periods.

After editing, the test station data contained records on 3,513 boars and the on-farm data sets contained records on 13,760 boars and 28,203 gilts. There were 838 sires represented by progeny in the test station data. Of these, 807 and 809 had male and female progeny on-farm. Further description of the data sets with respect to numbers of sires and dams and means and standard deviations of traits is given in Table 1.

Model

The data were analyzed according to the following model

$$ y_{ijklm} = \mu + h_i + g_j + s_{jk} + d_{ijkl} + e_{ijklm} $$

where $y_{ijklm}$ is a measure of days to 90 kg or backfat depth taken on-farm or at the test station on the $ijklm$th pig, $\mu$ is the population mean, $h_i$ is the fixed effect of the $i$th herd-year-season of birth, $g_j$ is the fixed effect of the $j$th year of birth of sire, $s_{jk}$ is the random effect of the $jk$th sire ($\sim N(0, \sigma^2_s)$), $d_{ijkl}$ is the random effect of the $ijkl$th dam (or litter) ($\sim N(0, \sigma^2_d)$) and $e_{ijklm}$ is the random error ($\sim N(0, \sigma^2_0)$). Season classes were January to June and July to December. The year of birth of sire effect was included to account for genetic trend. Some herd-year-season of birth, year of birth of sire and sire effects were common to both test station and on-farm data sets, but dam and error effects were independent.

Prior to analysis according to (1), test station data were corrected for the joint effects of month and year of entry into the test station (contemporary group) which were estimated by substituting them in the model instead of herd-year-season of birth.
**TEST STATION AND ON-FARM PERFORMANCE**

**TABLE 1. DESCRIPTION OF TEST STATION AND ON-FARM DATA**

<table>
<thead>
<tr>
<th>Item</th>
<th>Test station</th>
<th>On-farm boars</th>
<th>On-farm gilts</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of pigs</td>
<td>3,513</td>
<td>13,760</td>
<td>28,203</td>
</tr>
<tr>
<td>No. of sires</td>
<td>838</td>
<td>2,098</td>
<td>2,339</td>
</tr>
<tr>
<td>No. of dams (litters)</td>
<td>1,868</td>
<td>6,985</td>
<td>10,694</td>
</tr>
<tr>
<td>Days to 90 kg Mean</td>
<td>155.0</td>
<td>159.6</td>
<td>167.2</td>
</tr>
<tr>
<td>Days to 90 kg SD</td>
<td>10.2</td>
<td>16.4</td>
<td>16.4</td>
</tr>
<tr>
<td>Backfat, mm Mean</td>
<td>12.38</td>
<td>13.20</td>
<td>14.47</td>
</tr>
<tr>
<td>Backfat, mm SD</td>
<td>2.20</td>
<td>2.57</td>
<td>2.75</td>
</tr>
</tbody>
</table>

**Statistical Methodology**

Variances and covariances were obtained using a multiple trait extension of Henderson's approximate MIVQUE (Henderson, 1984). In matrix notation, let the model for the i\textsuperscript{th} trait be

\[ y_i = X_i b_i + Z_{s1} u_{s1} + Z_{d1} u_{d1} + e_i, \]

where \( b_i \) represents the fixed effects, \( u_{s1} \) the sire effects, \( u_{d1} \) the dam effects, \( e_i \) the error and \( X_i, Z_{s1} \) and \( Z_{d1} \) are the incidence matrices. Now let \( y_1 \) represent a measure taken at the test station and \( y_2 \) represent a measure taken on-farm. Then

\[
\text{Var}
\begin{bmatrix}
  y_1 \\
  y_2
\end{bmatrix}
= \begin{bmatrix}
  Z_{s1} Z_{s1} \sigma_{s1}^2 & Z_{s1} Z_{s2} \sigma_{s12} \\
  Z_{s2} Z_{s1} \sigma_{s12} & Z_{s2} Z_{s2} \sigma_{s2}^2
\end{bmatrix}
+ \begin{bmatrix}
  Z_{d1} Z_{d1} \sigma_{d1}^2 & 0 \\
  0 & Z_{d2} Z_{d2} \sigma_{d2}^2
\end{bmatrix}
\begin{bmatrix}
  \mathbf{I} \sigma_{e1}^2 \\
  \mathbf{I} \sigma_{e2}^2
\end{bmatrix}
\]

Note that under the model for this data structure

\[ \sigma_{d12} = \sigma_{e12} = 0. \]

After absorption of the fixed effects the mixed model equations are

\[
\begin{bmatrix}
  Z'_{s1} M_1 Z_{s1} + \lambda_1 & Z'_{s1} M_1 Z_{d1} \\
  \lambda_{12} & Z'_{s2} M_2 Z_{s2} + \lambda_2 \\
  \lambda_{21} & Z'_{s2} M_2 Z_{s2}
\end{bmatrix}
\begin{bmatrix}
  \hat{u}_{s1} \\
  \hat{u}_{s2} \\
  \hat{u}_{d1} \\
  \hat{u}_{d2}
\end{bmatrix}
= \begin{bmatrix}
  Z'_{s1} M_{1} y_1 \\
  Z'_{s2} M_{2} y_2
\end{bmatrix}
\]
where $M_1 = I - X_1(X_1'X_1)^{-1}X_1'$,
$M_2 = I - X_2(X_2'X_2)^{-1}X_2'$

with

$\lambda_1 = \frac{\sigma^2_{e_1}}{\sigma^2_{s_1}}, \quad \lambda_2 = \frac{\sigma^2_{e_2}}{\sigma^2_{s_2}}, \quad \lambda_{12} = \frac{\sigma^2_{e_1}}{\sigma^2_{s_{12}}}, \quad \lambda_{21} = \frac{\sigma^2_{e_2}}{\sigma^2_{s_{12}}},$

$\gamma_1 = \frac{\sigma^2_{e_1}}{\sigma^2_{d_1}}$ and $\gamma_2 = \frac{\sigma^2_{e_2}}{\sigma^2_{d_2}}$.

Let $D_{s_i} = \text{diag.} (Z_{s_i}'M_{s_i}Z_{s_i} + I_{\lambda_i})$
and $D_{d_i} = \text{diag.} (Z_{d_i}'M_{d_i}Z_{d_i} + I_{\gamma_i})$

Approximate solutions for the random effects are obtained as

$$\theta_{s_i} = D_{s_i}^{-1}Z_{s_i}'M_{s_i}y_i$$

and

$$\theta_{d_i} = D_{d_i}^{-1}Z_{d_i}'M_{d_i}y_i.$$

Then $\sigma^2_{s_1}, \sigma^2_{s_2}, \sigma^2_{d_1}, \sigma^2_{d_2}, \sigma^2_{e_1}, \sigma^2_{e_2}$ can be solved

$$E(\theta_{s_1}' \theta_{s_2}) = \text{tr}(D_{s_1}^{-1}D_{s_2}^{-1}Z_{s_1}'M_{s_1}Z_{s_2}Z_{s_1}'M_{s_1}Z_{s_2} \sigma_{s_{12}})$$

for in the usual way for single trait estimation by equating sums of squares of random effects solutions to their expectations. Computational details for this model are in Johansson and Kennedy (1983). Twenty-five cycles of iteration were performed for each trait. Convergence was obtained for all analyses.

The sire covariance between traits 1 and 2 can then be estimated relatively simply from

$$E(\theta_{s_1}' \theta_{s_2}) = \text{tr}(D_{s_1}^{-1}D_{s_2}^{-1}Z_{s_1}'M_{s_1}Z_{s_2}Z_{s_1}'M_{s_1}Z_{s_2} \sigma_{s_{12}})$$

### TABLE 2. ESTIMATES OF SIRE, DAM (LITTER) AND ERROR VARIANCES AND HERITABILITIES ($h^2$) AND ENVIRONMENTAL CORRELATIONS ($c^2$) OF DAYS TO 90 KG AND BACKFAT FOR TEST STATION AND ON-FARM DATA

<table>
<thead>
<tr>
<th>Variance</th>
<th>Test station boars</th>
<th>On-farm boars</th>
<th>On-farm gilts</th>
</tr>
</thead>
<tbody>
<tr>
<td>Days to 90 kg</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sire</td>
<td>4.45</td>
<td>6.22</td>
<td>9.46</td>
</tr>
<tr>
<td>Dam (litter)</td>
<td>16.78</td>
<td>66.93</td>
<td>69.28</td>
</tr>
<tr>
<td>Error</td>
<td>58.56</td>
<td>61.01</td>
<td>73.43</td>
</tr>
<tr>
<td>$h^2$</td>
<td>.22</td>
<td>.19</td>
<td>.25</td>
</tr>
<tr>
<td>$c^2$</td>
<td>.15</td>
<td>.45</td>
<td>.39</td>
</tr>
<tr>
<td>Backfat, mm</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sire</td>
<td>.175</td>
<td>.561</td>
<td>.575</td>
</tr>
<tr>
<td>Dam (litter)</td>
<td>.886</td>
<td>1.091</td>
<td>1.293</td>
</tr>
<tr>
<td>Error</td>
<td>1.656</td>
<td>2.691</td>
<td>3.394</td>
</tr>
<tr>
<td>$h^2$</td>
<td>.26</td>
<td>.52</td>
<td>.44</td>
</tr>
<tr>
<td>$c^2$</td>
<td>.26</td>
<td>.12</td>
<td>.14</td>
</tr>
</tbody>
</table>

### TABLE 3. ESTIMATES OF GENETIC CORRELATIONS BETWEEN TEST STATION AND ON-FARM MEASURES OF DAYS TO 90 KG AND BACKFAT

<table>
<thead>
<tr>
<th>Test station boars</th>
<th>On-farm days to 90 kg</th>
<th>On-farm backfat</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Boars</td>
<td>Gilts</td>
</tr>
<tr>
<td>Days to 90 kg</td>
<td>.80</td>
<td>.74</td>
</tr>
<tr>
<td>Backfat</td>
<td>.03</td>
<td>.09</td>
</tr>
</tbody>
</table>
and equating the computed value of $\hat{\theta}_{s_1}^{\prime} S_{s_1} \hat{\theta}_{s_1}$ to its expectation.

Paternal half-sib heritabilities were estimated as

$$h^2 = 4\sigma^2_{s_i} \left( \sigma^2_{s_i} + \sigma^2_{d_i} + \sigma^2_{e_i} \right)$$

and environmental correlations were estimated as

$$c^2 = (\sigma^2_{d_i} - \sigma^2_{s_i})/(\sigma^2_{s_i} + \sigma^2_{d_i} + \sigma^2_{e_i})$$.

The environmental correlation estimate assumes an additive genetic model. Dominance effects, if present, would be reflected in the $c^2$ term.

The genetic correlation between traits 1 and 2 was estimated as

$$r_{s_12} = \sigma_{s_12} / \sqrt{\sigma^2_{s_1} \sigma^2_{s_2}}$$

Pairwise estimates of genetic correlations between days to 90 kg and backfat measured on boars at the test station vs days to 90 kg and backfat measured on boars and gilts on-farm were obtained.

Results and Discussion

Estimates of sire, dam and error variances and heritabilities and environmental correlations are given in Table 2. Variances of test station measures all were lower than on-farm measures, presumably because of the more controlled environmental conditions at the test station.

Heritabilities for days to 90 kg were similar at the test station and on-farm and were similar for both gilts and boars on-farm. The estimates, which ranged from .19 to .25, were slightly lower than previous estimates obtained from similar data (Kennedy et al., 1985). For backfat, heritability at the test station was lower than on-farm. This was not due to selection of sires of test station boars. In this population, sires of test station boars were equal in estimated breeding value for backfat to sires of farm-tested boars and gilts (unpublished data). Also, genetic variability, as computed from estimated breeding values and accuracy of evaluation, was equal among sires of test station boars and sires of farm-tested boars and gilts. The fact that there was considerably less phenotypic variability for backfat at the test station than on-farm may have contributed to the lower heritability at the test station. Sampling error also may have contributed to the difference. The test station estimate was based on a relatively small number of observations. On-farm heritability estimates for backfat, which were .44 for gilts and .52 for boars, were similar to previous estimates obtained from similar data (Kennedy et al., 1985).

Dam or litter variability for days to 90 kg was very large on-farm but relatively small at the test station. The environmental correlation ($c^2$) at the test station was .15, compared to $c^2$ values of .39 to .45 on-farm. Although littermate boars were penned together at the test station, that did not contribute greatly to similarity between littermates for days to 90 kg. For on-farm days to 90 kg, $c^2$ terms were similar to those found previously (Kennedy et al., 1985) and were similar for boars and gilts. In the analysis of the on-farm data, contemporary effects were 6-mo periods in the same herd. Some of the variability over time within the 6-mo period would be reflected in the litter variances and hence in the $c^2$ values. In contrast, for the test station data, contemporary groups were more narrowly defined as all boars entering a single wing of the station over a short period of time.

For backfat, however, $c^2$ values were larger at the test station than on-farm. At the test station, littermates usually were probed for backfat on the same day; this was not necessarily the case for on-farm probes. However, the estimate of the sire variance for backfat at the test station was low, and an underestimate of the sire variance would be associated with an overestimate of the dam variance, because the two estimates are negatively correlated. This would result in an overestimate of the $c^2$ term.

Estimates of genetic correlations between test station and on-farm measures of days to 90 kg and backfat are given in Table 3. Estimates of genetic correlations between days to 90 kg at the test station and on-farm were .80 for boars and .74 for gilts. These values are considerably higher than most estimates from European data. In Sweden, Staal (1977) found a genetic correlation of .45 between
daily gain from birth of gilts on-farm and daily gain of boars at the test station. Roberts and Curran (1981), using British data, found low genetic correlations between on-farm and test station measures of weight for age of -.18 to .16, depending on sex. Recently, Merks (1988) reported genetic correlations of .42 to .57 between test station and on-farm measures of daily gain in data from the Netherlands.

Webb and Curran (1986) attributed these low correlations to differences in selection objectives, feeding level and number of pigs per pen; they expressed concern that genetic improvements for growth rate obtained in stations may not be expressed on farms. The results from this study using Canadian data are much more comforting. Although genetic correlations between on-farm and test station measures of growth were less than unity, they were high. In these data, feeds and feeding programs on-farm and at the test station were largely similar, but housing conditions varied considerably.

Differences in statistical methodology used also may have contributed to differences between these results and those of the European studies. The underlying principle behind this study and the European work (Roberts and Curran, 1981; Merks, 1988) was similar and was based on computed correlations or cross-products between sire progeny test evaluations on-farm and at the test station. The genetic correlation then was estimated from the sire progeny test correlation by adjusting it according to its expectation with respect to the true genetic correlation or genetic covariance. The European studies, however, computed these expectations from approximations of accuracy of the progeny test evaluation using selection index principles that ignored the reduction in accuracy from estimation of the fixed effects (contemporary group means). Accuracy of the sire progeny test evaluation might have been overestimated and the effect of this on the resulting genetic correlation estimate would be to bias it downward. This study computed the expectation of the cross-products of sire progeny test evaluations exactly [2] and accounted for the contribution from estimation of the fixed effects to the expectation.

Estimates of genetic correlations between test station and on-farm measures for backfat were .85 for boars and 1.04 for gilts and were higher than those for days to 90 kg. European studies also have found on-farm and test station genetic correlations for backfat to be higher than for growth rate, but not so high as our estimates (Standal, 1977; Roberts and Curran, 1981; Merks, 1988). In our data backfat measured at the test station is essentially the same trait genetically as backfat measured on-farm, although the lower estimated heritability for backfat at the test station (Table 2) is of concern. Genetic correlations between days to 90 kg and backfat were close to zero (.0 to .09) and differences between estimates were small.

For both traits, correlations between boars at the test station and boars on-farm were not greatly different from correlations between boars at the test station and gilts on-farm. This is consistent with the European work (Merks, 1988) and indicates that selection in one sex will result in similar genetic improvement of progeny regardless of sex.

Conclusions

In this study genetic correlations between two factors (d to 90 kg and backfat at 90 kg) taken at the test station and on-farm were high; there was no evidence of large interactions between genotype and testing environment. Also, genetic correlations between boars were similar to those between boars and gilts. Therefore, selection of boars on the basis of test station performance for growth rate and backfat would be expected to result in genetic improvement on-farm in both sexes under North American testing and production conditions.

Literature Cited


