

Fertility Breeding Values in New Zealand, the Next Generation

B. L. Harris, J. E. Pryce, Z. Z. Xu and W. A. Montgomerie

*Livestock Improvement Corporation Ltd,
Private Bag 3016, Hamilton, New Zealand*

Introduction

The reproductive performance of cows in New Zealand (NZ) is generally higher than most nonseasonal 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). The better reproductive performance of NZ cows is due to differences in management, milk production, nutrition, heat detection accuracy and breed composition including crossbreeding.

In seasonal production systems, good fertility is a fundamental part of the way in which farm systems operate. Feed requirements for production are matched to pasture supply on the majority of farms and an important management strategy is to have a single concentrated seasonal calving pattern so that feed usage is optimised. A concentrated calving pattern is achieved both by a high insemination rate and a high conception rate (Xu and Burton, 1996). In most countries the driver behind broadening breeding goals to include fertility has been the unfavourable genetic correlation with milk production. Although dairy cow fertility in New Zealand is good by international standards, selection for production could erode this advantage (Grosshans *et al.*, 1997; Harris *et al.*, 2000; Harris and Pryce, 2004). In-calf and empty rates are commonly used to assess the overall reproductive performance of seasonally mated herds. The submission pattern and conception rates achieved for artificial and natural breeding during the mating period determine performance. Submission rates are a function of both heat detection efficiency and the proportion of cows cycling. Days to first mating (DFM) 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 planned start of mating. This binary trait is abbreviated to PM21. A calving rate

trait (CR42) measured as the failure or success of calving in the first 42 days after the planned start of calving 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.

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 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 compared to fertility traits 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 redefine CAI as CR42; 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.

Data

The current 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 Livestock Improvement national dairy herd 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. 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. The mean PM21 has been reduced by using the CR42 and culling data to fill missing values for low fertility cows.

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

Genetic Parameter Estimation

Data for the variance component analyses were obtained from 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. Table 1 provides the heritabilities, genetic and phenotypic correlations between eight traits. They are consistent with those reported by Harris *et al.* (2000) among fertility and BCS consistent with those reported by Harris and Pryce (2004) among milk volume and fertility, and among fertility traits consistent with those reported by Harris *et al.* (2000).

Statistical Model for National Genetic Evaluation

The model for the national genetic evaluation of fertility is a multiple-trait (MT) animal model containing 8 traits where 270 day milk volume yield, BCS, PM21 parity 1, CR42 parity 1, PM21 parity 2, CR42 parity 2, PM21 parity 3, CR42 parity 3 are modelled as traits 1 to 8, respectively. The BCS records are pre-corrected for stage of lactation and type of scorer (liveweight operator or type score).

An individual trait record was modelled as:

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

where

y_{ijkno} is the record for ith trait, i denotes trait 1 to 8,

$hysa_{ij}$ is the jth 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 kth for trait i ,

ht_{is} is the linear regression coefficient for the sth heterosis effect for trait i ,

wh_{ins} is the sth heterosis covariate for animal n ,

rc_{is} is the sth linear regression coefficient for recombination loss for trait i ,
 wr_{ins} is the sth 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}

For the national fertility evaluation, 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.

Computational Strategy

The mixed model equations (MME) were solved using a preconditioned conjugate gradient solver (Stranden and Lidauer, 1999) and iteration on data with code reordering (Tsurata *et al.*, 2001). The convergence criteria for the MME was $<10^{-10}$ which required close to 1000 iterations and 30.5 hours processing time on a 2.2 Ghz AMD Opteron CPU.

National Evaluation Results

The distributions of BVs for first parity CR42 obtained across all breeds from sires enrolled in the national evaluation program are given in Figure 1. Table 2 provides within and across breed summary statistics for sires and a comparison with the current CAI fertility BV. 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 resembled normal distributions (Figure 2). The genetic trend for first parity CR42 by breed for the cow population is given in Figure 3. The first parity

CR42 BV was compared with the first parity CAI BV from the January 2005 national evaluation for enrolled sires. The CR42 BV had a greater standard deviation (5.33) compared to the CAI BV (3.61) which is due to the increased reliability for CR42 BV from increased fertility records and contributions from correlated traits. 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 missing valid sire records for the calving of their daughters and subsequently show the largest change in their CR42 BV compared to their CAI BVs. On average the reliability has increased from 34% to 42% and the 75% reliability quartile value increased from 52% to 68.8%. The increases in reliability are consistent with those calculated from selection index theory.

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. It is planned to implement the multiple trait fertility model in July 2005.

Table 2. Summary statistics for estimated breeding values for sires enrolled in the national evaluation.

	New National Evaluation CR42				
	Number	Mean	Standard Deviation	Maximum	Minimum
Across Breed	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 [†]	1188	-2.30	5.46	11.3	-26.4
	Current National Evaluation CAI [‡]				
	Number	Mean	Standard Deviation	Maximum	Minimum
Across Breed	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	6.15	14.6	-24.8
Other [†]	1188	-1.07	3.45	7.4	-17.1

[†] Predominantly Shorthorn, Guernsey and Brown Swiss

[‡] January 2005

References

- Grosshans, T., Xu, Z.Z., Burton, L.J., Johnson, D.L. & MacMillan, K.L. 1997. Performance and genetic parameters of fertility of seasonal dairy cows in New Zealand. *Livest. Prod. Sci.* 51, 41-51.
- Harris, B.L., Winkelman, A.M. & Burton, L.J. 2000. Comparisons of fertility measures in strains of Holstein-Friesian cows and their crosses. *Massey Dairy Farming Annual*.

- Harris, B.L. & Pryce, J.E. 2004. Genetic and phenotypic relationships between milk protein percentage, reproductive performance and body condition score in New Zealand dairy cattle. *N. Z. Soc. Anim. Prod.* 64, 127-131.
- Johnson, D.L. & Thompson, R. 1995. Restricted maximum likelihood estimation of variance components for univariate models using sparse matrix techniques and average information. *J. Dairy Sci.* 78, 449.
- Pryce, J.E., Coffey, M.P. & Brotherstone, S. 2000. The genetic relationship between calving interval, condition score and linear type and management traits in registered Holstein dairy cows. *J. Dairy Sci.* 83, 2664-2671.
- Royal, M.D., Darwash, A.O., Flint, A.P.F., Webb, R., Woolliams, J.A. & Lamming, G.E. 2000. Declining fertility in dairy cattle: changes in traditional and endocrine parameters of fertility. *Anim. Sci.* 70, 487-501.
- Stranden, I. & Lidauer, M. 1999. Solving large mixed linear models using preconditioned conjugate gradient iteration. *J. Dairy Sci.* 82, 2779-2787.
- Tsuruta, S., Misztal, I. & Strandén, I. 2001. Use of the preconditioned conjugate gradient algorithm as a generic solver for mixed-model equations in animal breeding applications. *J Anim Sci.* 79(5), 1166-72.
- Xu, Z.Z. & Burton, L.J. 1996. Reproductive efficiency in dairy cows. *Proc. N. Z. Soc. Anim. Prod.* 56, 34.

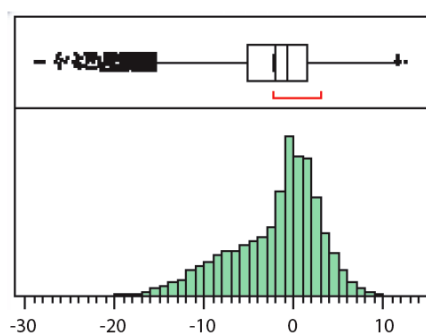


Figure 1. Estimated breeding values for first parity forty-two day calving rate (%) of enrolled sires.

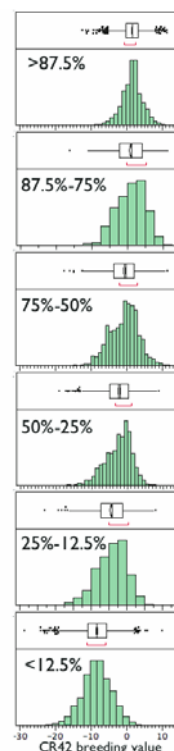


Figure 2. Estimated breeding values for first parity CR42 (%) by percentage NZ Friesian of enrolled Holstein Friesian sires.

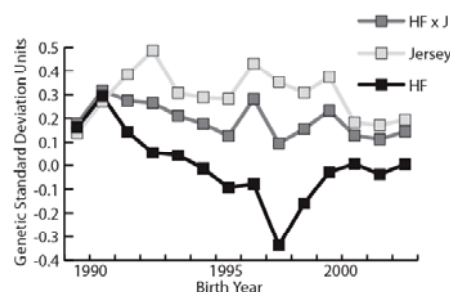


Figure 3. Forty-two day calving rate genetic trend by breed of cow.