VARIATION IN INBREEDING DEPRESSION BETWEEN ANCESTRAL LINES: A PRELIMINARY ANALYSIS OF FIRST LACTATION SOMATIC CELL COUNT FROM HOLSTEIN FRIESIANS IN AUSTRALIA

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SUMMARY

The overall level of inbreeding depression for this population is +0.0046±0.0017 log-transformed average somatic cell count (LSCC) for every 1% increase in inbreeding coefficient (F). Partial Fs were computed for a short-list of 100 ancestors that accounted for the largest proportion of the gene pool in 1996/1997-born cows. From this list, 11 ancestors with large numbers of cows inbred to them were used for this analysis. These 11 ancestors account for about 53% of overall F. Estimates of inbreeding depression of LSCC vary from –0.034 to +0.094 for every 1% increase in F, among ancestral lines, but this variation is not statistically significant, and may be simply the result of the large standard errors. Knowledge of variability in inbreeding depression can be useful for devising an optimal breeding structure. Based on this analysis alone, the lack of significant variation in inbreeding depression between different ancestral lines implies that the current method of reducing inbreeding depression is probably adequate in the context of between-line selection for inbreeding depression.

Keywords: Inbreeding depression, partial inbreeding coefficients, dairy cattle, somatic cell count

INTRODUCTION

Increasing efforts have been made to reduce the level of inbreeding in Holstein-Friesian populations. The main rationale for reducing inbreeding in the short term is to abate the economic cost of inbreeding depression. Theoretically, the extent of inbreeding depression depends on the frequency of favourable alleles and the extent to which they are dominant. Since not all ancestors have the same set of alleles, it follows that ancestral source of inbreeding may have an influence on the effect of inbreeding. Therefore, another way of reducing inbreeding depression may be to utilise variation in inbreeding depression between ancestral 'lines' by favouring lines that exhibit less depression (Wang, 2000). Variation in inbreeding depression between sire lines in experimental cattle populations was reported by Beckett *et al.* (1979) and Mi *et al.* (1965). Miglior *et al.* (1994) reported an analysis of variation in inbreeding depression for first lactation volume, fat and protein yield in commercial Holstein Friesians, in which each cow was categorized into one of 48 ancestral lines, according to the male common ancestor that had the highest additive genetic relationship to the cow. More recently, partial inbreeding coefficients due to the major founder lines have been used for analysis of variation in inbreeding depression between founder lines in a closed line of pigs (Rodriganez *et al.*, 1998). The present analysis uses this same approach in a national dairy population to partition the inbreeding coefficient (F) of animals in an age cohort, according to the direct contribution of important ancestors, and then estimates the variation in inbreeding depression in the cohort, between these ancestral lines. In certain breeding structures, this method of partitioning by ancestral lines can yield partial F with lower correlations than partitioning by founder lines, as genes tend to be more diffused through the population when they are traced back to the

founders. Hence, this can be a better context for an effective analysis of between-line variation in inbreeding depression, as there is less confounding of partial inbreeding effects.

MATERIAL AND METHODS

Phenotypic and pedigree records from the Australian Dairy Herd Improvement Scheme (ADHIS) were kindly provided by Drs Les Jones and Kevin Beard. The database has 301,951 Holstein-Friesian cows born in 1996 and 1997. The cohort for the current analysis comprised 145,261 cows:

- for which the equivalent number of generations of complete pedigree (judged by the harmonic mean of completeness from maternal and paternal sides of the pedigree; MacCluer, 1983) is equal to or greater than two;
- having a first lactation with two or more test-days records
- in herd-year-seasons with at least one inbred cow in a total of at least ten cows within the cohort.

Phenotypic data provided by ADHIS for the current analysis were expressed as log-transformed adjusted average somatic cell count (LSCC) for first lactations. These were derived from log-transformed somatic cell counts from individual test-day records and were provided as within-herd deviations adjusted to a common within-herd variance.

The algorithm for computation of the overall F was written by Tier (1990). The partial inbreeding contributed by each common ancestor was calculated using the path-searching algorithm (Stevens, 1975; modified by Boyce, 1983), which was adapted by the first author for this analysis. A short-list of 100 potential ancestors for computation of partial inbreeding was generated from a program for computation of effective number of ancestors in Boichard *et al.* (1997). This program iteratively searches for the next ancestor that gives the highest gene contribution to the current pool of individuals, after taking away the portion of its contribution that has been accounted for by ancestors from previous iterations. The partial inbreeding coefficient of each cow was then calculated for each of the short-listed ancestors that have a total gene contribution of more than 0.5% to the 1996/1997-born Holstein-Friesian cows that are inbred. The 11 ancestors with large numbers of 1996/1997-born Holstein-Friesian cows inbred to these ancestors (lowest = 585 cows for ancestor 5424) were included in this analysis. ASREML (Gilmour *et al.*, 1999) was used for the analysis of inbreeding effects on first lactation LSCC. The following mixed model was fitted:

$$y_i = bF_i + b_j F_{ij} + hys_k + animal_i$$

where y_i = standardized LSCC for the ith cow,

F_i = inbreeding contributed by all ancestors of the ith cow,

F_{ij} = inbreeding contributed by the jth common ancestor (j=1,…11) of the ith cow,

hys_k = the kth herd-year-season effect, and

$animal_i$ = random animal effect for the ith cow.

RESULTS AND DISCUSSION

Partial inbreeding coefficients. In all results, the 11 ancestors are ranked in descending order for their partial inbreeding contribution. Figure 1 shows the basic statistics for F in those 1996/1997-born cows that are inbred, i.e. mean and standard deviation of overall and partial F was calculated with respect to inbred cows only. The average F for the inbred 1996/1997-born cows is 1.8% and the sum of the partial inbreeding contributions of these 11 ancestors is about 53% of the overall F. Given the preliminary nature of this analysis, a more thorough search should give a list of ancestors that account for a much higher proportion of the overall level of inbreeding in the population. Preliminary results for this cohort indicated that the correlation between partial F is less than 0.25.
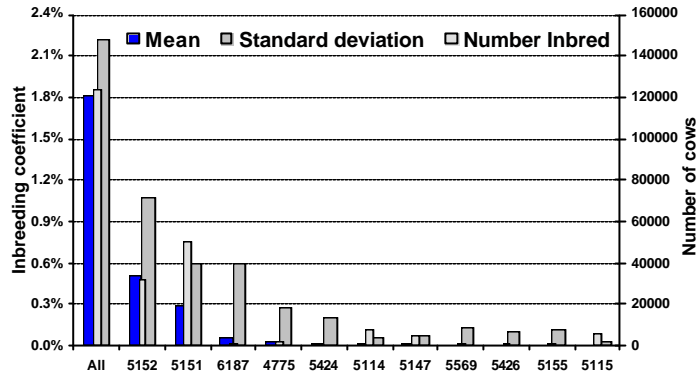
Figure 1. F due to all ancestors (first set of columns; ALL) and partial F due to 11 individual ancestors, in 1996/1997-born inbred cows. Number inbred is read from the right y-axis.

Inbreeding depression. In Figure 2 overall inbreeding depression in this population is 0.0046±0.0017 LSCC per 1% increase in F. The other bars show the variation in inbreeding depression between ancestral lines as their deviation from the overall level of depression. A wide range in inbreeding effect (from deviation of –0.039±0.028 to 0.089±0.048 LSCC for every 1% increase in inbreeding) is apparent, but this variation is not significant and the wide range is a reflection of the large standard errors in the estimates.
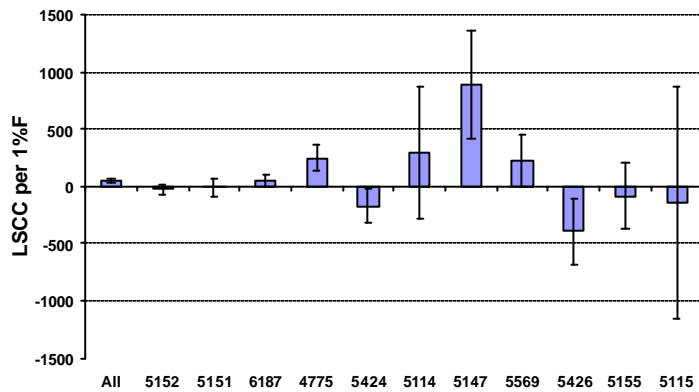

Figure 2. Effect of 1% increase in F on LSCC in standardized first lactation records. The mean change in LSCC per 1% increase in F is shown as columns with their standard errors shown as error bars.

CONCLUSION

Given commercial populations with complex breeding structures, various methods exist for distinguishing lineages so that between-line variation in inbreeding depression can be analysed. The method presented in this paper can give a more precise accounting of the inbreeding contributions from different common ancestors, compared with partitioning according to additive gene contribution. The present method also helps to overcome the problem of confounding in the partial inbreeding effects. However, the large standard errors in the results are most likely due to the low standard deviations of the partial inbreeding coefficients when this method is used.

The high inbreeding contribution from a small number of ancestors (53% of overall F from 11 ancestors) implies that control of inbreeding depression by limiting overall inbreeding in individuals may neglect the variation in effect of inbreeding from these ancestors and compromise the magnitude of improvement in production that can be achieved.

Knowledge of variability in inbreeding depression can be useful for devising an optimal breeding structure. It can provide information on the potential viability of developing strains within a breed and which ancestral line to use for these strains to take advantage of their favorable inbreeding "depression". If based on this analysis alone, there is a lack of significant variation in inbreeding depression between different ancestral lines, implying that the current method of reducing inbreeding depression is probably adequate in the context of between-line selection for inbreeding depression.

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