MODELING CROSSBRED INFORMATION IN GENETIC EVALUATION OF LITTER SIZE IN FINNISH PIG POPULATIONS

T. Serenius, M-L. Sevón-Aimonen and E.A. Mäntysaari

MTT Agrifood Research Finland, Animal Production Research, FIN-31600 Jokioinen, Finland

INTRODUCTION

Due to positive effect of heterosis on fertility, crossbreeding is widely used in piglet production. It seems also clear that response for selection will be maximized if all available information is used in breeding value estimation (Wei and van der Werf 1994; Bijma and van Arendonk 1998). However, crossbreeding causes some challenges for breeding value estimation. The estimation of non-additive genetic effects on individual level requires also reliable estimates for non-additive genetic parameters. In practice, reliable estimation of non-additive genetic parameters is hardly possible, and therefore the use of non-additive models in breeding value estimation has been limited.

Wei et al. (1991) showed that purebred and crossbred performance should be considered as two different traits, if there exists dominance and if gene frequencies differ between between parental populations. In Finland, the breeding objectives in the two main breeds, Landrace (LR) and Large White (LW), have been similar for many decades, and therefore, the breeds are very similar. In preliminary analyses, genetic correlation between crossbred and purebred performances in litter size were around 0.90 with high standard errors (> 0.10). Thus, preliminary analyses did not clearly indicate whether crossbred performance should be considered the same or different traits as purebred performance. The purpose of the present study was to examine how crossbred information would affect breeding value estimation of purebred pigs and how the effect of crossbreeding should be considered in breeding value estimation.

MATERIAL AND METHODS

Data from the Finnish litter recording scheme was used to estimate breeding values for number of piglets born alive in first parity of purebred LW and LR pigs. The full data set contained information on 86404 Landrace, 70749 Large White and 143133 crossbred litters (table 1). The reduced data set, contained information on 77306 Landrace, 62905 Large White, and 121598 crossbred litters. All the pedigrees were traced back to phantom parent groups. First the breeding values were estimated using either only purebred litter information or only crossbred information (F1 and first backcross litters). Next the full data was reduced by excluding the observations in 1998 or latter. The reduced data set was analyzed using 4 different methods to model crossbred information. The methods were compared by computing the correlations between the breeding value estimates of boars that had more than 40 daughters with a pure breed litter in the full data set but that had no daughters at any type of records in the reduced data set. Thus their pedigree indices computed using alternative models were compared to future evaluations as maternal grandsires of different types of litters. The following animal model was applied for purebred observations:
\[ Y_{ijklmno} = \mu + f_i + m_j + month_k + age_l + sire_m + dam_n + e_{ijklmno}, \]

where \( f_i \) is the fixed effect of farm and year, \( m_j \) is the fixed effect of mating type (artificial insemination or natural mating), \( month_k \) is the fixed effect of farrowing month, \( age_l \) is the fixed effect of age at first farrowing (1: under 330 days; 2: 330-360 days; 3: over 360 days), \( sire_m \) is the effect of sire of the litter, \( dam_n \) is the additive genetic effect of dam of the litter and \( e_{ijklmno} \) is the residual effect. Animal model breeding values for dam effects were estimated with MiX99 package (Lidauer et al. 2000). The reduced data was analyzed with following methods:

- **M1**: only purebred information included, same model as in purebred analysis,
- **M2**: M1 + crossbred information, same model as in purebred analysis,
- **M3**: M2 + data was scaled to the genetic variance of Landrace breed, and fixed effect of breed of the litter and regression effect of heterosis considered in the statistical model,
- **M4**: crossbred performances treated as different traits than purebred performances \((r_g = 0.90)\), crossbreeding was modeled as in M3.

The heterosis coefficients were as in Akbas et al. (1993): \( \text{Het} = P_s(1-P_d) + P_d(1-P_s) \), where \( P_s \) and \( P_d \) are the proportions of Large White breed in the sire and dam, respectively. Preliminary analysis showed that although heritabilities of litter size were similar between the breeds, the variances differed. In M3 and M4, the observations were scaled to the genetic variance of Landrace following the method presented by Madsen et al. (1995). The scaling multipliers \((\lambda)\) were obtained using the formula: \( \lambda = \frac{\sigma^2_{\text{L}}}{\sigma^2_{\text{L}} + \sigma^2_{\text{C}}} \), where \( \sigma^2_{\text{L}} \) is the additive genetic variance of Landrace breed (0.62), and \( \sigma^2_{\text{C}} \) is the additive genetic variance in the pure / crossbred population under consideration (0.66 for Large White, 0.76 for F1, 0.72 for first backcross). The scaling multipliers were 0.969, 0.903 and 0.928 for Large White, F1, and first backcross records, respectively.

### Table 1. Number of observations used in analysis of estimated breeding values with full and reduced data

<table>
<thead>
<tr>
<th></th>
<th>Landrace</th>
<th>Large White</th>
<th>Crossbred</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Full data</strong></td>
<td>86404</td>
<td>70749</td>
<td>143133</td>
</tr>
<tr>
<td><strong>Reduced data</strong></td>
<td>77306</td>
<td>62905</td>
<td>121598</td>
</tr>
</tbody>
</table>

**RESULTS AND DISCUSSION**

The comparison was based on the fact that accuracy of estimated breeding values \((r_{TI})\) should increase with increase in amount of information. If the accuracy of estimated breeding values \((\text{ACC}_{EBV})\) is known, the accuracy of pedigree breeding value \((\text{ACC}_{PI})\) is proportional to the
correlation between pedigree breeding value and more reliable one: \( \text{ACC}_{\text{PT}} = r_{\text{PLEBV, ACC}} \) (Reverter et al. 1994). In present study, the comparison was carried out amongst maternal grandsires with at least 40 daughters with a purebred litter in full data. Thus, the accuracy of maternal grandsires in full data is at least 0.71 (\( r_{\text{TR, progeny testing}} = \sqrt{\frac{P}{P} + \frac{4 - \hat{h}^2}{\hat{h}^2}} \)), where \( p \) is the number of daughters), and therefore, accuracy of pedigree index is at least \( r_{\text{PLEBV}} \times 0.71 \).

In general, correlations between pedigree breeding values (reduced data) and breeding values estimated using full purebred data ranged from 0.662 to 0.685 in Landrace, and from 0.699 to 0.758 in Large White grandsires (table 2). Correlations were highest for \( M_4 \), where the crossbred performance was treated as a different trait for both the breeds. Thus, although breeding objectives of LR and LW have been similar for many decades, the breeds seem to have different gene frequencies.

The pedigree breeding values were more accurate with \( M_1 \), where only purebred performances were included, than with \( M_2 \) and \( M_3 \), where crossbred performance was treated as a same trait as the purebred one (table 2). Also this indicates that genetic correlation between purebred and crossbred performance is not one, or that crossbreeding is not properly modeled. Table 3 shows the correlations between breeding values estimated from the full data but using only the crossbred records, and the pedigree indices from the reduced data estimated with models \( M_1 \) to \( M_4 \). Obviously, there is so much more information on crossbred litters than on purebred LR or LW litters (table 1) that estimated breeding values with \( M_2 \) and \( M_3 \) are more correlated to breeding values of crossbred performances than breeding values of purebred performances (tables 2 and 3).

Table 2. Correlations between breeding values of grandsires estimated using the purebred records on full data and the estimates from reduced data analyzed with methods described before (\( M_1 \) – \( M_4 \)). In \( M_4 \), the correlation is between “purebred traits”

<table>
<thead>
<tr>
<th>Breed</th>
<th>( M_1 )</th>
<th>( M_2 )</th>
<th>( M_3 )</th>
<th>( M_4 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Landrace (n = 61)</td>
<td>0.677</td>
<td>0.671</td>
<td>0.662</td>
<td>0.685</td>
</tr>
<tr>
<td>Large White (n = 34)</td>
<td>0.747</td>
<td>0.699</td>
<td>0.708</td>
<td>0.758</td>
</tr>
</tbody>
</table>

Analyses suggest that breeding values should preferably be estimated using only purebred information than by considering crossbred information as in \( M_2 \) or \( M_3 \) (Table 2). However, it should be remembered that the objective of litter size selection is to enlarge both purebred and crossbred litters. In any case, \( M_4 \) gives breeding value estimates for both purebred and crossbred traits, and thus, might be used in practical breeding value estimation.

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Table 3. Correlations between breeding values of grandsires estimated using only the crossbred records on full data and the estimates from reduced data analyzed with methods described before (M₁ – M₄). In M₄, the correlation is between “crossbred traits”

<table>
<thead>
<tr>
<th></th>
<th>Landrace (n = 61)</th>
<th>Large White (n = 34)</th>
</tr>
</thead>
<tbody>
<tr>
<td>M₁</td>
<td>0.570</td>
<td>0.534</td>
</tr>
<tr>
<td>M₂</td>
<td>0.810</td>
<td>0.770</td>
</tr>
<tr>
<td>M₃</td>
<td>0.809</td>
<td>0.761</td>
</tr>
<tr>
<td>M₄</td>
<td>0.829</td>
<td>0.794</td>
</tr>
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</table>

CONCLUSION
Pedigree breeding values estimated with a model where crossbred performance is treated as a different trait than the purebred one (M₄) showed highest correlation to breeding values estimated using full purebred data. This would suggest that such a model could be implemented for the practical breeding value estimation of pig breeds where the production comes equally from pure breed and crossbreed litters.

REFERENCES