

Computing Inbreeding Coefficients and Effects of Inbreeding, Heterosis and Recombination Loss on Evaluations for Lifespan and Somatic Cell Count in the UK

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1. Introduction

A recent study on the Holstein/Friesian (HOL) breed has indicated that the rapid rise in percentage Holstein genes in the United Kingdom (UK) has been accompanied by an increasing rate of inbreeding (Kearney *et al.*, 2004). They reported an average inbreeding rate of 0.17% per year since 1992. Some of the consequences of inbreeding, for instance, inbreeding depression, are expected to be more pronounced in fitness traits such as somatic cell count (SCC) and lifespan (LS).

Van Raden (1992) introduced the concept of accounting for the covariance between unknown parent groups (UPGs) when calculating inbreeding coefficients. The algorithm of Quass (see Mrode, 1996) for computing inbreeding was modified to account for the covariance between UPGs. Initially, the modified algorithm is briefly presented. Then the study examines the effects of inbreeding on SCC and LS in the UK for the HOL, Ayrshire (AYR) and Jersey (JER) breeds. Also the effects of heterosis and recombination loss are studied in the HOL only. Using the JER breed, the estimate of inbreeding depression for SCC from an animal model is compared with that from a random regression model.

2. Materials and Method

The pedigree information for registered HOL, AYR and JER animals used for this study was obtained from the respective UK Breed Societies. For non-registered cows, pedigree data were obtained from the lactation record files from Milk Recording Organisations. The pedigree files analysed consisted of 6891169, 221095 and 157888 animals for the HOL, AYR and JER breeds respectively born between 1956 and 2002. The base population was defined as animals born before or in 1960.

Unknown ancestors were assigned to UPGs on the basis of the sex and date of birth of their progeny and the sex and country of origin of the parent.

Initially, inbreeding coefficients were calculated using the algorithm of Quass with no grouping of ancestors and assuming base animals and unknown ancestors were unrelated and not inbred. The inbreeding coefficients were then averaged by year of birth of animals. In the second step, unknown ancestors were then assigned to UPGs. The UPGs were assigned inbreeding coefficients equal to the average inbreeding coefficients of known parents born in the same time period (Van Raden, 1992). The relationship of an UPG with animals born in year t with other UPGs consisting of animals born in years 1 to $t-1$ was assumed to be twice the inbreeding coefficient of the UPG with animals born in year t (Wiggans *et al.*, 1995). Inbreeding coefficients were re-calculated accounting for the covariance between UPGs. The algorithm of Quass was modified to account for the contribution of UPGs to estimates of inbreeding coefficients of animals. With the usual algorithm of Quass, the inbreeding coefficient of animal x , (F_x) is;

$$F_x = \sum_{m=1}^{nc} l_{sm} l_{dm} D_m$$

with

$$D_m = 0.25 - 0.125 (F_s + F_d), \text{ assuming that } F_0 = -1.0$$

where l_{sm} , l_{dm} are the proportion of genes which the m^{th} common ancestor contributed to the sire (s) and dam (d) of animal x respectively, D_m is half the variance of Mendelian sampling for the common ancestor m , and nc is the number of common ancestors for the sire and dam of animal x . Note that F_s

and F_d in the equation for D_m above, refer to the inbreeding coefficients of the sire and dam of the m^{th} common parents respectively.

In accounting for the covariance between UPGs the inbreeding coefficient of animal x was calculated as usual with the Quaas algorithm but with UPGs treated as unknown ancestors which are unrelated and not inbred and the inbreeding coefficient of animal x augmented by the contribution from UPG as:

$$F_x = F_x + \sum_{i=1}^{ns} 0.5(l_{s, \text{UPGi}})(l_{d, \text{UPGj}})(\text{cov}(\text{UPGi}, \text{UPGj})); i \neq j$$

where $(l_{s, \text{UPGi}})$ is the proportion of genes which the sire of animal x contributed to the i^{th} UPG, $(l_{d, \text{UPGj}})$ is the proportion of genes which the dam of animal x contributed to the j^{th} UPG, and ns and nd are the number of UPG's to which ancestors of the sire and dam are assigned. If the sire and dam of animal x are unknown parent groups, the equation above reduces to:

$$F_x = F_x + 0.5 \text{ cov}(\text{UPGi}, \text{UPGj}); i \neq j$$

The estimates of inbreeding depression were obtained by including the inbreeding coefficients of animals as a covariate in the usual animal model used for the national evaluation of $\log_e$ SCC (LSCC) and lifespan in the UK (Interbull, 2000). However, only first lactation LSCC were analysed. A bivariate animal model for lifespan score (number of lactations an animal has completed or is expected to complete) and an index of type trait was used to compute LS evaluations. The inverse of the A^{-1} matrix used in the analyses were computed accounting for inbreeding. For the HOL breed only, an analysis including inbreeding coefficients, heterosis and recombination loss of animals as covariates in the usual national genetic evaluation models for LSCC and LS was implemented, to estimate their effects on both traits. For the JER only, inbreeding coefficients were fitted as a covariate in a random regression model (RRM) for SCC with orthogonal polynomials of order 2 and 3 for animal and permanent environment effects. Results were compared with those from the lactation model.

3. Results and Discussion

The trends in mean inbreeding coefficients by year for the breeds are shown in Figure 1. Consistent with the results of Kearney *et al.* (2004), there is an increasing trend in inbreeding in recent years for the HOL and AYR breeds. However, inbreeding peaked in the JER breed in the early 1990s and has subsequently declined. This might be due to the importation of different bloodlines from foreign populations in recent years. The inbreeding levels reported here are less than those reported by Kearney *et al.* (2004) as both pedigree and non-pedigree animals have been analysed and the study has focused on cows with records and their ancestors.

It can be seen from the proportion of animals at different levels of inbreeding for animals born between 1990-1995 and 1996-2001 in Table 1, that the increase in rates of inbreeding in the HOL and AYR breeds, is mainly due to the increased proportion in animals which are becoming inbred rather than an increase in the proportion of animals with higher levels of inbreeding.

The regression coefficients of LSCC for a 1% increase of inbreeding were 0.0039, 0.0080 and 0.0043 for HOL, AYR and JER respectively. These estimates are rather low and implies that cows that are inbred by 25%, for example, had LSCC on average higher by 0.10, 0.20 and 0.11 than an average non-inbred cow for HOL, AYR and JER respectively. These correspond to an increase in SCC of about 6000 cell/ml for HOL, 15556 cell/ml for AYR and 8013 cell/ml for JER above an average non-inbred cow. The average increase in population mean of LSCC from a 10% increase of inbreeding is equal to 6% (HOL), 11% (AYR) and 6% (JER) of the standard phenotypic standard deviation (0.71). These estimates of inbreeding depression for HOL and JER are lower than those reported by Miglior *et al.* (1992) for the Canadian Holstein, but, the estimate for AYR is similar.

The estimate of inbreeding depression for SCC from the RRM for the JER breed was 0.0038 per 1% inbreeding; which is similar to the estimate from the lactation model. However, fitting inbreeding coefficients by days in milk, indicated that inbreeding tended

to increase SCC at the beginning and end of lactation (Figure 2).

The estimates of the effects of heterosis and recombination (HOL only) on LSCC were also very low. Assuming 10% heterosis and recombination the effects are -0.012 and -0.016 LSCC respectively.

The regression coefficients of lifespan for 1% increase of inbreeding were -0.0219, -0.0145 and -0.0145 lactations for HOL, AYR and JER respectively. A cow that is 25% inbred for instance, has an average lifespan of 0.55 of a lactation less than an average cow for the HOL and 0.36 of a lactation less for both AYR and JER. The average reduction in population mean from a 10% increase of inbreeding was equal to 9% (HOL) and 6% for both AYR and JER of the phenotypic standard deviation (2.36). The estimates of the effect of heterosis and recombination rate (HOL only) were low for LS. These were 0.153 lactation at 10% heterosis and -0.013 lactation at 10% recombination rate.

The rank correlations between bull predicted transmitting abilities with and without inbreeding coefficients fitted were about 0.99 for LSCC and LS in the three breeds; indicating little re-ranking due to accounting for inbreeding.

4. Conclusion

The recent increase in inbreeding rate in the HOL and AYR is due to a higher proportion of animals that are becoming inbred at levels ≤

6.25%. The importation of foreign bloodlines has resulted in a decrease in the inbreeding rate in the JER since the late 1990s. The effects of inbreeding on SCC and LS observed are rather low and may only have significant effects at high levels of inbreeding, eg 25%. The effects of, heterosis and recombination loss were much lower and were close to zero.

5. References

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Table 1. The frequency of bulls and cows by class of inbreeding (%F) for two time periods for Holstein Friesian and Ayrshire.

Class of inbreeding %F	Holstein Friesians				Ayrshire			
	1990-1995		1996-2001		1990-1995		1996-2001	
	Cows	Bulls	Cows	Bulls	Cows	Bulls	Cows	Bulls
0	51.3	58.8	36.7	46.5	8.6	11.8	2.4	1.9
0 - 6.25	47.3	39.5	61.5	50.9	88.0	85.8	93.3	94.4
6.26 - 12.5	0.9	1.5	1.4	2.5	2.2	1.2	2.7	3.1
12.6 - 18.8	0.3	0.2	0.3	0.1	1.0	1.1	1.2	0.3
≥ 18.9	0.2	0	0.1	0.1	0.3	0.2	0.3	0.3
No of Animals	943013	14483	733436	7259	37794	1027	18977	323

Figure 1. Mean inbreeding per year for Holstein, Ayrshire and Jersey Breeds.

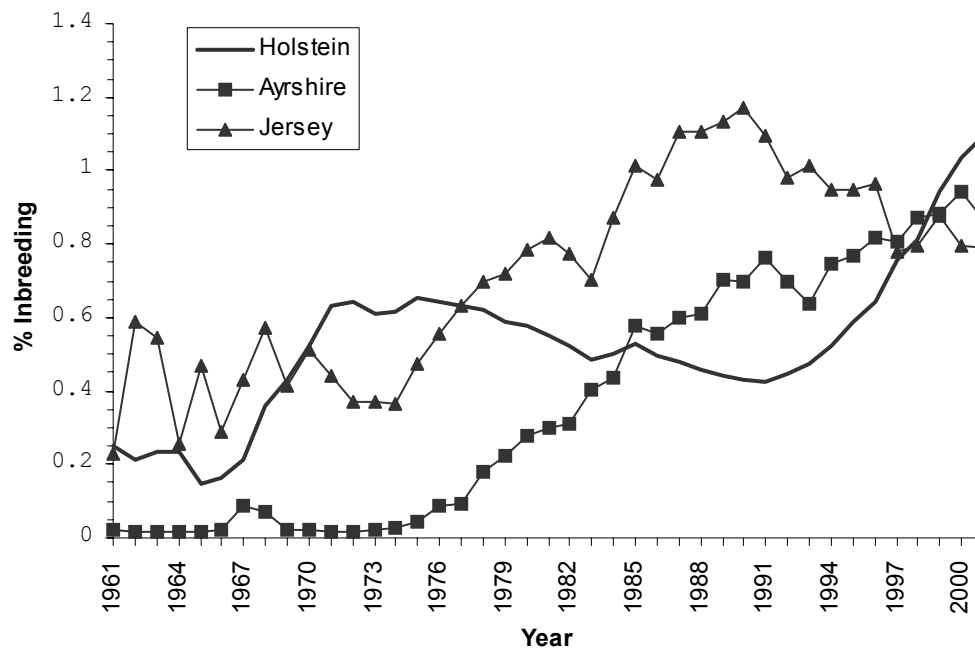


Figure 2. Mean LSCC per DIM with 0% inbreeding or assuming 25% inbreeding.

