Assessing Connectedness Among German Swine Herdbook Populations

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Introduction

In Germany, swine breeding traditionally is organised on the level of the federal states with one herdbook association in each state. Pigs are tested centrally in regional test stations, and EBV are calculated separately for each herdbook association, resulting in a very limited exchange of animals among populations. This structure has changed somewhat in recent years. Because of the increasing use of AI, there was less demand for sire breed boars for natural service. At the same time, sow herds have become larger. Their need for large groups of replacement gilts is often difficult to fulfill by the traditionally small-scale herdbook breeders. The number of herdbook breeders has decreased considerably. First steps have been taken towards a closer collaboration of the German herdbook associations. Structural improvements are likely, and greater genetic gains may be achieved, allowing herdbook associations to compete with pig breeding companies.

With a joint genetic evaluation based on data from all German herdbook associations, animals would be ranked on a national level while breeding, at least in the past, has been on a regional level with limited connections among herdbook associations. If herdbook associations have different genetic levels and connectedness is insufficient, comparison of EBV among animals from different associations may be biased. A number of studies have dealt with the importance of connectedness in genetic evaluation (e.g. Foulley et al., 1992; Laloë, 1993; Kennedy and Trus, 1993; Hanoqc et al., 1996). Among the measures proposed to evaluate connectedness are the coefficient of determination (CD) of contrasts among units (e.g. Laloë, 1993; Fouilloux et al., 2008), the connectedness correlation (Lewis et al., 1999, 2005), and the connectedness rating (Mathur et al., 2002). Comparing different connectedness scenarios, Kuehn et al. (2007) found that only CD had a consistent relationship with bias reduction across all scenarios, but considered it difficult to calculate for routine genetic evaluation. In a simulation study, Kuehn et al. (2008) measured connectedness as connectedness correlation ($r_{ij}$) and suggested benchmark levels for $r_{ij}$ for minimising the risk of comparing animal EBV among units.

If German herdbook associations decide to collaborate, the level of connectedness among these populations needs to be analysed. Usually, risk of biased comparisons is of concern in species where comparisons are among animals across herds. This has been analysed in beef cattle (e.g. Fouilloux et al., 2008; Tarres et al., 2010) and in sheep (e.g. Kuehn et al., 2009). Similar analyses may be possible in pigs if test stations are regarded as ‘herds’. The objective

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of this study was to assess the connectedness level among the Piétrain populations from Saxony and Bavaria by calculating connectedness correlations for test stations.

**Material and methods**

Data from Saxony were provided by the regional herdbook association (MSZV) and the regional computation center (LfULG) and included performance records from Piétrain animals tested in the Saxon test station (Koellitsch) as well as pedigree information. Up to six males and females from one litter were tested.

For this analysis, the Bavarian population was divided into two subpopulations since there are two test stations (Schwarzenau, Grub). Breeders from Northern Bavaria tend to have their animals tested in Schwarzenau while animals from breeders in Southern Bavaria are tested in Grub. According to the testing scheme, approximately 10% of the animals (two females from a litter) registered for testing in one station are sent to the other station when the piglets are collected on the farms. Performance records and pedigree information were extracted from the central database maintained by the Bavarian herdbook association (EGZH), the Bavarian recording organization (LKV), and the Bavarian State Research Center for Agriculture (LfL).

Data from Saxony and Bavaria were joined. For this analysis, identifying animals that appeared as sires or dams in both populations was critical. There is no unique animal identification across herdbook associations. An animal registered in one herdbook may receive a new identification when it or its progeny is registered in another herdbook. Performance records for loin muscle area were edited with respect to year of test (2005 to 2009) and number of observations per test station*fattening period*compartment (at least 5).

Characteristics of the data are presented in Table 1.

**Table 1: Characteristics of data for three test stations and the joint data set.**

<table>
<thead>
<tr>
<th></th>
<th>Schwarzenau</th>
<th>Grub</th>
<th>Koellitsch</th>
<th>Joint data set</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of performance records</td>
<td>1621</td>
<td>1066</td>
<td>767</td>
<td>3454</td>
</tr>
<tr>
<td>No. of contemporary groups</td>
<td>140</td>
<td>92</td>
<td>65</td>
<td>297</td>
</tr>
<tr>
<td>No. of sires</td>
<td>311</td>
<td>221</td>
<td>148</td>
<td>572</td>
</tr>
<tr>
<td>No. of dams</td>
<td>885</td>
<td>607</td>
<td>188</td>
<td>1651</td>
</tr>
</tbody>
</table>

*Test station*fattening period*compartment

There were 101 sires and 18 dams, respectively, with progeny tested in both Bavarian stations, Grub and Schwarzenau, i.e. progeny from one litter was tested in Schwarzenau and progeny from another litter was tested in Grub. Between Schwarzenau and the Saxon test station, there were only seven common sires and eleven common dams, respectively. There was merely one sire with progeny tested in Grub and Koellitsch, and no such dam. An analysis of the pedigree revealed that animals tested in the three stations also had common ancestors in earlier generations. In order to assess the effect of common ancestors on connectedness, the number of generations added from the joint pedigree for each animal with a performance record was varied from 1 (only parents assumed to be known) to 6.
The DMU package (Madsen and Jensen, 2000) was used to set up and solve the mixed model equations and to obtain prediction error variances and covariances. The loin muscle area observation \( y_{ijklmn} \) on an animal was modeled by
\[
y_{ijklmn} = \mu + h x_{ijkl} + \alpha_i + \beta_{jk} + A_{ij} + c_{ijkl} + e_{ijklmn},
\]
where \( \mu \) is the mean of loin muscle area; \( h x_{ijkl} \) is the carcass weight as a linear covariate; \( \alpha_i \) is the fixed effect of test station*fattening period*compartment; \( \beta_{jk} \) is the fixed effect of sex; \( A_{ij} \) is the random additive-genetic animal effect; \( c_{ijkl} \) is the random effect of litter; and \( e_{ijklmn} \) is the random residual effect. An estimated heritability of 0.475 was used.

The connectedness correlation proposed by Lewis et al. (1999, 2005) was calculated for test stations \( i \) and \( j \) as
\[
r_{ij} = \frac{\text{PEC}(\hat{a}_i, \hat{a}_j)}{\sqrt{\text{PEV}(\hat{a}_i) \times \text{PEV}(\hat{a}_j)}},
\]
where \( \hat{a}_{i(j)} \) is the mean EBV of all animals tested in station \( i(j) \), \( \text{PEC}(\hat{a}_i, \hat{a}_j) \) is the prediction error covariance between these means, and \( \text{PEV}(\hat{a}_i) \) and \( \text{PEV}(\hat{a}_j) \) are the prediction error variances of the mean EBV of test stations \( i \) and \( j \).

**Results and discussion**

Figure 1 shows the connectedness correlations for test stations from Bavaria (Schwarzenau, Grub) and Saxony (Koellitsch). With one generation of pedigree information added for each animal with a performance record, i.e. only parents of tested animals assumed to be known, \( r_{ij} \) was 0.23 for Schwarzenau and Grub, the Bavarian test stations. There was a large increase in \( r_{ij} \) with 2 generations added, and only a moderate increase when more generations were added. With 6 generations of pedigree information, \( r_{ij} \) was 0.89. Since a large percentage of sires are AI boars and since the testing scheme is aimed at a sufficient connectedness among test stations, this \( r_{ij} \) can be regarded as the upper level of connectedness for test stations and populations, respectively. In sheep, the largest \( r_{ij} \) found for two flocks was 0.69 (Kuehn et al., 2008).

As could be expected from the small numbers of sires and dams with progeny tested in both Schwarzenau or Grub and Koellitsch, \( r_{ij} \) for Schwarzenau/Grub and Koellitsch was close to 0 when just parents of tested animals were assumed to be known. These \( r_{ij} \) increased almost steadily when more generations were added, but they were always considerably lower than \( r_{ij} \) for the Bavarian stations. Throughout, \( r_{ij} \) for Schwarzenau and Koellitsch was somewhat larger than for Grub and Koellitsch.

**Conclusion**

The benchmarks for \( r_{ij} \) of 0.05 and 0.10 proposed by Kuehn et al. (2009) were clearly reached for Bavaria and Saxony once a sufficient number of generations was considered in the genetic evaluation. These results indicate that a sufficient level of connectedness can be reached even if the number of linking sires and dams with progeny with performance records
in two populations is low. Animals in earlier generations can contribute considerably to the level of connectedness. Therefore, it is important to identify common animals correctly.

Figure 1: Connectedness correlations ($r_{ij}$) for test stations from Bavaria (Schwarzenau, Grub) and Saxony (Koellitsch).

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References