Genetic correlations between reproduction and production traits in swine

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ABSTRACT: Genetic correlations between reproduction and production traits were estimated in swine. Reproduction traits investigated were age at first service (AFS), number of live-born piglets in the first litter (NBA1), interval from weaning to first service after first litter (WTS1), number of live-born piglets in the second litter (NBA2), and interval from weaning to first service after the second litter (WTS2). Females generating the data were Norwegian Landrace born in nucleus herds between 1990 and 2000, and the number of records ranged from 13,792 to 56,932. Genetic correlations were estimated among the main production traits in the breeding goal: adjusted age at 100 kg live weight (A100), percentage of lean meat content (LMC), individual feed consumption from 25 to 100 kg (FC), and bacon side quality (BSQ). Average adjusted backfat thickness (BF) was included as a production trait. The A100 and BF traits were recorded on gilts on-farm with 190,454 records, whereas LMC, BSQ, and FC were recorded on-station with the number of records ranging from 12,487 to 12,992. Analyses were carried out with a multivariate animal model using average information restricted maximum likelihood procedures by first running each reproduction trait with A100 and BF, followed by each reproduction trait with LMC, BSQ, and FC. Average heritabilities for reproduction traits were as follows: AFS (0.38), NBA1 (0.11), WTS1 (0.06), NBA2 (0.12), and WTS2 (0.03); and for production traits: A100 (0.30), BF (0.44), FC (0.22), LMC (0.58), and BSQ (0.23). The highest genetic correlation was estimated between A100 and AFS (rg = 0.68), also resulting in a positive genetic correlation between FC and AFS. Growth (A100) was negatively (i.e., unfavorably) genetically correlated to NBA1 and NBA2 (rg = 0.60 and rg = 0.42 respectively), and so the genetic correlation to FC also became unfavorable (rg = 0.23 and rg = 0.20). Single-trait selection for enhanced LMC would also affect NBA1 and NBA2 unfavorably (rg = −0.12 and rg = −0.24). Correlations between BF at 100 kg live weight and reproduction traits were close to zero; however, a low genetic correlation between BF and WTS1 was obtained (rg = −0.12), indicating that selection toward reduced BF at 100 kg live weight may have an unfavorable impact on WTS1.

Key Words: Genetic Parameters, Heritability, Litter Traits, Pigs, Production, Reproduction

Introduction

The Norwegian Landrace (NL) has developed into a lean and efficient breed over the last decade. A large body of literature suggests zero covariance between production and reproduction traits in swine (Rydhmer, 1993; Ducos and Bidanel, 1996; Rydhmer, 2000). In NL, selection has been based on a total merit index with multivariate BLUP-EBV for production traits and a separate repeatability model for litter size. Phenotypic trends in NL reflect the predicted genetic progress, with the exception of growth traits, both on-farm and on-test (Norsvin, 2002), questioning the assumption of zero covariances between the two blocks of information. Dunnington (1990) argued, based on experience from poultry, that if genetic changes are too rapid, the population might not be able to adapt to the changes imposed by selection, creating unfavorable genetic correlations between fitness traits and production traits. In addition, increased leanness induces deterioration in reproductive performance due to deterioration in the body’s ability to mobilize lipid (Johansson and Kennedy, 1983; Kersey De Nise et al., 1983). As NL is regarded as a very lean breed, possible antagonistic genetic correlations due to low fat resources could be expected.

Several studies regarding genetic correlations between production and reproduction traits were based on experimental data or selected field data. Selection bias could be avoided by including all selected traits in the genetic analyses (Henderson, 1975; Gianola et al., 1989; Meyer, 1990). This study used the entire breeding popu-
lation of NL from 1990 to 2000, including data on the most important traits in the breeding goal. The objectives were to estimate genetic correlations between production and reproduction traits, and to draw inferences on how selection for efficiency, growth, and leanness would impact sow reproduction.

Materials and Methods

In NL, pure breeding is carried out in nucleus herds. Herd managers record on-farm events such as inseminations and farrowings through the national recording scheme. Technicians from the Norsvin breed association perform on-farm tests on all live females, and the nucleus herds sell boars for boar tests, gilts to multiplying herds, and sibs of boars to one of two commercial market hog producers for sib testing (Vangen and Sehested, 1997). Multiplying herds also report on-farm events on their sows through the national recording scheme. The Norsvin breed association operates all these activities as well as the only boar stud in Norway. In this study, an average of 7,300 litters was born per year in nucleus and multiplying herds, 96% of them by AI. In 1990, the average number of litters born in nucleus and multiplying herds was 49 and 64, respectively, vs. 92 and 95 litters in 2000. In 2000, the breeding program included 59 nucleus herds and 100 multiplying herds.

Lean meat content and growth accounted for 23 and 20% of the annual genetic merit in the last part of the decade, respectively. Litter size accounted for 29% of the annual genetic merit, whereas feed consumption and bacon side quality accounted for 15 and 10%, respectively (our unpublished data).

Reproduction Traits

Data on purebred NL born between January 1990 and January 2000 were sampled from nucleus and multiplying herds recorded in the national recording scheme. The following traits were extracted: age at first service (AFS), number of live-born in first litter (NBA1), weaning to first service interval after first litter (WTS1), number of live-born in the second litter (NBA2), and weaning to first service interval after second litter (WTS2). Individual records were set to a missing value when not observed within intervals: 120 to 500 d for AFS; 1 to 50 d for WTS1 and WTS2; and 0 to 22 piglets for NBA1 and NBA2. Before statistical analysis, a logarithmic transformation was performed for intervals of 6 d and more for both WTS1 and WTS2, according to ten Napel et al. (1995), and used by Hanenberg et al. (2001):

$$
\frac{\ln(WTS)}{\ln(6) - \ln(5)} - \left(\frac{\ln(6)}{\ln(6) - \ln(5)} - 6\right)
$$

Descriptive statistics for reproduction traits are presented in Table 1.

### Table 1. Number of records, means, and SD of female reproduction traits as recorded in the national recording scheme for Norwegian Landrace born between 1990 and 2000

<table>
<thead>
<tr>
<th>Trait**</th>
<th>No.</th>
<th>Mean</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>AFS, d</td>
<td>56,932</td>
<td>219.65</td>
<td>31.59</td>
</tr>
<tr>
<td>NBA1</td>
<td>36,102</td>
<td>10.41</td>
<td>2.87</td>
</tr>
<tr>
<td>WTS1, d</td>
<td>25,168</td>
<td>8.42</td>
<td>7.95</td>
</tr>
<tr>
<td>NBA2</td>
<td>19,243</td>
<td>11.40</td>
<td>3.06</td>
</tr>
<tr>
<td>WTS2, d</td>
<td>13,793</td>
<td>7.00</td>
<td>6.56</td>
</tr>
</tbody>
</table>

*Age at first service (AFS), number of live-born first litter (NBA1), interval from weaning to first service after first litter (WTS1), number of live-born second litter (NBA2), and interval from weaning to first service after second litter (WTS2). Results for WTS1 and WTS2 are untransformed.

Production and Carcass Traits

The breed organization measured growth on females in nucleus herds as adjusted age at 100 kg of live weight (A100) using the following formula:

$$
A100 = \frac{\text{age}}{[(0.383) + (0.00617 \times \text{weight})]} 
$$

where age and weight were individually observed. The same females were measured for back fat thickness (BF), in mm, by ultrasound (Krautkramer USK7, Krautkramer NDT; Cologne, Germany) in four different locations: 2.5 cm in front of the last rib, immediately behind the shoulder blades, and the highest and lowest values measured by sliding the probe from loin to ham. All measurements were taken mid-dorsal along the length of the axis of the animals, and an average BF measure was calculated using the four measures before being adjusted to 100 kg live weight using the formula:

$$
BF = \frac{\text{average BF}}{[(0.432) + (0.00577 \times \text{weight})]} 
$$

Feed consumption (FC) was recorded from 25 to 100 kg of live weight on boars fed ad libitum, using feed intake recording equipment (Hunday Electronics Ltd., Newcastle, U.K.). The measured variable can also be defined as feed conversion rate because the gain interval was identical for all individuals. Lean meat content (LMC) was calculated by dissecting the animals from the sib test. Animals were slaughtered at one of two slaughterhouses, and the left part of each carcass was sent for complete dissection at the Norwegian Meat Cooperative’s research unit in Oslo. The LMC was calculated by taking into account the weight of each muscle group, the weight of the bones, the weight of the fat, and the amount of fat in the different muscle groups. In the same animals, bacon side quality (BSQ) was subjectively scored for a combination of meat and fat content ratio and distribution of fat content in the bacon on a scale from 1 to 5, with superior quality represented by
the smallest value. Descriptive statistics for production and carcass traits are presented in Table 2.

Methods

Initially, several fixed effects and covariates were examined for their significance (P < 0.05) in univariate models using ordinary least squares. Computations were performed using SAS Proc GLM (SAS Inst., Inc., Cary, NC). For each trait, the following fixed effects were tested: sex of the animal (female or castrate), herd in which the animal was born (105 levels), litter breed, which denoted purebred Landrace or Landrace ¥ Yorkshire litters, parity of the dam (1, 2, ≥3), double insemination (0, 1 if a new insemination occurred within 2 d after the first insemination), mating type (natural mating, professional- or owner-executed AI), and a herd-year-season effect for traits recorded on-farm (January to March, April to June, etc.). For AFS, NBA, and WTS, season referred to time of sow insemination, farrowing, and first service after weaning, respectively. For A100 and BF, both recorded in nucleus with 10 visits annually, season was month of visit. For traits recorded on-station (FC, LMC, and BSQ), station ¥ pen ¥ batch was used as the contemporary group. The minimum number of observations within level of contemporary groups was set to four. The effects included in the models for the different traits are presented in Table 3.

Ideally, a multiple-trait analysis would have been desirable to account for selection bias. However, due to large computational requirements, several analyses were run. First, traits recorded on-station (LMC, BSQ, and FC) were analyzed jointly with each reproduction trait in a four-variate animal model:

\[
y = \begin{bmatrix}
y_1 \\
y_2 \\
y_3 \\
y_4 
\end{bmatrix} = \begin{bmatrix}
X_1 & 0 & 0 & 0 \\
0 & X_2 & 0 & 0 \\
X_3 & 0 & X_4 & b_1 \\
0 & 0 & X_4 & b_2 
\end{bmatrix} b_1 + \begin{bmatrix}
X_1 & 0 & 0 & 0 \\
0 & X_2 & 0 & 0 \\
X_3 & 0 & X_4 & a_1 \\
0 & 0 & X_4 & a_2 
\end{bmatrix} a_1 + \begin{bmatrix}
X_1 & 0 & 0 & 0 \\
0 & X_2 & 0 & 0 \\
X_3 & 0 & X_4 & e_1 \\
0 & 0 & X_4 & e_2 
\end{bmatrix} e_1
\]

where \( y_1, b_1, a_1, \) and \( e_1 \) are vectors of observations, fixed effects, animal additive genetic effects, and residuals for trait \( i \), respectively. The variance–covariance matrices for the random additive genetic and residual effects were:

\[
 \text{var}[a] = G \otimes A, \quad \text{with } G = \begin{bmatrix}
\sigma^2_{a1} & \sigma_{a12} & \sigma_{a13} & \sigma_{a14} \\
\sigma_{a12} & \sigma^2_{a2} & \sigma_{a23} & \sigma_{a24} \\
\sigma_{a13} & \sigma_{a23} & \sigma^2_{a3} & \sigma_{a34} \\
\sigma_{a14} & \sigma_{a24} & \sigma_{a34} & \sigma^2_{a4} 
\end{bmatrix}
\]

and

\[
 \text{var}[e] = R \otimes I, \quad \text{with } R = \begin{bmatrix}
\sigma^2_{e1} & \sigma_{e12} & \sigma_{e13} & \sigma_{e14} \\
\sigma_{e12} & \sigma^2_{e2} & \sigma_{e23} & \sigma_{e24} \\
\sigma_{e13} & \sigma_{e23} & \sigma^2_{e3} & \sigma_{e34} \\
\sigma_{e14} & \sigma_{e24} & \sigma_{e34} & \sigma^2_{e4} 
\end{bmatrix}
\]

where \( A \) is the numerator relationship matrix among the animals, \( I \) is an identity matrix, \( \sigma^2_{ai} \) and \( \sigma^2_{ei} \) are direct additive genetic variance and residual variances for trait \( i \), and \( \sigma_{aij} \) and \( \sigma_{eij} \) are corresponding additive genetic and residual covariances between traits. The individual pedigree file used to create \( A \) was compiled using animals in the data set as the starting point, followed by tracing their relatives back at least five generations whenever possible. This file contained 227,525 animals, originating from 1,097 known sires and 32,476 known females.

For traits measured in different test systems, the residual covariances were set to zero. Secondly, trivariate analyses were carried out for production traits recorded on-farm (A100 and BF) and each reproduction trait (R), in turn, by using the following linear animal model:

\[
\begin{bmatrix}
y_{A100} \\
y_{BF} \\
y_R 
\end{bmatrix} = \begin{bmatrix}
X_{A100} & 0 & 0 \\
0 & X_{BF} & 0 \\
0 & 0 & X_{R}
\end{bmatrix} \begin{bmatrix}
b_{A100} \\
b_{BF} \\
b_R
\end{bmatrix} + \begin{bmatrix}
Z_{aA100} & 0 & 0 \\
0 & Z_{aBF} & 0 \\
0 & 0 & Z_{aR}
\end{bmatrix} \begin{bmatrix}
a_{A100} \\
a_{BF} \\
a_R
\end{bmatrix} + \begin{bmatrix}
Z_{eA100} & 0 & 0 \\
0 & Z_{eBF} & 0 \\
0 & 0 & Z_{eR}
\end{bmatrix} \begin{bmatrix}
e_{A100} \\
e_{BF} \\
e_R
\end{bmatrix}
\]

where \( y, X, b, Z, a, \) and \( e \) are as explained previously, and \( e \) denotes the common environmental effect of litter. The additional (co)variance structure added to this model compared with that given previously in Eq. [5] and [6] was:

\[
 \text{var}[e] = P \otimes I, \quad \text{with } P = \begin{bmatrix}
\sigma^2_{eA100} & \sigma_{eA100,BF} \\
\sigma_{eA100,BF} & \sigma^2_{eBF}
\end{bmatrix}
\]

where \( I \) was an identity matrix.

Estimates

(Co)variance estimation was carried out with the statistical package DMU (Madsen and Jensen, 2003) using the average information restricted maximum likelihood procedure. If an update exceeded the parameter space, a stepwise expectation maximization algorithm was used to maximize the restricted likelihood (Jensen et al., 1997). The convergence criterion for all runs was 10^{-6}. The SE of heritabilities and correlations were obtained by Taylor series approximations.
Table 2. Number of records, means, and SD of production and carcass traits as recorded for Norwegian Landrace born between 1990 and 2000

<table>
<thead>
<tr>
<th>Trait</th>
<th>Recorded</th>
<th>No.</th>
<th>Mean</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>A100, d</td>
<td>On-farm test, females</td>
<td>190,454</td>
<td>149.84</td>
<td>16.02</td>
</tr>
<tr>
<td>BF, mm</td>
<td>On-farm test, females</td>
<td>190,453</td>
<td>9.89</td>
<td>1.43</td>
</tr>
<tr>
<td>FC, kg</td>
<td>Boar test, males</td>
<td>12,992</td>
<td>157.14</td>
<td>13.42</td>
</tr>
<tr>
<td>LMC, %</td>
<td>Sib test, females and castrates</td>
<td>12,487</td>
<td>60.53</td>
<td>3.05</td>
</tr>
<tr>
<td>BSQ, pointsb</td>
<td>Sib test, females and castrates</td>
<td>12,589</td>
<td>2.71</td>
<td>0.88</td>
</tr>
</tbody>
</table>

aAdjusted age at 100 kg live weight (A100), average and adjusted back fat thickness (BF), feed consumption (FC), lean meat content (LMC), and bacon side quality (BSQ).

bSubjectively scored with a preferred value of 1 (range = 1 to 5).

Results

Variance Components and Heritabilities

Variance components and heritabilities are presented in Table 4 as average of all 10 analyses. For female reproduction traits, the heritability estimates were quite low, ranging from 0.03 to 0.10, with an exception for AFS (h² = 0.37). Heritability estimates for production traits ranged from 0.22 to 0.58, and were similar to those used by the breeding association in the actual period (H. Tajet and D. Olsen, personal communication). For A100 and BF, a substantial proportion of the total variation could be explained by the common environment of the litter in which the gilt was born, more so for A100.

Genetic Correlations

Estimated genetic correlations between reproduction traits and A100 and BF are given in Table 5. Several sow reproduction traits had moderate to high genetic correlations with some production traits. For example, using 1.96 × SE as an approximate criterion for significance (P < 0.05), A100 was significantly correlated to all reproduction traits here. The largest estimate was between A100 and AFS, suggesting that selection solely for increased growth would decrease age at first service. More surprisingly, the genetic correlation between A100 and NBA₁/NBA₂ was highly unfavorable (i.e., selection for reduced A100 would decrease litter size). However, A100 tended to have a moderately favorable genetic correlation with WTS₁ and WTS₂. Estimated genetic correlations between reproduction traits and traits recorded on-station (LMC, BSQ, and FC) are shown in Table 6. Again, using 1.96 × SE as an approximate criterion for significance (P < 0.05), FC showed an unfavorable genetic correlation with NBA₁ and NBA₂, but a favorable genetic correlation with AFS. There was a moderate to low unfavorable genetic correlation between LMC and NBA₂. A small unfavorable genetic correlation was estimated between BF and WTS₁. The SE of genetic correlations ranged between 0.02 and 0.17 (SE = 0.08), implying that genetic correlations were estimated accurately.

Discussion

Results here indicate that genetic variation exists in NL for age at first service (AFS), the number of live-born piglets (NBA₁ and NBA₂), and interval from weaning to first service (WTS₁ and WTS₂). Sizeable genetic correlations were estimated between these reproduction traits and several production, carcass, and efficiency traits, with a particularly high genetic correlation between growth and litter size.

Table 3. Classification effects and covariates included in the models for traits analyzed

<table>
<thead>
<tr>
<th>Trait</th>
<th>Classification effects</th>
<th>Covariates</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Sex</td>
<td>Herd</td>
</tr>
<tr>
<td>AFS</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>NBA₁</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>NBA₂</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>WTS₁</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>WTS₂</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>A100</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>BF</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>FC</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>LMC</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>BSQ</td>
<td>X</td>
<td>X</td>
</tr>
</tbody>
</table>

aSee Tables 1 and 2 for trait names.
bSex of animal (Sex), herd in which animal was born (Herd), litter breed (LB), parity of dam (PD), double insemination (DI), mating type (MT), herd-year-season (HYS), and station-pen-batch (SPB).
cLactation length (LL), number weaned (NW).
Table 4. Estimates of variance components and heritabilities for reproduction and production traits in Norwegian Landrace born between 1990 and 2000 as averages of the analyses conducted

<table>
<thead>
<tr>
<th>Traitb</th>
<th>$\sigma_a^2$</th>
<th>$\sigma_e^2$</th>
<th>$\sigma_c^2$</th>
<th>h²</th>
</tr>
</thead>
<tbody>
<tr>
<td>AFS, d</td>
<td>257.04</td>
<td>436.19</td>
<td>0.37 ± 0.01</td>
<td></td>
</tr>
<tr>
<td>NBA₁</td>
<td>0.76</td>
<td>7.12</td>
<td>0.10 ± 0.01</td>
<td></td>
</tr>
<tr>
<td>WTS₁, d</td>
<td>0.63</td>
<td>10.50</td>
<td>0.06 ± 0.02</td>
<td></td>
</tr>
<tr>
<td>NBA₂</td>
<td>0.90</td>
<td>8.11</td>
<td>0.10 ± 0.01</td>
<td></td>
</tr>
<tr>
<td>WTS₂, d</td>
<td>0.19</td>
<td>6.14</td>
<td>0.03 ± 0.02</td>
<td></td>
</tr>
<tr>
<td>A100, d</td>
<td>52.14</td>
<td>50.25</td>
<td>68.32 ± 0.30</td>
<td></td>
</tr>
<tr>
<td>BF, mm</td>
<td>0.66</td>
<td>0.18</td>
<td>0.67 ± 0.04</td>
<td></td>
</tr>
<tr>
<td>FC, kg</td>
<td>17.79</td>
<td>64.84</td>
<td>0.22 ± 0.03</td>
<td></td>
</tr>
<tr>
<td>LMC, %</td>
<td>2.76</td>
<td>1.99</td>
<td>0.58 ± 0.04</td>
<td></td>
</tr>
<tr>
<td>BSQ (1 to 5)</td>
<td>0.13</td>
<td>0.42</td>
<td>0.23 ± 0.03</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Traitb</th>
<th>$\sigma_a^2$</th>
<th>$\sigma_e^2$</th>
<th>$\sigma_c^2$</th>
<th>h²</th>
</tr>
</thead>
<tbody>
<tr>
<td>NBA₂</td>
<td>0.24</td>
<td>6.14</td>
<td>0.02 ± 0.01</td>
<td></td>
</tr>
<tr>
<td>WTS₂</td>
<td>0.05</td>
<td>0.16</td>
<td>0.13 ± 0.03</td>
<td></td>
</tr>
</tbody>
</table>

aSee Table 1 for variable definitions.

bSubjectively scored, with a preferred value of 1.

Table 5. Genetic correlations (rᵍ) between female reproduction traits and average adjusted back fat thickness (BF)

<table>
<thead>
<tr>
<th>Traita</th>
<th>A100</th>
<th>BF</th>
</tr>
</thead>
<tbody>
<tr>
<td>AFS</td>
<td>0.68 ± 0.02</td>
<td>−0.03 ± 0.02</td>
</tr>
<tr>
<td>NBA₁</td>
<td>0.60 ± 0.05</td>
<td>−0.00 ± 0.05</td>
</tr>
<tr>
<td>WTS₁</td>
<td>0.16 ± 0.07</td>
<td>−0.12 ± 0.06</td>
</tr>
<tr>
<td>NBA₂</td>
<td>0.42 ± 0.06</td>
<td>0.08 ± 0.05</td>
</tr>
<tr>
<td>WTS₂</td>
<td>0.20 ± 0.10</td>
<td>0.03 ± 0.10</td>
</tr>
</tbody>
</table>

aSee Table 1 for trait definitions.

Table 6. Genetic correlations (rᵍ) between female reproduction traits and lean meat content (LMC), bacon side quality (BSQ), and feed consumption (FC)

<table>
<thead>
<tr>
<th>Traitb</th>
<th>LMC</th>
<th>BSQb</th>
<th>FC</th>
</tr>
</thead>
<tbody>
<tr>
<td>AFS</td>
<td>0.02 ± 0.05</td>
<td>−0.09 ± 0.06</td>
<td>0.20 ± 0.06</td>
</tr>
<tr>
<td>NBA₁</td>
<td>−0.12 ± 0.07</td>
<td>0.04 ± 0.08</td>
<td>0.23 ± 0.08</td>
</tr>
<tr>
<td>WTS₁</td>
<td>−0.09 ± 0.10</td>
<td>0.08 ± 0.12</td>
<td>0.04 ± 0.11</td>
</tr>
<tr>
<td>NBA₂</td>
<td>−0.24 ± 0.09</td>
<td>0.17 ± 0.10</td>
<td>0.20 ± 0.10</td>
</tr>
<tr>
<td>WTS₂</td>
<td>0.05 ± 0.16</td>
<td>0.13 ± 0.13</td>
<td>0.01 ± 0.17</td>
</tr>
</tbody>
</table>

aSee Table 1 for variable definitions.

these findings. Fast growing gilts reach puberty earlier than gilts growing at a lower rate (Brien, 1986; Bidanel et al., 1996).

The current study estimated the genetic correlation between A100 and WTS₁, and between A100 and WTS₂ to be 0.16 and 0.20, respectively. Selection for decreased A100 will also favorably decrease the interval from weaning to first service. This is contrary to results of ten Napel and Johnson (1997) and ten Napel et al. (1998), which suggested that selection for increased daily gain and reduced BF would increase the probability of a long WTS interval. They found no correlation to the interval from weaning to first service treated as a continuous trait, and they also questioned the accuracy of using WTS on a continuous scale.

Individual amount of feed consumed by boars from 25 to 100 kg of live weight (feed conversion ratio) in the current study was estimated to have a positive (unfavorable) genetic correlation with litter size. There is a conflict of interest between market hog producers and piglet producers regarding feed consumption and appetite. Market hog producers prefer animals that require as little feed as possible to grow, whereas piglet producers prefer sows with large appetites to avoid substantial weight losses during lactation. Karsten et al. (2000) estimated a similar genetic correlation between individual feed intake by boars and number of live-born piglets in a selection experiment for improved feed efficiency. They also stated that the genetic antagonism between production and reproduction increased with a decrease in feed intake. The finding of a positive (favorable) genetic correlation between FC and AFS means that selection for reduced FC will decrease AFS. On the other hand, Kerr and Cameron (1996), using data from a selection experiment, found that selection for low daily feed intake resulted in increased farrowing age, whereas selection for lean growth, on scale feeding, reduced farrowing age. King and Dunkin (1986), using research farm data, stated that decreased energy and AA intake during lactation was associated with long WTS intervals. Koketsu et al. (1996), using field data, stated that both the amount and pattern of feed intake during lactation influenced subsequent reproductive performance. Here, no significant genetic correlation was estimated between...
FC and WTS, indicating that there was not a high genetic correlation between FC in boars from 25 to 100 kg and appetite of sows.

Among other traits, litter size can be viewed as a component of female reproductive fitness (Falconer and Mackay, 1996). Fitness components often show internal negative genetic correlations and with production traits (Beilharz et al., 1993). Dunnington (1990) argued that if genetic changes were sought too rapidly, the population might lack the time required to adapt to the changes imposed by selection, and the homeostatic balance of the animals would be at risk. The greater the loss of balance, the more unfavorable the genetic correlations between production- and fitness-related traits would become to counteract this loss. Dunnington (1990) made these assumptions based on poultry, and a generalization to mammals might be questionable; however, the considerable weight that traditionally has been given to growth in NL resulting in rapid genetic progress might explain the build up of correlation between litter size and growth. Actual phenotypic level of the animals used is another issue. The NL breed is somewhat leaner, faster-growing, and has a higher litter size than the animals used in the studies by Ducos and Bidanel (1996; A100 = 158.1 d; BF = 12.9 mm; NBA1, 2 = 10.4 and 10.6), Rydhmer et al. (1995; ADG = 525 g/d; BF = 11.9 mm; NBA1, 2 = 9.8 and 10.2), and Peskovicova et al. (2002; ADG = 540 g/d; NBA1, 2+ = 9.8 and 10.2) where no major genetic correlations between reproduction and production were estimated.

Biologically, selection for growth places demands on the young sow, requiring it to use resources for growth, which in turn has a negative genetic influence on her ability to give birth to a large litter. As pointed out by Brien (1986), gilts with a high growth rate might be less sexually mature at the same weight than gilts growing at a lower rate, again having an effect on the gilt’s uterine capacity. Taylor (1980) also argued that selection for lean meat content and growth has enhanced mature weight (finishing weight). Consequently, pigs seem to be bred at a lower proportion of their mature size and, inevitably, breeding pigs are challenged simultaneously rather than sequentially with the drive to grow and to reproduce (Whittemore, 1994).

Lean meat content showed a low to moderate genetic correlation to litter size, and the genetic correlation was largest for NBA2. Again, using resources for adding protein to the sow’s body mass leaves it with fewer resources for producing offspring.

Back fat thickness had little genetic correlation to any reproduction trait investigated. There are studies where an unfavorable genetic correlation between BF and litter size has been estimated (Chen et al., 2003), but in reviews by Rothschild and Bidanel (1998) and Peskovicova et al. (2002), genetic correlations between reproduction traits and BF were generally low, and with varying sign. Johansson and Kennedy (1983) and Kersey De Nise et al. (1983) suggested that an increase in carcass leanness results in deterioration of reproductive performance due to deterioration in the body’s ability for lipid mobilization during gestation or the suckling period. Viewing BF as a source of energy for the sow, one could expect that BF would play a role in the sow’s rebreeding capacity. In addition, WTS1 was the only reproduction trait that had a small genetic correlation with BF (r_g = −0.12 ± 0.06). It is possible that fat content at 100 kg is not a critical measure of the animal’s energy supply later in their reproductive life, and that selection toward reduced BF at 100 kg will not have a major unfavorable effect on rebreeding performance of gilts and sows. Kemper and Evans (1979) stated that during growth, the various fat depots develop at different rates, causing changes in fat distribution as the animal matures. Data from tomography studies on Norwegian swine show that there is genetic variation in fat depot use between animals, and that a decrease in BF requires use of other fat depots (Kolstad, 1996). There may be a threshold for BF at 100 kg of live weight because decreased BF to some extent also is associated with a decrease in other fat depots, and the genetic correlation between BF and rebreeding performance may increase if the BF value is forced below this threshold. Bacon side quality, which reflects the amount and distribution of fat in the bacon side, also revealed no significant genetic correlation to any of the analyzed reproduction traits.

Results here suggest that selection for production and efficiency will affect the reproductive performance of sows, whereas selection toward decreased fat content at 100 kg of live weight will not. In a lean, efficient, and prolific breed such as NL, it seems that growth has become more unfavorably genetically correlated to reproduction of the sow than leanness and fat content at 100 kg live weight.

Implications

Variance components for several reproduction and production traits were successfully estimated on Norwegian Landrace. Selection for increased efficiency and productivity will affect reproduction traits of the gilt and the sow. The breeding objective should therefore include both production and reproduction traits, and to maximize accuracy of breeding values, estimation should take the genetic correlations between the two blocks of information into account. Litter size and growth especially revealed a highly antagonistic genetic association, whereas selection for decreased back fat thickness at 100 kg of live weight is not expected to show any major effect on the reproductive performance of sows later in life.

Literature Cited
