Degree of connectedness among herds and sires of current candidates for selection in Afrikaner cattle with reported weaning weights

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Summary

Systems of national cattle evaluation seek to facilitate comparisons of candidates for selection across contemporary groups. Thus, it is prediction error variance (PEV) for the difference between EBV of two competing candidates that is important rather that the accuracy of each EBV. The PEV for the difference between EBV is reduced when the competing candidates are well-connected in the genetic evaluation. Pedigree and weaning performance data for Afrikaner cattle was obtained from the South African National Database. The connectedness correlation and PEV for the difference in EBV were estimated for sires of the current candidates for selection and these estimates were averaged to determine connectedness between herds. Seventeen of the 28 herds were found to have weak connectedness and therefore pose some risk of bias in using EBV to compare candidates for selection across herds. The average number of sires per contemporary group was 1.5 providing a rationale for the generally weak connectedness among sires. Use of a sire referencing scheme by Afrikaner breeders is anticipated to improve connectedness, reduce potential for bias to adversely affect comparisons among selection candidates and therefore facilitate genetic improvement.

Keywords: connectedness, genetic evaluation, reference sire, genetic progress

Introduction

Genetic evaluation is conducted to facilitate comparison of candidates for selection based on their merit. Henderson’s mixed model equations (Henderson, 1973) are frequently used to separate predictions of breeding value (EBV) and environmental effects. This potentially allows for the fair comparison of animals in different contemporary groups. However, differences in average genetic merit among contemporary groups will be attributed to the environment in the absence of adequate genetic connections among the groups.

Connectedness, in a statistical sense relates to the estimability of contrasts among fixed effects. However, connectedness is not required in order to predict random breeding values (Fernando et al., 1983), and disconnected subsets of records do not lead to biased predictions of breeding values, provided that breeding values of animals that were present at the start of performance recording were randomly and identically distributed across the entire population (Tosh & Wilton, 1990). If selection or genetic drift occurs before pedigree and performance recording begin and causes genetic means to differ among contemporary groups, then this assumption is violated. The risk of bias when comparisons are made across herds is increased when connectedness is poor.
Afrikaner cattle are indigenous to South Africa, with very little evidence of *Bos indicus* in the modern day Afrikaner (Makina *et al*., 2016). The breed can thus be described as a fairly unique and tropically adapted taurine breed type. The breed is recognized for environmental adaptation and cost-effective beef production under harsh conditions with limited food and water (Scholtz & Mamabolo, 2016). Pienaar *et al.* (2014) found four distinct genetic clusters in an analysis of samples from 37 herds of Afrikaner cattle. There has also been recent, albeit limited, introgression of Bonsmara germplasm in some herds, (Vermaak *et al*., 2016).

This population segmentation gives rise to concern for unbiased comparison of candidates for selection in the Afrikaner breed when they may originate from different herds. Thus, the objectives of this study were to determine connectedness among the herds of Afrikaner that are currently engaged in performance recording and to further estimate connectedness among sires of current candidates for selection.

**Material and methods**

Data recorded for the Afrikaner breed in the national database were extracted for use in this study and were used with the permission of the Afrikaner Cattle Breeders’ Society of South Africa. The pedigree comprised of 258 841 individuals and extended back in time to the point at which there was no known ancestry for any animal that was contained therein. There were 22 275 animals for which neither parent was identified and an additional 21 485 animals with only one identified parent. Of those animals having only one identified parent, paternity was unknown for 11 404 and maternity was unknown for 10 081. Animals born after 2014 were divided among 28 herd-year-season subclasses that contained an average of 46 head. These cattle were sired by 139 bulls.

Two statistics were used to summarize connectedness. The connectedness correlation (rij) was calculated as:

\[
\text{r}_{(i,j)} = \frac{\text{a}_{(i,j)}}{\sqrt{\text{a}_{(i,i)} \cdot \text{a}_{(j,j)}}},
\]

where \(a_{(i,j)}\) was the prediction error covariance between animals \(i\) and \(j\), and \(a_{(i,i)}\) and \(a_{(j,j)}\) were the prediction error variances (PEV) for animals \(i\) and \(j\), respectively.

The second statistic was the scaled PEV of the difference in EBV between animals:

\[
\text{d}_{(i,j)} = \frac{\text{a}_{(i,i)} + \text{a}_{(j,j)} - 2\text{a}_{(i,j)}}{\sigma_a^2},
\]

where \(\sigma_a^2\) was the additive genetic variance for the trait of interest.

These statistics for all pairs of animals in different herds were averaged to evaluate connectedness between the herds.

In order to identify animals represented in the Afrikaner breed society’s performance recording scheme, the weaning weight records were downloaded from the database, adjusted to an average age at weaning of 210 days (which was the actual average), and edited to conform to a window of ages at weaning between 165 and 255 days. Connectedness statistics (see below) were calculated for this trait based on prediction error variances from an animal model that included contemporary groups (defined by herd, year and weaning date), classes defined by the cross-classification of sex and age of dam, and feed levels. The *a priori* assumed heritability was 0.2, which is approximately equal to the 0.19 estimate of heritability.
for direct effects on weaning weight that is used in the current genetic evaluation of Afrikaner.

Results and discussion

A summary of connectedness among the herds that produced the recent Afrikaner candidates for selection is displayed in Figure 1. Alternative definitions of contemporary groups could affect these results and are a topic of ongoing research. Between herd average thresholds of $r_{ij} > 0.10$, $0.10 \leq r_{ij} \leq 0.05$, and $r_{ij} < 0.05$ were identified by Kuehn et al (2008a) as indicating strong connectedness with little risk of bias in comparisons among animals in the different herds, moderate connectedness with small risk of bias, and weak connectedness with greater risk of bias, respectively. Using these standards, 17 of the 28 herds were found to have weak connectedness and therefore pose some risk of bias in using EBV to compare candidates for selection in those herds with other animals in the breed. The average scaled prediction error variance for differences in EBV indicates that comparison of animals from four of the herds would be particularly inaccurate.

![Graph showing connectedness among herds](image)

**Figure 1.** Measures of connectedness among herds of Afrikaner cattle enrolled in the breed’s performance recording scheme.

The dendrogram shown in Figure 2 illustrates the relationships among herds and supports the contention of Pienaar et al. (2014) that the Afrikaner population in South Africa is segmented. Improved connectedness among herds could be accomplished through exchange of breeding bulls between the well-connected herds and those that are less well-connected. Alternatively, artificial insemination could allow this exchange to occur, perhaps at significantly less cost and greater effectiveness because it would then be feasible to use multiple potential sires without a commensurate commitment of the number of cows needed to employ the same number of bulls. Implementation of a sire referencing scheme in Afrikaner would facilitate increasing the rate of genetic progress and reduce inbreeding (Kuehn et al., 2008b).
The average number of sires per contemporary group was only 1.5 and the average number of progeny per sire was 17.7 (minimum = 1, maximum = 124). This relatively poor representation of sires across contemporary groups provides a rationale for the weak connectedness among sires (Figure 3.).

Within herds, this situation could be improved by spreading weaning over as few days
as possible each year without compromising the number of calves that fall into the prescribed age range for the age-adjusted weaning weight. Connectedness among sires could also be improved through use of AI in a sire referencing scheme and this would reduce the potential for bias in comparisons among sires based on their EBV. Such a scheme could use relatively few sires to periodically produce a fairly small number of progeny in each of the Afrikaner herds (Lewis & Simm, 2000; Kuehn et al., 2008b).

**List of References**


