Genetic Parameters for Beef Traits Measured on Future AI-bulls and Their Daughters Production

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Summary

Genetic correlations between different traits measured on future AI-bulls being performance tested for beef traits and lactation records from the field were estimated in a bivariate animal sire model using the AI-REML algorithm.

Records from three Danish beef performance test stations from 1984 to 1994 on 7641 bull calves of three Danish dual-purpose and dairy populations, i.e. Red Danish (RDM), Danish Black and White (SDM) and Danish Jerseys (DJ), were obtained for estimation of genetic and phenotypic parameters for feed intake capacity (Ku), feed efficiency (EFF), average daily gain (ADG) and area of M. Longissimus Dorsi (LD).

218,457, 1,215,918 and 250,846 first lactation records from RDM, SDM and DJ cows, respectively, calved after January 1st 1986 were included in the analysis as well.

Genetic correlations of 0.16, 0.25 and 0.43 between Ku and protein yield were obtained for RDM, SDM and DJ, respectively. Genetic correlations of 0.44, 0.19 and 0.47 between ADG and protein yield were obtained for RDM, SDM and DJ, respectively. Genetic correlations around zero between EFF and protein yield were obtained for all three breeds. The genetic correlation between protein yield and LD was also close to zero for SDM, while it was -0.31 for RDM.

Introduction

The main purpose of a performance test is to determine the breeding value for ADG, Ku and LD for potential AI bulls (Andersen et al., 1992). By raising the bull calves at central performance test stations the environmental variance will be reduced and a higher heritability will be obtained for the traits of interest.

The total merit of the performance test depends on the direct effect on the measured traits and the effects on correlated traits. The purpose of this research was to determine the genetic correlations between the meat production traits measured on bulls during their performance test and their daughters yield. If these correlations are strong, measurement from the performance test can be used as an early predictor for milk yield.

Materials and Methods

Beef traits on future AI-bulls

The bull calves were weighed with 4-weeks intervals and the corresponding average daily feed intake was obtained on the basis of the individually daily recording of feed intake expressed as Scandinavian Feed Units (SFU) and Fill Factor of Growing Cattle (FFu) of the feed ration. Feed efficiency (EFF) was calculated as the ratio of expected energy intake (Strudsholm et al., 1992) to observed energy intake from 1.5 to 11 months of age.
The calves were fed ad libitum with a total mixed ration. 7641 potential AI bulls (2280 RDM, 4323 SDM, 1038 DJ) have completed the performance test in the period 1984 to 1994.

Lactation records

The original data sets contained 218.457, 1.215.918 and 250.846 first lactations of RDM, SDM and DJ, respectively, calved after January 1st 1986. Yield and pedigree records were from the national database.

The following editing rules were used:
- cows with uncompleted records
- daughters of private bulls (no herdbook number)
- daughters of bulls with less than 5 progeny (for SDM less than 20 progeny)
- daughters of bulls with progeny in less than 3 herd-years
- cows from herds, with less than 4 first lactations within a year

The pedigree was traced back as far as possible.

Both young sires and proven bulls were sires of cows in the data. The variation between proven bulls is therefore expected to be reduced compared to the variance between test bulls (Bulmer, 1971). To improve the data structure young bulls were therefore treated as random and proven bulls as fixed effect. To be classified as a young bull there must be less than 60 months between the day of birth of the bull and the day of birth of his daughter.

Models

The statistical analyses had to take into account the recent immigration from external breeds into the Danish populations. Breed proportions as well as additive breed and heterosis effects were included in the model under the assumption that heterosis is due to dominance effects. The RDM population included four breeds (original RDM, American Brown Swiss (ABS), Red Canadian Cattle (RCC) and "other red breeds"), the SDM population included proportions of three breeds (original SDM, HF and "other black & white breeds") and the DJ population included four breeds (original DJ, American Jersey (USJ), New Zealand Jersey (NZJ) and "other Jersey breeds"). Proportions of heterozygosity for each breed combination was summed up to a general heterozygosity within each population.

Model for yield traits

Traits measured on the cows were analysed with the following sire model:

\[
Y_{ijkm(n)} = H_{Y} + Y_{MR_j} + A_{R_k} + P_{B_j} + \sum_{m=1}^{n} b_m \cdot P_{m(l/n)} + b_1 \cdot H_{(l/n)} + Y_{B_n} + e_{ijkm(n)} \tag{1}
\]

where

- \(Y_{ijkm(n)}\) is the observation of milk, fat or protein yield
- \(H_{Y}\) is the fixed effect for herd*year
- \(Y_{MR_j}\) is the fixed effect for year*month*region
- \(A_{R_k}\) is the fixed effect for age at first calving*region
- \(P_{B_j}\) is the fixed effect of proven bull
- \(b_m\) is regression on proportion of genes of the \((l/n)\)'th bull originating from the \(m\)'th breed
- \(P_{m(l/n)}\) is proportion of genes of the \((l/n)\)'th bull originating from the \(m\)'th breed
- \(n\) is the number of breeds within each population
- \(b_1\) is regression on general heterozygosity
- \(H_{(l/n)}\) is general heterozygosity of the \((l/n)\)'th bull
- \(Y_{B_n}\) is random effect of young bull \(n\) and
- \(e_{ijkmn}\) is random residual.

Data were precorrected for days open by use of correction factors from the Danish breeding value estimation system for yield.
Model for feed intake (Ku), average daily gain (ADG) and feed efficiency (EFF) measured on bulls

Traits measured on the performance test bulls were analysed with the following animal model:

\[ Y_{ijk} = HYS_{j(i)} + b_1 * L_{j(i)} + \sum_{k=1}^{n} b_k * P_{kj(i)} + b_2 * H_{j(i)} + A_{j(i)} + e_{ijk} \]  [2]

where

- \( Y_{ijk} \) is the observation of Ku, ADG or EFF
- \( HYS_{j(i)} \) is the fixed effect of the \( j \)th bull in the \( i \)th herd*year*season
- \( b_1 \) is regression on age at arrival to performance test station
- \( L_{j(i)} \) is age of bull \( j \) at arrival to the performance test station
- \( b_k \) is regression on proportion of genes of the \( j \)th bull originating from the \( k \)th breed
- \( P_{kj(i)} \) is proportion of genes of the \( j \)th bull originating from the \( k \)th breed
- \( n \) is the number of breeds within each population
- \( b_2 \) is regression on general heterozygosity
- \( H_{j(i)} \) is general heterozygosity
- \( A_{j(i)} \) is random effect of bull \( j \) and
- \( e_{ijk} \) is random residual.

Model for area of Longissimus Dorsi (LD) measured on bulls

LD measured on the performance test bulls was analysed with the following repeatability animal model:

\[ Y_{ijk} = H_{ij} + b_1 * W_{ij} + b_2 * W_{ij}^2 + \sum_{k=1}^{n} b_k * P_{kj} + b_3 * H_j + P_j + A_j + e_{ijk} \]  [3]

where

- \( Y_{ijk} \) is the observation of LD
- \( H_{ij} \) is the fixed effect of herd*day of measurement
- \( b_1 \) is regression on weight of bull at measurement
- \( W_{ij} \) is weight of bull at measurement
- \( b_2 \) is regression on weight of bull at measurement squared
- \( W_{ij}^2 \) is weight of bull at measurement squared
- \( b_k \) is regression on proportion of genes of the \( j \)th bull originating from the \( k \)th breed
- \( P_{kj} \) is proportion of genes of the \( j \)th bull originating from the \( k \)th breed
- \( n \) is the number of breeds within each population
- \( b_3 \) is regression on general heterozygosity
- \( H_j \) is general heterozygosity
- \( P_j \) is random effect of permanent environment affecting bull \( j \)
- \( A_j \) is random effect of bull \( j \) and
- \( e_{ijk} \) is random residual.

Model for traits measured on first lactation cows and performance test bulls

Genetic correlations between yield traits measured on cows and Ku, EFF, ADG and LD measured on performance test bulls were estimated in a bivariate animal-sire model.

Algorithms

Genetic and phenotypic parameters were estimated by Restricted Maximum Likelihood (REML) (Patterson & Thompson, 1971). Average Information Restricted Maximum Likelihood (AI-REML) was used for estimation of variance and covariance components (Madsen et al., 1994). AI-REML is included in the DMU-package (Jensen & Madsen, 1993).

Results and discussion

Genetic correlations between traits measured on performance test bulls of the three dairy
In Table 1 the genetic correlations between muscle area and yield traits can be seen for RDM and SDM, respectively. Correlations close to zero were estimated for SDM, while correlations around -0.30 were estimated for RDM between LD and the yield traits.

A correlation of zero was obtained between EFF measured on performance test bulls and daughters yield for RDM and SDM. While a small negative correlation was found for Jersey. In other investigations (e.g. Nieuwhof et al., 1992; Jensen et al., 1995) negative correlations between feed efficiency of the bulls and daughters yield were estimated. This difference can be caused by differences in feeding strategies and difference in definition of feed efficiency.

Here, Ku is defined as feed intake capacity at a constant weight and therefore the obtained correlations can be difficult to compare to investigations, where correlations are estimated between for example total dry matter intake and milk yield.

**Conclusion**

The genetic correlation between ADG and yield is positive for all three populations. The highest correlations were found for RDM and Jersey, and a smaller correlation for SDM.

Similar correlations were found between Ku and yield, but in general, the correlations were lower than for ADG.

The genetic correlation between LD and yield was negative for RDM but negligible for SDM.

**References**


Patterson, H.D. and Thompson, R. 1971. Recovery of inter-block information when block sizes are unequal. Biometrika 58, 545-554.

Table 1. Genetic correlations ($r_g$) between Ku, ADG, EFF and LD measured on performance test bulls and first lactations of milk, fat and protein measured on their daughters.

<table>
<thead>
<tr>
<th>Population</th>
<th>Trait</th>
<th>Milk $r_g$ ± s.e.</th>
<th>Fat $r_g$ ± s.e.</th>
<th>Protein $r_g$ ± s.e.</th>
</tr>
</thead>
<tbody>
<tr>
<td>RDM</td>
<td>Ku</td>
<td>-0.17 ± 0.08</td>
<td>0.08 ± 0.08</td>
<td>0.16 ± 0.08</td>
</tr>
<tr>
<td></td>
<td>ADG</td>
<td>0.42 ± 0.06</td>
<td>0.39 ± 0.06</td>
<td>0.44 ± 0.06</td>
</tr>
<tr>
<td></td>
<td>EFF</td>
<td>0.05 ± 0.06</td>
<td>0.07 ± 0.06</td>
<td>0.03 ± 0.06</td>
</tr>
<tr>
<td></td>
<td>LD</td>
<td>-0.28 ± 0.05</td>
<td>-0.25 ± 0.05</td>
<td>-0.31 ± 0.05</td>
</tr>
<tr>
<td>SDM*</td>
<td>Ku</td>
<td>0.24 ± 0.07</td>
<td>0.03 ± 0.07</td>
<td>0.25 ± 0.07</td>
</tr>
<tr>
<td></td>
<td>ADG</td>
<td>0.05 ± 0.05</td>
<td>0.06 ± 0.05</td>
<td>0.19 ± 0.05</td>
</tr>
<tr>
<td></td>
<td>EFF</td>
<td>-0.09 ± 0.06</td>
<td>0.10 ± 0.05</td>
<td>0.00 ± 0.06</td>
</tr>
<tr>
<td></td>
<td>LD</td>
<td>-0.07 ± 0.05</td>
<td>0.01 ± 0.05</td>
<td>-0.06 ± 0.05</td>
</tr>
<tr>
<td>DJ</td>
<td>Ku</td>
<td>0.33 ± 0.11</td>
<td>0.40 ± 0.11</td>
<td>0.43 ± 0.11</td>
</tr>
<tr>
<td></td>
<td>ADG</td>
<td>0.31 ± 0.11</td>
<td>0.50 ± 0.11</td>
<td>0.47 ± 0.11</td>
</tr>
<tr>
<td></td>
<td>EFF</td>
<td>-0.13 ± 0.11</td>
<td>-0.09 ± 0.11</td>
<td>-0.18 ± 0.11</td>
</tr>
</tbody>
</table>

*) The original data set for yield was split in three smaller subsets for the genetic analyses. The correlations in Table 1 are calculated as average of the estimated correlations from the three subsets. This is the reason for the missing standard errors for the correlations stated for the SDM population.