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Development of new fertility breeding values in the dairy industry

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ABSTRACT

This paper provides the basis for a new method for calculating fertility breeding values. The objective of this study was to: firstly, investigate the data extract of mating and calving records from Livestock Improvement's national database to identify improvements, secondly investigate the definition of the fertility trait from percent of calves born from artificial insemination (AI) to 42 day calving rate, and thirdly explore the inclusion of milk production and body condition score information. The overall aim was to improve the accuracy of the fertility breeding values available when a sire's daughters have completed their first lactation (i.e., the time of the sire's first proof). A new procedure for routine national evaluation of these traits is outlined. Results from the new system are given. Possible future enhancements to the new system are discussed. The new method improves the accuracy of the fertility breeding value for first crop sires with 80 daughters from 45% to 52%. The inclusion of body condition score and milk production in the calculation of the fertility breeding value improves the response to selection for fertility within breeding worth index by 34% per annum. The improvement in response to selection is worth 0.18 \$/cow/year or approximately \$700,000 annually to the dairy industry.

Keywords: Fertility; genetic evaluation; multi-trait model; dairy cows.

INTRODUCTION

Maintaining good cow fertility is a fundamental component in the way in which farm systems operate in a seasonal environment. The type of farming system requires concentrated calving pattern which is achieved both by a high insemination rate and a high conception rate (Xu and Burton, 1996). Commonly used measures to assess the overall reproductive performance of seasonally mated herds are in-calf and empty rates. Reproductive performance is determined by the submission pattern and conception rates achieved for artificial and natural breeding during the mating period. Submission rates are a function of both heat detection efficiency and the proportion of cows cycling.

A large number of studies from many countries have reported a decrease in the fertility of dairy cows. In the United States, the conception rate at first insemination has decreased by 0.45% per year over a twenty year period (Beam and Butler, 1999) and the number of inseminations required for conception, has increased from 1.75 to more than 3 over a period of 20 years (Lucy, 2001). Similarly, at first insemination a decrease of the approximately 1% per year in the conception rate has been reported in the UK (Royal *et al.*, 2000). Also, the Netherlands have reported a decrease in the conception rate at first insemination from 55.5% to 45.5% over a 10 period (Jorristma *et al.*, 2003.) However, the reproductive performance of

cows in New Zealand (NZ) is generally considered higher than most non-seasonal dairying countries with conception rates of around 60% being commonly reported (Xu and Burton, 1996) compared to about 50% in countries with predominantly non-seasonally calving herds (e.g. Royal *et al.*, 2000). However, there are no reports showing the national trends in the fertility of cows in New Zealand over the last ten-year interval.

The existence of negative genetic correlations among production and fertility could lead to erosion of cow fertility from continual selection for production (Grosshans *et al.*, 1997; Harris *et al.*, 2000; Harris and Pryce, 2004). Consequently, a number of countries including New Zealand have now broadened their selection objectives to include fertility as a separate trait to limit the negative effect on fertility of selecting for milk production alone. Since 2001, New Zealand has included cow fertility in the national breeding objective, Breeding Worth Index.

Body condition score (BCS) has been suggested as a suitable selection criterion for genetic improvement of fertility (Pryce *et al.*, 2000). Harris and Pryce (2004) reported genetic correlation estimates between BCS and percent of cows mated in the first 21 days after the planned start of mating (PM21) and percent calves born to artificial insemination (CAI) to be 0.48 and 0.38, respectively. These correlations along with a higher heritability for BCS, 0.20, compared to fertility traits, 0.02-0.05, make BCS a useful additional

predictor in a multiple-trait fertility model. Also, a milk production trait could be used to increase the accuracy of the fertility breeding values due to the negative genetic correlation between fertility and milk production. The negative genetic correlations between production and fertility estimated using NZ data (Grosshans *et al.*, 1997; Harris *et al.*, 2000; Harris and Pryce, 2004) are greatest in magnitude for milk volume yield. Milk volume is the logical choice of production trait as an additional predictor in a multiple-trait model for estimating the fertility BV.

The objectives of this study were to: review rules for a new national fertility data extract and redefinition of the fertility traits; use the national fertility data extract to provide national statistics on cow fertility; explore the use of BCS and milk volume yield as predictors in a multiple-trait model for estimating the fertility BV; and develop a new national fertility evaluation system.

MATERIALS AND METHODS

Data

Survival, milk production, body condition score, mating and calving records were extracted from the NZ national database. The extract was done in April 2005 and included all herd test milk records from 1987 onwards. All mating and calving records from 1990 were included in the extract, records prior to 1990 were excluded due to data quality issues. The previous national data extract for fertility has several restrictions; for a given parity PM21 had to be present but CAI could be coded as missing; for a CAI record to be valid a sire record for the calf born is required. These restrictions were removed when the data was extracted from the National database for this analysis. Included in the data were the date of first mating and the calving date at the start of the subsequent parity. Only records from first to third parity were included. Not all cows had all traits recorded. Contemporary groups were defined on a parity-herd-season-year basis. Season was defined as spring or autumn calving. Pedigree and breed data were extracted from the Animal Evaluation routine genetic evaluations for production. Ancestors were traced back to 1939. Animals born before 1960 were considered to be the base population. Culling records were used to fill in missing calving records for cows culled for fertility reasons in the appropriate year-season.

Days to first mating (DFM) from the planned start of mating is a practical measure to use as a proxy for submission rate. DFM is recoded to a binary trait according to whether the cow was presented for mating in the first 21 days after the

start of mating. This binary trait is abbreviated to PM21. If DFM was not recoded and the number of days were used, cows who cycle early relative to the start of mating would be given credit which would be incorrect since, a cow's ability to cycle within a 21 day period is a random chance event. The previous extract used calves born to artificial insemination as the calving trait. This trait definition requires the identification of the sire for each calving and restricts the amount of calving data used in the analysis. The calving rate trait was redefined as the failure or success of calving in the first 42 days after the planned start of calving (CR42). The CR42 trait was used as the in-calf rate fertility measure. Forty-two day calving rate is a commonly used management measure to evaluate reproductive performance and is well understood by farmers, whereas, CAI is difficult to explain. Compared to the current data set used for national evaluation the effects of removing the restriction on requiring a PM21 record and a valid sire record for the mating has resulted in a considerable increase (17%) in the quantity of data.

Genetic Parameter Estimation

The data for the variance component analyses was a subset of the dataset described above containing Livestock Improvement's Sire Proving Scheme (SPS) herds in the years 1990 to 2004. First-, second- and third- lactation fertility, first lactation milk volume and first lactation body condition score records on a total of 221,224 cows were used for this study. The breed composition of the cows was 1% Ayrshires, 52% Friesians, 22% Jerseys, and 25% crosses of these breeds. A sire-maternal-grandsire model that included all eight traits simultaneously allowing for missing data was used. The estimation of (co)variance components used restricted maximum likelihood with a multivariate linear sire model using the average information algorithm of Johnson and Thompson (1995). There were 4270 sires in the pedigree.

Statistical Model for National Genetic Evaluation

A multiple-trait (MT) animal model was used for the national genetic evaluation of fertility on the entire dataset. The model could cope with missing data on any combination of traits. The model used 8 traits; 270 day milk volume yield, BCS parity 1, PM21 parity 1, CR42 parity 1, PM21 parity 2, CR42 parity 2, PM21 parity 3, CR42 parity 3. The BCS records were pre-corrected for stage of lactation at the time of measurement.

Each individual trait record was modelled as:

$$y_{ijkno} = hysa_{ij} + age_{ik} + \sum_{s=1}^6 ht_{is} w_{ns}^h + \sum_{s=1}^6 rc_{is} w_{ns}^r + a_{in} + e_{ijkno}$$

where

- y_{ijkno} is the record for i th trait,
- $hysa_{ij}$ is the j th herd-year-season-age fixed effect for trait i , with season referring to spring or autumn calving period,
- age_{ik} is the age in days at calving covariate for parity k th for trait i ,
- ht_{is} is the linear regression coefficient for the s th heterosis effect for trait i ,
- w_{ns}^h is the s th heterosis covariate for animal n ,
- rc_{is} is the s th linear regression coefficient for recombination loss for trait i ,
- w_{ns}^r is the s th recombination loss covariate for animal n ,
- a_{in} is the random additive genetic effect of animal n for trait i ,
- e_{ijkno} is the random residual associated with record y_{ijkno}

Heterosis and recombination loss factors were fitted to account for the effects of crossbreeding, different factors were fitted by breed combination to account for different genetic distances among the major breeds. Genetic groups were assigned by breed, gender of missing parent, birth year and country of origin. Four breed classes were assigned genetic grouping, namely, Holstein-Friesian, Jersey, Ayrshire-Red, and other breeds. Genetic groups were assigned in 5-year intervals from 1960 to 1980 then yearly, with the first birth year group being prior to 1960. Country of origin was defined as NZ, North American and other. Gender of missing parent was defined as female or male. If a genetic group had less than 200 animals per group birth years were clustered. No clustering occurred across breed, origin or gender genetic groups. The mixed model equations were solved using a preconditioned conjugate gradient solver (Stranden and Lidauer, 1999) and iteration on data with code reordering (Tsurata *et al.*, 2001).

RESULTS

The average PM21 and CR42 across parities 1 to 3 based on 9,067,318 fertility records were 80.0% and 62.3%, respectively. The average PM21 and CR42 by season are shown in Figure 1. A declining phenotypic cow reproductive performance with time is evident for CR42 but not PM21 in Figure 1. It is likely that the improvement in CR42 since 2001 is a combination of improved management, climate and the effects of selection.

FIGURE 1: Phenotypic averages by season for percent mated in the first 21 days after the start of mating and the 42 day calving rate.

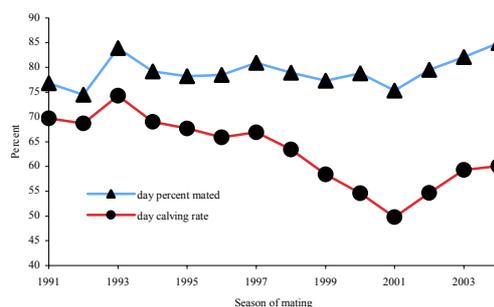


Table 1 provides the heritabilities, genetic and phenotypic correlations between the eight traits used in the national evaluation. They are consistent with those reported by Harris *et al* (2000), among fertility and BCS with those reported by Harris and Pryce (2004) among milk volume and fertility, and among fertility traits with those reported by Harris *et al* (2000). The magnitudes of the heritabilities are consistent with values reported in other countries.

TABLE 1: Heritabilities (diagonal), genetic (below diagonal) and phenotypic (above diagonal) correlations between the six fertility traits, milk volume and body condition score.

	Milk	BCS	PM21 ¹	CR42 ¹	PM21 ²	CR42 ²	PM21 ³	CR42 ³
Milk	0.308	-0.088	-0.017	-0.008	-0.033	-0.008	-0.021	-0.013
BCS	-0.071	0.187	0.112	0.06	0.066	0.038	0.052	0.027
PM21 ¹	-0.167	0.461	0.05	0.135	0.137	0.056	0.092	0.027
CR42 ¹	-0.163	0.357	0.896	0.022	0.071	0.071	0.029	0.048
PM21 ²	-0.233	0.429	0.915	0.821	0.05	0.179	0.148	0.053
CR42 ²	-0.165	0.441	0.753	0.856	0.724	0.026	0.082	0.084
PM21 ³	-0.234	0.492	0.845	0.816	0.918	0.725	0.036	0.147
CR42 ³	-0.176	0.24	0.632	0.764	0.668	0.832	0.689	0.015

¹Parity 1

²Parity 2

³Parity 3

TABLE 2: Summary statistics for 42 day calving rate and percent calves born to artificial insemination sire breeding values.

42 day calving rate sire breeding values					
	Number	Mean	Standard Deviation	Minimum	Maximum
All Breeds	20449	-2.05	5.33	13.6	-29.7
Holstein-Friesian	10185	-3.02	5.61	11.6	-28.7
Jersey	7484	0.72	2.63	13.6	-13.8
Ayrshire	1562	-6.98	6.15	11.7	-29.7
Other Breeds	1188	-2.03	5.46	11.3	-26.4

Percent calves born to artificial insemination sire breeding values					
	Number	Mean	Standard Deviation	Minimum	Maximum
All Breeds	20449	-1.04	3.61	14.6	-24.9
Holstein-Friesian	10185	-1.98	3.68	12.6	-24.9
Jersey	7484	0.76	2.07	12.0	-17.9
Ayrshire	1562	-3.55	3.15	14.6	-24.8
Other Breeds	1188	-1.07	3.45	7.4	-17.1

The estimates for breed heterosis from the national evaluation analysis show that the first cross HFxJersey cow has an advantage of 4.3% PM21 and 3.4% CR42 compared to the average of the parental breeds for first parity. Results for parities 2 and 3 show a similar advantage to the HFxJersey cow. A bi-modal distribution for enrolled Holstein Friesian sires was observed due to the mixture of NZ Friesian and Holstein sires. When the distributions are graphed within categories of percentage Holstein they resemble normal distributions as shown in Figure 2. A within and across breed summary statistics for sires and a comparison with the current CAI fertility BV and the first parity CR42 BV is given in Table 2. Comparing the first parity CR42 BV with the first parity CAI BV from the January 2005 national evaluation for enrolled sires it can be seen that the CR42 BV had a greater standard deviation (5.33) compared to the CAI BV (3.61). The increase in standard deviation is due to the increased reliability for CR42 BV from increased fertility records and contributions from correlated traits. The genetic trend for first parity CR42 by breed for the cow population is given in Figure 3. The improvement in the genetic trend in the HF breed since concedes with a marked reduction in the use of 100% Holstein proven sires.

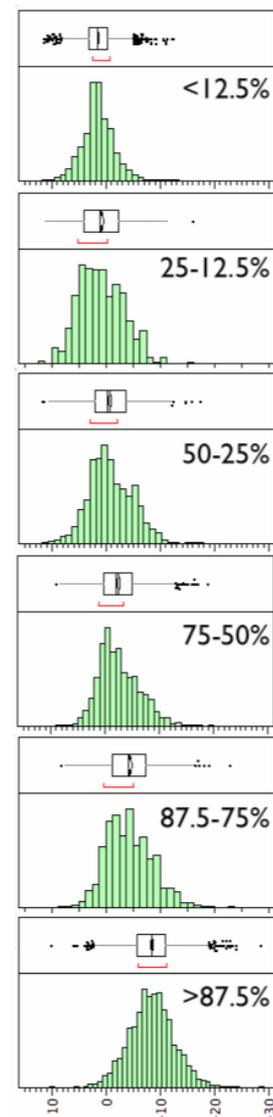
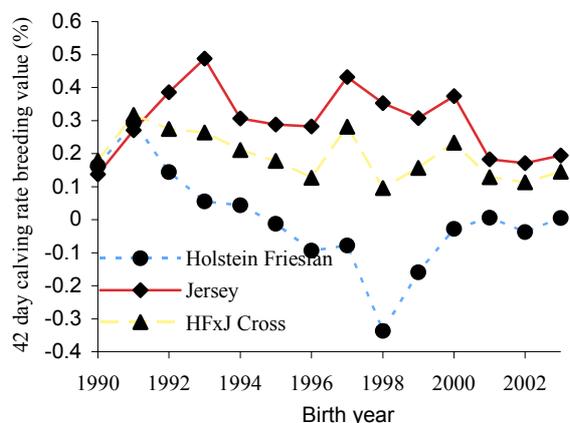
FIGURE 2: Estimated breeding values for first parity CR42 (%) by percentage overseas Holstein of enrolled Holstein Friesian sires.

FIGURE 3: Genetic trend for 42 day calving rate in the national cow population.



DISCUSSION

The phenotypic averages from national database show a decline in CR42 that is consistent with a number of studies from many countries reporting similar trends in dairy cow fertility. The figures in the graph exclude the calving data from first calving heifers and include the information on cows culled for infertility. Thus, the CR42 rates achieved on farm will be higher by approximately 10%.

Changing the calving-rate trait definition from CAI to CR42 decreased the amount of data exclusion in the national fertility analysis. The results from the national analysis with the new data show that the sires with larger percentages of overseas Ayrshire and overseas Holstein genes on average had a greater percent of calving records excluded in the CAI BV calculations due to missing PM21 records or problems with sire determination of the resulting calf. Subsequently, these sires show the largest change in their CR42 BV compared to their CAI BVs. Figure 2 shows a declining fertility with increase percent of overseas Holstein genes in the Holstein-Friesian sires. The magnitude of the difference is consistent with fertility results from the Dexcel strain trail (Macdonald et al, 2005).

The multiple trait fertility model provided improved accuracy than the current fertility evaluation as a result of including a greater number fertility records and inclusion of BCS and milk volume traits. The use of a multiple trait model improved the reliability of the breeding values from 45% to 52% for first proof sires. The increases in reliability are consistent with those calculated from selection index theory. The response to selection from using CR42 in place of CAI in the BW index

was calculated. Inclusion of body condition score and milk production in the calculation of the CR42 fertility breeding value improves the response to selection for fertility within breeding worth index by 34% per annum. The improvement in response to selection is worth 0.18 \$/cow/year or approximately \$700,000 annually to the dairy industry.

A new method for estimating fertility breeding values has been developed that includes information on correlated traits; milk volume and body condition score; in addition to fertility records. The model improved the accuracy of the estimated breeding values and should improve the response to selection for fertility under BW.

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