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Impact of Nonadditive Genetic Effects in the Estimation of Breeding Values for Fertility and Correlated Traits

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ABSTRACT

The effects of inbreeding, heterosis, recombination loss, and percentage Holstein on the estimation of predicted transmitting abilities for fertility traits (calving interval, number of days from calving to first insemination, nonreturn rate, number of inseminations) and correlated traits (milk yield at test nearest d 110 and body condition score) were examined in a mixed population of Holstein and Friesian cattle. An unfavorable effect of percentage Holstein on calving interval was observed, resulting in a 12-d increase for pure Holsteins compared with pure Friesians. Insemination traits were less affected by percentage Holstein, with 3% more animals returning to first service within 56 d and 0.1 more inseminations required for Holstein animals. Heterosis and recombination loss affected some of the traits. Heterosis had a favorable effect on yield, with a 0.35-kg difference between a pure and cross-bred animal for test milk. There was a reduction of 1 d to first insemination between a pure and first-crossbred animal. Inbreeding had a significant and unfavorable effect on all traits. The difference between a noninbred animal and an animal with an inbreeding coefficient of 10% was a 2.8-d increase in calving interval, a 1.7-d increase in days to first insemination, a 1% increased probability to return to estrus at first service, 0.03 more inseminations, a 0.27-unit decrease in body condition, and a 0.54-kg decrease in milk on test nearest d 110. The effect of inbreeding depression was more pronounced at higher levels of inbreeding. The rank correlations between the predicted transmitting abilities for fertility and correlated traits, with and without the additional nonadditive effects in the model, were over 0.99. Steps should be taken to control the rise in inbreeding, or the effects on fertility and correlated traits such as milk production will begin to manifest themselves.

(**Key words:** nonadditive genetic effect, inbreeding, fertility)

Abbreviation key: CI = calving interval, **DFS** = number of days from calving to first insemination, **F** = inbreeding coefficient, **F_1** = first cross breeding, **INS** = number of inseminations per conception, **MILK** = daily milk yield at d 110, **NR56** = nonreturn rate after 56 d.

INTRODUCTION

Genetic evaluations often ignore nonadditive genetic effects, such as dominance and epistasis, and their expression in the forms of heterosis and inbreeding depression. In many cases, this is justified by the relatively minor impact they make on the outcome of selection decisions. However, as breeding goals become more complex in recognition of the need to maintain fitness as well as improve productivity, there may be a need to review this position, particularly because nonadditive effects are considered to have a greater impact upon traits associated with fitness, which are more likely to exhibit dominance or epistasis than production-related traits.

Within a breed, the nonadditive genetic effects commonly expressed are associated with either inbreeding or crossbreeding. Inbreeding arises from the mating of related individuals and results in reduced heterozygosity, and when there is dominance, this reduction in heterozygosity is expected to lead to inbreeding depression. The management of inbreeding is becoming increasingly important in domestic livestock populations as genetic evaluation procedures, such as BLUP, are more accurate in identifying elite bulls and, when used in combination with truncation selection, increase the rate of inbreeding, largely caused by a greater tendency to select related animals. This increased potential for inbreeding has been exacerbated by the use of reproductive technology, allowing an increase in the selection intensity through the extensive worldwide use of semen and increasing the reproductive rate of elite females. The crossing of breeds increases the heterozygosity in

the offspring, whereby crossbred progeny have a performance advantage over the midparent mean for that trait (Shull, 1914). Interbreeding the crosses or backcrossing breaks up epistatic gene combinations present in each breed but to different amounts in different crosses (Dickerson, 1969). The impact of these phenomena can be observed in heterosis and recombination loss, respectively. Many countries, including the UK, analyze Holstein and Friesian animals together. However, in the UK they are considered distinct breeds, and, therefore, the heterosis and recombination loss between the 2 breeds is accounted for in the genetic evaluation of production (Brotherstone and Hill, 1994).

The consequences of inbreeding include inbreeding depression, which is a reduction of the mean phenotypic value, particularly for traits connected with reproduction or fitness (Falconer, 1989). Inbreeding depression has been shown to decrease milk production by approximately 9 to 26 kg of milk per lactation for each 1% of inbreeding (Thompson et al., 2000a, b). Smith et al. (1998) estimated an economic loss in relative net income of approximately $22 to $25 (losses expressed in terms of production index) for registered cows per 1% increase in inbreeding over the lifetime of a cow. Very little data exist for nonproduction related traits, such as fertility, but it is expected that inbreeding depression could be substantially greater for such fitness-related traits than for production traits. Studies that have considered the effect of inbreeding on fertility and related traits have found a nonsignificant or small effect (Smith et al., 1998; Cassell et al., 2003).

Little work has been done to estimate inbreeding in the UK dairy population. Roughsedge et al. (1999) found the average inbreeding coefficient of cows born in 1997 to be 0.4% relative to a base population born in 1960. There has been a recent move away from Friesian genes to North American Holstein genes, with 76% of the cow population in 1997 having North American Holstein founder origins (Roughsedge et al., 1999). Although inbreeding was low at 0.4%, it can be hypothesized that the rate of inbreeding will follow that of the US population but with a generation lag. Kearney et al. (2004) showed that current levels of inbreeding in the UK Holstein population were 2.6% for females and 3.1% for males relative to a base population born in 1940, using a more complete pedigree file than that available to Roughsedge et al. (1999). Kearney et al. (2004) showed that the mean level of inbreeding is currently rising at a rate of 0.17%/yr. The average inbreeding coefficient of the US Holstein population is now approximately 5% with a current average annual increase of 0.2% (AIPL, USDA, 2004).

The UK dairy population was predominately Friesian until the 1980s (Roughsedge et al., 1999; Kearney et al., 2004), but a large influx of North American Holstein genes has occurred over the past 20 yr, resulting in a steep increase in the proportion of Holstein in the population. Therefore, historical data will include cows of varying proportions of Friesian and Holstein. However, a small population of "pure" and distinct Friesians still exist. Substantial crossing and upgrading has occurred in the UK dairy population, which still retains a reasonable spread of crosses. Estimates of heterosis effects for dairy cattle performance vary across studies and traits. For example, Ahlborn-Breier and Hohenboken (1991) described a heterotic effect of 6.1% for milk yield and 7.2% for fat yield in a Holstein-Jersey cross. Akbas et al. (1993) found a lower heterotic effect of 1.8 to 2.2% for 305-d milk, fat, and protein kg between Holsteins and Friesians.

Studies suggest that poor fertility has become a major reason for involuntary culling of dairy cows in the UK (Esslemont, 1993) and worldwide (Olori et al., 2002). Research has recently led to the development of a fertility index for dairy cattle in the UK to counter this decline (e.g., Wall et al., 2003). The index is based on data from calving, insemination records, milk yield, and BCS. Published fertility proofs in the UK are based on calving interval and nonreturn rate after 56 d weighted by their relative economic weights (independent of culling). The development of genetic analyses for fertility has created an opportunity for evaluation of the possible differential impact of nonadditive genetic variation for fertility, a trait directly associated with fitness, and production traits.

The purpose of this study was to estimate the effects of inbreeding, heterosis, recombination loss, and proportion of Holstein genes on dairy cow fertility and production and to examine their potential impact on selection decisions in the UK dairy population by comparing the outcomes of genetic evaluations made with and without these effects.

MATERIALS AND METHODS

A number of fertility traits were defined using information on inseminations and calvings from national milk recording databases, including: a) calving interval (**CI**), b) number of days from calving to first insemination (**DFS**), c) number of inseminations that resulted in a second calving (**INS**), d) a binary trait measuring a return to service within 56 d of first insemination (**NR56**), e) milk yield in kilograms around d 110 (**MILK**), and f) BCS. Body condition score was recorded during the first lactation for animals participating in the type classification scheme operated by Holstein UK and expressed on a scale of 1 to 9, where 1 represented thin and 9 represented fat. This score was adjusted for

Table 1. Mean, SD, range (minimum [Min] and maximum [Max]), and numbers of records in the analysis.

	Mean	SD	Min	Max	no.
Calving interval, d	395.20	54.30	300	600	274,489
Days to first service	86.03	31.34	1	200	358,326
Nonreturn rate, 0/1	0.69	0.46	0	1	357,507
Number of inseminations, count	1.65	0.99	1	10	258,271
Body condition score, 1 to 9 scale	4.44	1.67	−1.5	10.5	110,383
Milk at test nearest d 110, kg	23.87	5.93	5	60.0	408,847
Age, mo	28.90	4.10	18	40	408,847
Inbreeding, %	1.7	2	0	38	408,847
Recombination loss, units	17	11	0	50	408,847
Heterosis, %	36	27	0	100	408,847
Percentage Holstein	75	24	0	100	408,847

effect of the recording officer by scaling the records to make the standard deviations for each field officer equal to the mean standard deviation of all field officers (Jones et al., 1999). This scaling procedure resulted in some scores being beyond the 1 to 9 range.

Production records for first-lactation Holstein-Friesian animals with at least 3 test days were taken from 1992 until the end of 2002. Validation and editing rules were applied to these data as described in Wall et al. (2003). The pedigree of all cows in the data set was extracted from the Holstein UK database. Animals with ≥4 complete generations of pedigree information were extracted, leaving 408,847 records. Only animals with this degree of pedigree completeness were considered for this analysis because of the problems in estimating accurate inbreeding coefficients for animals with incomplete pedigrees (Cassell et al., 2003).

Inbreeding coefficients were calculated for all animals using the algorithm of Meuwissen and Luo (1992). Each animal was also assigned to an inbreeding class of 0, 1, 2, ..., 10; 10 to 15; or 15; where the zero class included non-inbred animals, class 1 animals had inbreeding coefficients >0% but ≤1%, and so on, with class 15 consisting of animals with inbreeding of ≥15% . Percentage Holstein was calculated for all animals in this data set, based on the average percentage Holstein of the parents. Additional assumptions on percentage Holstein based on the breed code or country of origin and date of birth of a sire or dam were also applied. For example, all registered US animals were considered to be 100% Holstein, while the older UK bulls in the pedigree were considered to be 100% Friesian. Heterosis and recombination loss were calculated for all cows as follows (Akbas et al., 1993):

$$\text{heterosis} = P_S(1 - P_D) + P_D(1 - P_S)$$
$$\text{recombination loss} = P_D(1 - P_D) + P_S(1 - P_S)$$

where P_S and P_D are the proportion of Holstein for the sire and dam, respectively. Thus, (heterosis, recombina-

tion loss) took values (1, 0), (0.5, 0.25), (0.25, 0.188), (0.125, 0.109) for the first cross (F_1) and the subsequent 3 backcrosses to Holstein, respectively.

More than 67% of cows had information on CI, over 27% had BCS information, and 88% had at least one insemination record; 63% had a record for INS. A total of 11,354 sires were included, all with ≥3 daughters in the data set that also represented 32,264 herd-year seasons. Table 1 gives summary statistics for the data set.

These data were analyzed with a sire model using an exact solver in PEST (Groeneveld et al., 1990) instead of an iterative procedure so that the standard errors for each solution (fixed effects, covariates, and breeding values) would be produced. Bivariate analyses for MILK paired with each of the other 5 traits (BCS, CI, NR56, DFS, and INS) were carried out to account for selection on yield in the analysis. The (co)variance between traits is presented in full in Wall et al. (2003). Unknown ancestors were set to missing in the sire pedigree file instead of being allocated to genetic groups because of the potential confounding between percentage Holstein and these groups:

$$P_{ijk} = \mu + \text{hys}_i + \text{month}_j + \beta_1 X_a + \beta_2(X_a)^2 + \beta_3 X_F + \beta_4 X_\% + \beta_5 X_{het} + \beta_6 X_{rec} + \text{sire}_k + e_{ijk}$$

$$T_{ijk} = \mu + \text{hys}_i + \text{month}_j + \beta_1 X_a + \beta_2(X_a)^2 + \beta_7 X_{d\_t} + \beta_8(X_{d\_t})^2 + \beta_3 X_F + \beta_4 X_\% + \beta_5 X_{het} + \beta_6 X_{rec} + \text{sire}_k + e_{ijk}$$

$$V_{ijk} = \mu + \text{hysc}_i + \text{month}_j + \beta_1 X_a + \beta_2(X_a)^2 + \beta_9 X_{d\_c} + \beta_{10}(X_{d\_c})^2 + \beta_1 X_F + \beta_3 X_F + \beta_4 X_\% + \beta_5 X_{het} + \beta_6 X_{rec} + \text{sire}_k + e_{ijk}$$

where P_{ijk} = an observation for CI, DFS, NR56, or INS; T_{ijk} = MILK; V_{ijk} = BCS; hys_i = fixed effect of herd-by-year-by-season of calving interaction i; hysc_i = fixed effect of herd-by-year-by-season of visit interaction i on BCS; month_j = fixed effect of the month of calving i; β_1 to β_{10} = linear and quadratic regression coefficients of the dependent variable (P, T, or V) on age of animal at
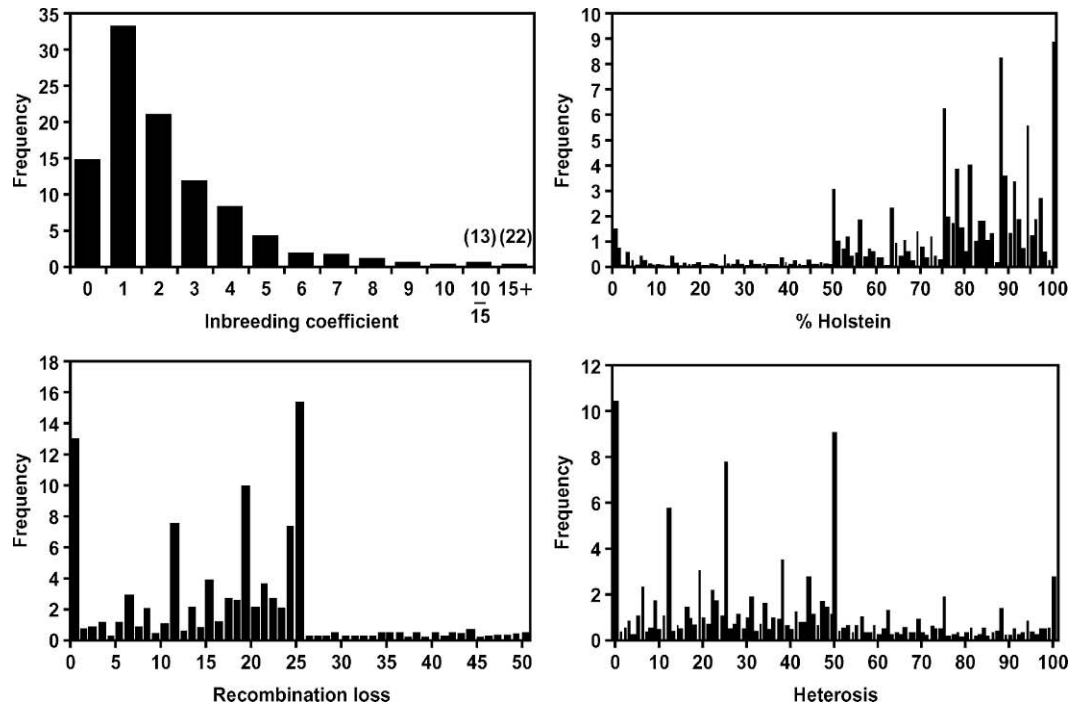
Figure 1. Distribution of inbreeding coefficient (midpoints for last 2 classes), percentage Holstein, recombination loss, and heterosis.

calving (X_a), DIM at test (X_{d_t}), DIM at BCS measurement visit (X_{d_c}), inbreeding coefficient (X_F), percent Holstein ($X_\%$), heterosis (X_{het}), and recombination loss (X_{rec}) expressed as deviations from their mean; $sire_k$ = the random genetic effect of sire k; and e_{ijk} = residual random error term.

The significance of each of the solutions for each of the covariates was tested using a 2-way *t*-test. Fitting inbreeding as a simple covariate in the model assumes that the effect of inbreeding depression on a trait is linear. The curvilinearity of inbreeding depression was also tested by including inbreeding as a classification variable (inbreeding class, as defined in Figure 1, added as a fixed effect in the previous models).

A covariate was added to the model for a given trait if it was found to have a significant effect after the previously mentioned analyses. Separate BLUP analyses were run with and without fitting these additional effects in the model. The effect of their inclusion was estimated by the rank correlation between the 2 BLUP analyses.

RESULTS

Percentage Holstein

The mean percentage Holstein of cows with data was 75% (SD 24%; Table 1), with nearly 75% of the cows

born in 2000 being at least 86% Holstein (Figure 2). Percentage Holstein had a statistically significant impact upon all traits, with percentage Holstein (or breed substitution from 100% Friesian to 100% Holstein) predicted to increase the mean MILK by 13% but to decrease BCS by 43% (Table 2). Phenotypic values for all fertility traits decreased as percentage Holstein increased, with the effect ranging from a 3 to 7% reduction
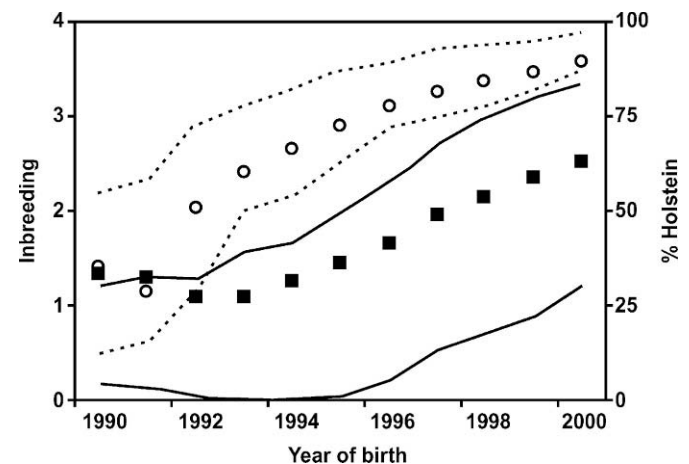
Figure 2. Recent trends and interquartile ranges in inbreeding (■, ——) and percentage Holstein (○, ····) in cows in the data born since 1990.

Table 2. Estimates (est.) of the effect of percentage Holstein (breed substitution of Friesian by Holstein), heterosis in the F₁ (first cross breeding), and recombination loss (SE) in absolute terms. Effects of percentage Holstein, heterosis, and recombination loss are expressed as a percentage of the mean (% mean) and the phenotypic standard deviation (% SD).

	Percentage Holstein (breed substitution)				Heterosis				Recombination loss			
	est.	SE	% mean	% SD	est.	SE	% mean	% SD	est.	SE	% mean	% SD
Calving interval (d)	12.200	1.250***	3.08	22.46	−1.610	0.720*	0.41	2.97	−1.270	1.240	0.32	2.34
Days to first service (d)	3.950	0.600***	4.59	12.60	−1.140	0.340**	1.33	3.64	−0.040	0.610	0.04	0.13
Nonreturn rate (0/1)	−0.031	0.010**	4.52	6.68	−0.010	0.006	1.46	2.16	−0.016	0.010	2.33	3.45
Inseminations (no.)	0.113	0.024***	6.84	11.40	−0.020	0.014	1.21	2.02	−0.049	0.026	2.97	4.94
Body condition score (1 to 9 scale)	−1.930	0.130***	43.46	115.57	−0.130	0.070	2.93	7.78	−0.013	0.067	0.29	0.78
Milk at test nearest d 110 (kg)	3.125	0.109***	13.09	52.74	0.355	0.059***	1.49	5.99	−1.454	0.088***	6.09	24.54

***$P < 0.001$.
**$P < 0.01$.
*$P < 0.05$.

of the mean (Table 2). Among the traits analyzed, the impact of percentage Holstein was less dramatic on the traits directly associated with fertility (CI, DFS, NR56, and INS) than on BCS and MILK.

Heterosis

Average heterosis was 36% (SD 27%; Table 1), indicating that the benefits from heterosis in the current population are approximately one-third of that seen in an F₁. Figure 1 shows that some crosses between pure Holstein and pure Friesians were present in the data (3%), resulting in 100% heterosis for these animals. However, the UK is mainly an upgrading population from Friesians to Holsteins, as the distribution is skewed to the right (100% Holstein).

Heterosis was shown to have a small but statistically significant effect on MILK, CI, and DFS (Table 2). Heterosis had a favorable effect on yield, with an estimated difference of 0.36 kg/d between an F₁ and the average of Friesian and Holstein. However, this quantity corresponded to only 1.4% of the mean. Heterosis had a favorable effect on DFS and CI, reducing them by 1.1 and 1.6 d, respectively.

Recombination Loss

The mean recombination loss was 17% (SD 11%; Table 1). The only statistically significant effect of recombination loss was upon MILK (Table 2), resulting in a 1.45-kg loss in milk on test nearest d 110. The loss caused by recombination seen in MILK was larger, in absolute terms, than the gain achieved from the favorable heterosis. The joint impact on the F₁ and the subsequent 3 backcrosses to Holstein was 0.355, −0.186, −0.185, and −0.112 kg, respectively, suggesting that while the F₁ was marginally better than expected from the additive breed composition, the subsequent crosses were marginally worse.

Inbreeding

Average inbreeding was 1.7% (SD 2.0%; Table 1), with nearly 94% of animals having an inbreeding coefficient of <5% (Figure 1). Over 85% of cows in this data set were inbred to some degree relative to a base population of 1940. However, a small number of cows in this population had a high inbreeding coefficient (**F**), up to 38%.

Figure 2 shows the trend in average F and percent Holstein by year of birth of the 408,847 cows in the data set. A steady increase in F occurred over the period shown, and the current rate of increase in inbreeding of 0.2%/yr (based on linear regression) is equal to recent

Table 3. Estimates of inbreeding depression (noninbred to 100% inbred) in absolute terms (est.) and its SE. Decrease of trait per 10% rise in inbreeding coefficient is expressed as a percentage of the mean (% mean) and as a percentage of the phenotypic standard deviation (% SD).

| | Inbreeding depression | | | |
	Est.	SE	% mean	% SD
Calving interval (d)	27.75	5.52***	0.70	5.11
Days to first service (d)	16.75	2.58***	1.86	5.34
Nonreturn rate (0/1)	−0.099	0.045*	1.44	2.13
Inseminations (no.)	0.270	0.115*	1.63	2.72
Body condition score (1 to 9 scale)	−2.72	0.25***	6.13	16.29
Milk at test nearest d 110 (kg)	−5.39	0.35***	2.26	9.10

***$P < 0.001$.

**$P < 0.01$.

*$P < 0.05$.

estimates in the current US population and in the complete UK Holstein population (Kearney et al., 2004). The average F of cows born in 2000 is 2.5% (Figure 2), with nearly 98% of animals being inbred to some degree. The most recent (born since 1995) sires represented in this data set have a mean F of just under 3%, with a similar rate of increase as seen in their daughters.

Table 3 shows that inbreeding had a significant and unfavorable effect on all traits. The difference between a noninbred animal and an animal of F = 10% was a 2.8-d increase in CI, a 1.7-d increase in DFS, a 0.27-unit decrease in BCS, and a 0.54-kg decrease in MILK. This pattern of change is similar, but opposite, to the predicted heterosis in the F_1 between the Friesian and Holstein. As for heterosis, the impacts of F on the traits directly related to fertility were not clearly larger than those on MILK and BCS.

Figure 3 shows the effect of inbreeding class on each of the traits, which was generally more severe at extreme levels of inbreeding (≥8%). The deviations of the inbreeding class solutions from that estimated from linear regressions were all within one standard error up to the inbreeding class of 8%, suggesting that the effect of inbreeding on a trait is linear up to this point. The difference between animals in F class 0 (non-inbred) and F class 10 was +5 d in CI, +1 d in DFS, −0.6 in BCS, and −0.3 kg in MILK. These results were not significantly different from the result estimated from the linear regression, with the exception of BCS. The effect of inbreeding depression on all traits for animals with inbreeding <3% was unfavorable but small, with the effect of inbreeding being most pronounced for animals in higher inbreeding classes. For example, animals in the highest 3 inbreeding classes (inbreeding >9%) had a CI that was approximately 6 d longer than a non-inbred animal. Animals with inbreeding coefficients between 15 and 30% produced 1.16 kg less MILK

compared with a noninbred animal, a 5% decline in the phenotypic mean for that trait. Inbreeding had a similar (and significant) effect on DFS to that had on CI, with highly inbred animals (≥15%) having 4.5 additional d to first insemination compared with noninbred animals.

Although not statistically significant, Figure 3 shows that the effect on MILK of the 0% inbreeding class was actually lower than that of the next 3 classes (1 to 3%). Figure 3 shows that the majority of the effect of inbreeding depression on BCS occurred at quite low levels of inbreeding. The effect of inbreeding depression on BCS for animals in inbreeding class 3 (F = 2 to 3%) compared with noninbred animals was 0.37 units. This result is nearly 50% of the effect of inbreeding depression for animals with F >15%. However, inbreeding depression only causes a major effect at the higher inbreeding classes (>6%) for the other traits in the analysis. For example, inbreeding depression caused a 0.37-d increase in CI for animals in inbreeding class 3, which was only 6% of the effect of inbreeding depression for animals with F >15%.

Wall et al. (2003) estimated the genetic decline in fertility and associated traits. Over the period from 1980 to 2000, a 4.9-d increase in CI and 3.6-d increase in DFS was observed. Distribution of inbreeding for sires born in 1980, 1990, and 2000 was obtained from the results of Kearney et al. (2004). Given these distributions, the effect of inbreeding on each trait at the 3 time points was examined. Over the 20-yr period, inbreeding depression accounted for a 0.6-d increase in CI, 11% of the genetic decline observed in that trait, while 8.3% of the genetic decline in DFS was attributed to inbreeding depression.

Effect of Nonadditive Genetic Effects on Breeding Value Estimation

Inbreeding was included as a covariate in the model for each trait. Heterosis was added to the models for MILK, CI, and DFS, while recombination loss was included in the model for MILK only. The effect of inbreeding was fitted as a covariate in the model because of how similar the inbreeding class solutions were to linear regression solutions up to 8%. Percentage Holstein was significant for all traits. However, this effect is already accounted for in the prediction of fertility indices by fitting genetic groups in the sire model with pedigree. Using both of these effects would result in some confounding.

Including nonadditive effects in the model, on average, caused a very slight and unfavorable change in the index and its components (Table 4). The mean value for CI increases (0.16 d), and NR56 decreased. The stan-
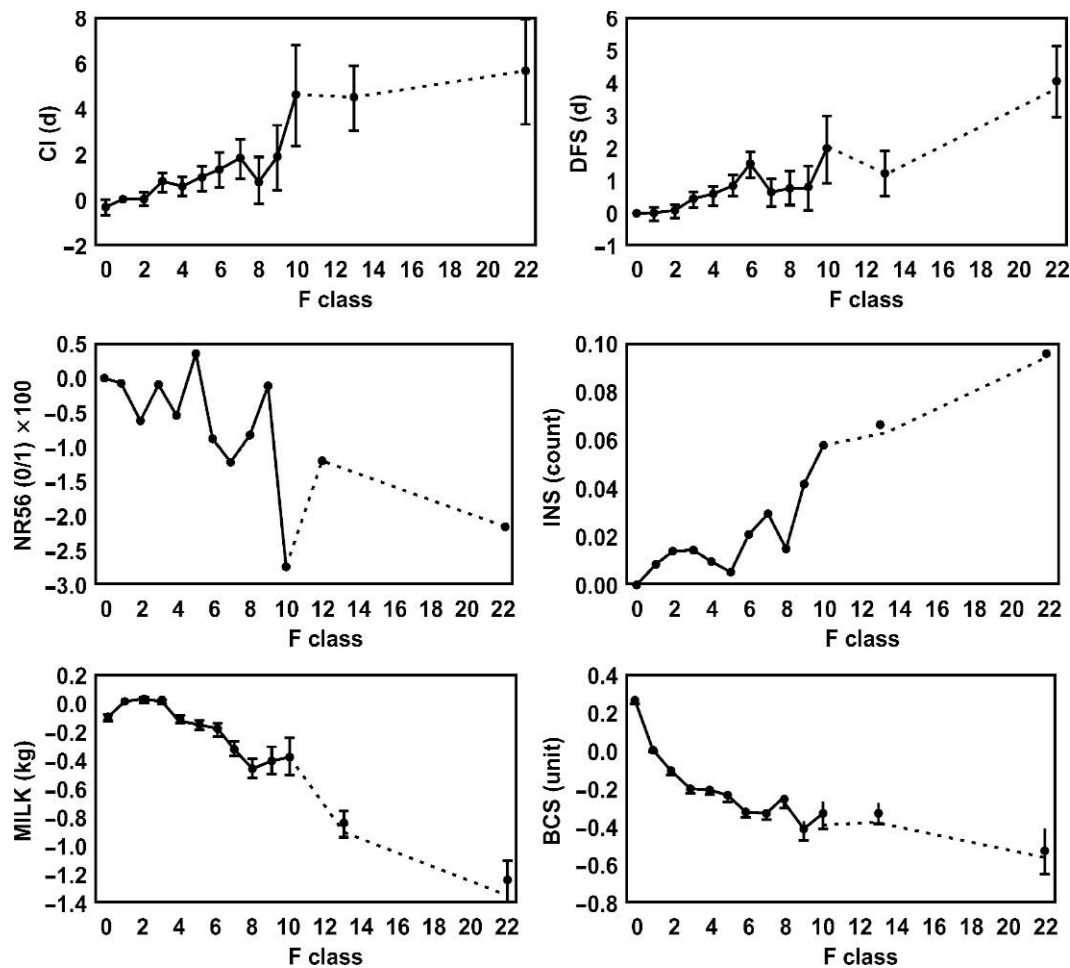
Figure 3. Effect of inbreeding class (plotted against the class midpoint) on calving interval (CI), days to first service (DFS), nonreturn rate (NR56), number of inseminations (INS), BCS, and milk at test d 110 (MILK). For NR56 and INS, unable to estimate a SE.

dard deviation of the PTA for each trait was slightly larger with the inclusion of the nonadditive genetic effects in the model. However, there was little change in overall rank of animals by fitting these additional effects in the model. The rank correlations between the trait PTA calculated with the nonadditive effects fitted in the model and trait PTA calculated without the nonadditive genetic effects fitted in the model were consistently >0.99. Although overall ranking of bulls remained relatively unchanged, the change in position of

Table 4. Changes in the mean and SD of the PTA when significant nonadditive effects are included or not included to the model of the trait. Rank correlation between PTA with or without nonadditive genetic effects in the model (corr).

| | Nonadditive effects | | | | |
| | Included | | Not included | | |
	Mean	SD	Mean	SD	Corr
Calving interval (d)	1.04	3.46	0.88	3.40	0.997
Days to first service (d)	0.61	2.39	0.54	2.37	0.999
Nonreturn rate (0/1)	−0.0068	0.0199	−0.0064	0.0197	0.999
Inseminations (no.)	0.010	0.041	0.009	0.041	0.997
Body condition score (1 to 9 scale)	−0.12	0.33	−0.11	0.32	0.996
Milk at test nearest d 110 (kg)	0.45	1.47	0.45	1.48	0.999
Fertility index (£GBP)	−1.39	3.70	−1.27	3.64	0.999

some individual bulls was considerable. Some bulls (out of 2000) dropped in ranking more than 90 positions, and others moved up more than 60 places when ranked on the fertility index.

For currently (October 2003) available bulls (ranked on the national profit index, £PLI) in the UK, the rank correlation in the fertility index with or without nonadditive genetic effects in the model was very close to unity. None of the top 100 bulls dropped more than 4 places or rose more than 5 places with the inclusion of nonadditive effects in the models.

DISCUSSION

Inbreeding depression was observed for all fertility traits, but significant heterosis between Friesian and Holstein was observed only for CI and DFS. The magnitude of the effect of inbreeding and heterosis in relation to the mean or the phenotypic standard deviation was smaller than for MILK and BCS, and when included in the model used for genetic evaluation, this impact on the ranking of bulls was negligible. At the current levels of inbreeding, losses in production caused by inbreeding depression were likely to have been offset by genetic gain. Nevertheless, inbreeding can reduce performance in traits not currently considered in selection indices in the UK, such as fertility traits.

Miglior et al. (1995) found that 10% inbreeding caused a 4% decrease in the phenotypic mean of total lactation yield. This analysis found a smaller effect of inbreeding depression on MILK, with a 2.3% decrease in the phenotypic mean for each 10% rise in inbreeding. Smith et al. (1998) found that inbreeding depression increased CI by 2.6 d per 10% rise in inbreeding, similar to the 2.8 d seen with this analysis. Cassell et al. (2003) found a nonsignificant effect of inbreeding on days to first insemination. However, Hoeschele (1991) found that each 10% rise in inbreeding caused a 1.3-d increase in days open, much closer to the significant 1-d increase in days to first insemination seen here. Weiner et al. (1992) showed that conception at first service in sheep declined by 4.2%, with a 10% rise in inbreeding, compared with the 0.6% increase in animals returning to first service observed in this study. In the current study, the impact of inbreeding on BCS (6.1% of the mean for a 10% rise in inbreeding), when expressed as a proportion of the phenotypic standard deviation (16.3%), was similar to results described by Falconer (1989) for BW in pigs (15%), litter size in mice (23%), and milk yield in cattle (17%).

The genetic trend in MILK from 1980 to 2000 was 2.7 kg in daily milk yield at d 110 (Wall et al., 2003). Inbreeding seemed to have a slightly favorable effect (nonsignificant) on MILK for animals in inbreeding classes 1 to 3, suggesting that inbreeding has improved MILK by 0.015 kg in the past 20 yr. A similar trend was seen for test day milk after d 70 in the American Holstein population (Thompson et al., 2000a). Figure 2 shows how inbreeding increased with time, as has genetic merit for production. Therefore, in the past 2 decades, cow inbreeding has increased as well as their genetic merit, and this could be a reason for the estimated favorable effect of low inbreeding on MILK. Modeling all of the nonadditive and additive effects (and trends) precisely may be difficult, and this problem could at least partially explain this apparent artifact resulting in a favorable effect of low inbreeding on production. However, if inbreeding in the UK continues to rise in line with the US, more animals will be in the higher inbreeding classes. Thus, in 10 yr (following current trends), inbreeding will have a negative effect on MILK, reducing it by 0.12 kg.

This study examined the effects of inbreeding in a population with relatively low levels of inbreeding and a historically low rate of inbreeding. Other studies have shown that as animals move into these higher inbreeding classes and the rate of inbreeding increases, the effects on overall performance are much larger than observed in this study. For example, Weiner et al. (1994) showed an almost linear decline in overall profitability in sheep (£1.27) with each percentage rise in F in rapid inbreeding.

Interestingly, the effects of Friesian genetics were favorable for all traits (3 to 7% better fertility than for the Holstein) except MILK, where the Holstein had a 13% benefit over the Friesian. The effect of heterosis MILK, CI, and DFS was low (0.5 to 1.4%). Other studies have found much higher effects of heterosis of the order of 9 to 20% for fertility and productivity traits (e.g., McAllister et al., 1994) but generally in crosses of more diverse breeds (e.g., Holstein × Ayrshire). The effect of recombination loss was as expected for MILK, with the favorable heterosis being lost because of recombination and, therefore, breakdown of the epistatic effects between the genes with additional crossing. Brotherstone and Hill (1994) saw a similar pattern attributable to crossing for lactation yields for 5 lactations; for example, heterosis resulted in a 100-kg increase of first lactation milk, with recombination resulting in a 156-kg loss. Some studies have shown a negative effect of recombination on fertility traits (e.g., Koenen et al., 1994). Distl et al. (1998) showed a favorable recombination effect on days open, which agrees with our results.

To date, no countries include inbreeding in the genetic evaluation model for production or fitness traits (INTERBULL, 2003). This may have to change if inbreeding continues to rise in dairy populations and the effects of inbreeding depression become more pro-

nounced, but this may require a review of the presentation of breeding values. For example, if bull A has all daughters with F = 12.5% and bull B has daughters with F = 0%, accounting for inbreeding depression by adjusting all individuals to a common F (e.g., F = 0 or the mean of the population) would improve the estimated breeding value of bull A relative to B. However, this may be misleading if A is more related to the population, as the offspring of A will be expected to display greater inbreeding depression than those of B. This presentational problem can be resolved by reference to the definition of breeding value (Falconer, 1989) and, hence, transmitting ability. Thus, the transmitting ability of an individual is the difference between the mean performance of its offspring and the population mean, assuming random mating. With this definition, it is clear that an individual male's PTA should be estimated at an F equal to its coefficient of coancestry with the population of breeding females. Thus, for presentation, each individual PTA is adjusted to a different value of F.

It is important that this adjustment for presenting breeding values is not confused with the separate task of managing genetic variation and the rate of inbreeding in the population. Studies have examined the optimization of contributions of selection candidates for maximizing genetic gain at a given rate of inbreeding in dairy cattle (Weigel and Lin, 2002; Kearney et al., 2004). This would have the most effect when combined with the selection of bulls and bull dams by breeding companies, since this is a) the subpopulation that is critical for managing the long-term gene flow and b) where the contributions of the bulls and dams of greatest impact can be most easily managed. Such decisions should be based upon the group coancestry of all breeding males and females, including coancestry among the breeding males and among the breeding females, and not upon the inbreeding coefficient of the offspring. This cannot be achieved by individual breeders, as they have little control over the total contributions of individual animals to the population and can only be achieved by the cooperation of worldwide breeding organizations. Some help can be given to breeders to minimize the impact of inbreeding depression in their herd. Breeding companies can recommend matings that avoid related individuals, which can be done by providing information on the expected inbreeding of daughters.

The differences between Holsteins and Friesians in the UK are accounted for in genetic evaluations of production traits by dividing founders in the pedigree into genetic groups and including heterosis and recombination loss coefficients in the model of analysis. This accounts for the benefits and costs in crossing the 2 breeds, as occurs frequently in the UK dairy population.

Crossbreeding of dairy breeds is practiced by a small proportion of dairy farmers in many countries across the world to capture the benefits of the heterosis in F_1 populations and the epistatic interaction of genes of purebred animals. Ideally, this practice should be part of a population-wide controlled program of breeding, maintaining both pure and crossbred populations. However, implementation of genetic evaluation procedures that allow for the full exploitation of the advantages of crossbreeding may prove difficult, as it would require the estimation of and accounting for relevant genetic parameters of fixed breed, heterosis, and recombination effects for all crosses (Swan and Kinghorn, 1992). The estimates of the effect of heterosis will be different depending on the 2 purebreds in question. This study showed a small heterotic advantage of a crossbred progeny over that of the average of purebred Holsteins and Friesians. Brotherstone (personal communication, 2004) also found small heterotic effects for the majority of traits of interest and only found useful heterosis in SCS for various crosses in the UK. The estimation of each of the nonadditive effects between each potential cross of breeds in a country is a large task but essential to allow for the development of crossbreed and multibreed evaluations.

The approach to the presentation of PTA accounting for F (described earlier) could be extended to the other forms of nonadditive variation discussed in this paper, such as heterosis and recombination loss; however, the advisability of this is more dependent on the breeding system in which the multiple breeds are used. In a population that is subject to breed substitution and otherwise unmanaged interbreeding, it may be appropriate to consider presentation of breeding values adjusted to expected levels of heterosis or recombination loss arising from random mating. However, where crossbreeding systems are more tightly managed, this practice would be less inappropriate, and more direct predictions of crossbred performance would be more informative.

CONCLUSIONS

Nonadditive effects of inbreeding, heterosis, recombination loss, and percentage Holstein were shown to have a significant effect on some or all of the traits used in the UK Fertility Index. On closer examination, it was shown that the effect of inbreeding was more severe at higher levels of inbreeding than at lower levels. This study provided little support for the hypothesis that reproductive traits in dairy cattle were more strongly influenced by nonadditive genetic variation than were traits associated with milk production. It is the recommendation of this study that inbreeding and other sig-

nificant nonadditive effects be accounted for in the models of evaluation for fertility and production traits. However, it may not be possible to assign all animals an accurate inbreeding coefficient as a result of missing pedigree, and the presentation of results may be difficult in practice. At current rates of inbreeding, a greater proportion of animals will soon be in the higher inbreeding classes, where the effect of inbreeding in the evaluations will be more pronounced. Steps should be taken to control this rise in inbreeding, or the effects on fertility and correlated traits such as milk production could be detrimental.

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