Fertility Breeding Values for Seasonal Dairying

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Introduction

Most dairy farms in New Zealand use a low input, pastoral feeding system. Feed demand is matched with the seasonal pasture supply by achieving a single concentrated seasonal calving pattern. The objective for herd reproductive performance is to achieve high pregnancy rates in a short time period following the planned start of mating, and to maintain calving intervals very close to 365 In this type of system, successful davs. reproduction depends on two factors which display genetic variation. The first factor is the ability of the cow to resume cycling soon after calving, and to be mated early in the herd's mating period. The second factor is the cow's ability to conceive, sustain a pregnancy and calve early in the herd's subsequent calving period. The objective of this research project was to develop a genetic evaluation of cow fertility that incorporated both these aspects of successful reproductive performance in seasonal dairying.

Material and Methods

Trait Selection

Prior studies identified substantial genetic variation in the ability of cows to be presented for mating early in the herd's mating period (Grosshans et al., 1997). Substantial genetic variation in the ability of cows to calve early in the herd's calving period was also identified (Harris et al., 2000). Binomial traits were defined for national evaluation. Days to first mating (DFM) was scored 1 for the cows that were mated in the first 21 days of the mating period of the herd-year-season, and 0 for cows which failed to be mated in the first 21 days of the herd's mating period.

Standard practice in New Zealand is to present cows for artificial insemination (AI) for a period of approximately 30 days from the commencement of mating. After this period, natural service bulls are pastured with the herd. In these circumstances, successfully bearing a calf to artificial insemination (CAI) is a close proxy for calving early in the herd's calving period. CAI was scored 1 for cows which successfully sustained an AI pregnancy through to calving.

Only records from first to third parity were included. Consequently the analysis proceeded with six traits – DFM in the first three parities, and the associated CAI in the second, third and fourth lactations.

National Evaluation Data

In the national data 57% of cows have greater than ³⁄₄ Holstein-Friesian ancestry, 20% are Holstein-Friesian Jersey crossbred, 18% have greater than ³⁄₄ Jersey ancestry, 3% are crossbreds involving breeds other than solely Holstein-Friesian and Jersey, and 2% have greater than ³⁄₄ Ayrshire ancestry. Mixed breed herds are common. Average herd size has exceeded 160 cows in each year since 1990, and currently exceeds 240 cows.

Data was extracted from mating and calving records from 1990 to February 2001. To determine the date of the planned start of mating in a herd-year-season the date of mating records were sorted in ascending order. In a normal herdvear-season, approximately one third of the cows are expected to be mated within the first week of the herd's planned mating period. The numbers of cows mated in each week for each herd-yearseason were calculated. This number was the observed value in the Chi-square test. The expected value was set to one third of all the cows in the herd-year-season. If the Chi-square statistic had a probability of more than 0.01 with 1 degree of freedom, records in this week were considered as data errors and not used to determine the planned start of mating. After the planned start of mating was determined for each herd-year-season, the mating dates for each cow were expressed as deviations from the appropriate planned start of mating.

After editing there were 9,610,501 records for DFM. The mean days from the herd's start of mating to the cow's first recorded mating was 12.7 with a standard deviation of 9. DFM was taken as a binomial trait even though the underlying data is recorded in days. An interval of 2 days between the herd's planned start of mating and the cow's first mating does not necessarily imply superior fertility compared to an interval of 18 days. In each case the cow has been presented for mating in the earliest possible period. The shorter interval reflects an accident of timing relative to the planned start of mating rather than a biological signal. In these circumstances it is preferable to take DFM as a binomial trait. This argument is also supported by the presence in the data of cows which have received unrecorded fertility treatments in order to be presented for mating very early in the herd's mating period.

CAI was coded "missing" for cows which left the herd prior to the calving period for reasons other than low fertility, or which had not yet had the opportunity to calve to the recorded mating. Nineteen per cent of CAI records were coded missing. Of the remainder, 72% were records of successful calving to artificial insemination.

Contemporary groups were defined on a parity-herd-year-season basis. Season was defined as spring or autumn calving. Ancestors were traced back to 1939. Breed information was available in 16ths for all animals.

Estimation of (Co)variance Components

Co(variance) components were estimated from a subset of the national data set, collected on cows in herds that participated in the Livestock Improvement Corporation's sire proving scheme in seasons 1990 through to 2000. There were 2534 sires in the pedigree with 125,252 daughters.

(Co)variance components were estimated with a multivariate linear sire model allowing for missing observations, using the average information algorithm of Johnson and Thompson (1995). The model was of the form:

y = herd-year-season-parity + heterosis + age-at-calving + sire + genetic group + error. Estimated heritabilities were 5% for DFM in first parity; 3% for DFM in later parities, and 2% for each CAI trait. Estimated genetic correlations between DFM and the associated CAI were 0.93, 0.84, and 0.44 for parities 1, 2, and 3 respectively.

National Multiple Trait Evaluation

All animal models were of the following form:

y = herd-year-season-parity + heterosis + age-at-calving + animal + genetic group + error.

Both linear and quadratic age-at-calving effects were fitted. To account for differences in mean genetic merit of unknown ancestors over time, common genetic groups for sires and dams were included as proposed by Westell et al. (1987). These genetic groups were based on birth year, breed, country of origin and sex of unknown parent.

Linear models were adopted. Testing with the subset of the data used for (co)variance component estimation, and using ASREML software (Gilmour et al., 2001), revealed that there was a greater loss of efficiency by adopting the feasible single trait logit models compared to the feasible multiple trait linear models.

There are no methods for utilising canonical transformation with missing data and different models per trait. To overcome the infeasibility of analysing all six traits simultaneously, three bivariate analyses were conducted (DFM and CAI analysed simultaneously within parity). The analyses utilise bivariate can canonical transformation with missing data since the model was the same for DFM and CAI within parity (Ducrocq and Besbes, 1993). The reliability of the breeding values was calculated using the method of Harris and Johnson (1998). For each sire the resulting CAI breeding values were combined using selection index procedures, and reported to the industry as a single sire breeding value (BV) for cow fertility. The reported BV relates to the comparative percentage likelihood of a bull's daughters re-calving for their second lactation in the herd's AI calving period.

Results

Marked additive genetic variation in the AI sires has been reported to the industry. A summary of the sire breeding values reported for AI sires born since January 1980 and with at least one daughter with a fertility record is shown in Table 1.

Table 1. Sire Breeding Values for Cow Fertility				
Ν	Max	Min	St	
	BV (%)	BV	Dev	
		(%)		
3417	10.4	-22.5	4.0	
1704	7.8	-10.3	2.6	
	N 3417	N Max BV (%) 3417 10.4	N Max BV (%) Min BV (%) 3417 10.4 -22.5	

National evaluation was consistent with the prior studies in revealing substantial heterosis effects for the fertility traits. Heterosis effects for Holstein-Friesian and Jersey first cross are shown in Table 2.

Table 2. Heterosis estimates,

Holstein-Friesian x Jersey, First Cross

Parity	DFM (%)	CAI (%)
1	3.8	3.5
2	3.2	2.8
3	2.3	2.5

Discussion

Some traits used for cow fertility evaluations in the Northern Hemisphere have limited applicability for New Zealand's intensively seasonal herd reproductive management system. For example, available mating records are very accurate during a herd's period of AI mating but often are less complete for the period after the AI matings have finished. For this reason, research projects with New Zealand data have found little genetic variation in non-return rate measures. For seasonal dairying, measures based on the interval from the planned start of mating to the first recorded mating are preferred to measures based on the interval from calving to first recorded Given the reproductive management mating. system, a short interval from calving to first service gives an ambiguous fertility signal. In the current season it serves as a positive fertility indicator. However, it is usually associated with a late calving date - which indicates impaired fertility in the previous season. Grosshans et al. (1997) found very low heritabilities and coefficients of genetic variation for the interval from calving to first service.

DFM in the first parity is the most highly heritable of the cow fertility traits investigated for New Zealand's seasonal dairying. Daughter information for DFM is available early in the life cycle of AI sires. The high genetic correlation between DFM in the first parity and the other cow fertility traits facilitates the provision of timely information by the national genetic evaluation system.

Cow fertility exhibits quite a large additive genetic variation despite its low heritability. This is demonstrated by Figure 1, which shows the distribution of sire BVs for the Holstein-Friesian and Jersey AI sires born from 1979 to 1995 and with two-year-old daughters commencing lactation since 1995. The greater variation in the Holstein-Friesian sires is partially attributable to the higher frequency of overseas genes in the national Holstein-Friesian population than in the national Jersey population (Harris and Kolver, 2001).

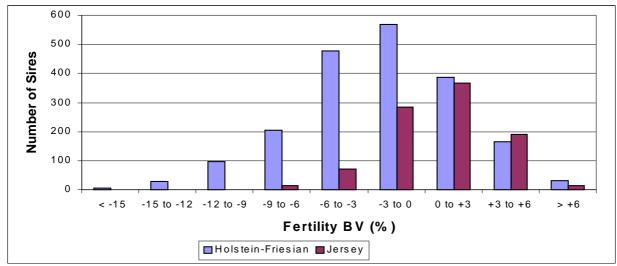


Figure 1. Distribution of sire breeding values for cow fertility

Conclusions

Female fertility traits based on the interval from the herd's planned start of mating to the cow's first service are appropriate for measuring reproductive performance of dairy cows in the New Zealand seasonal production system. Fertility traits based on the success of the cow in conceiving and bearing an AI calf are also appropriate in this system.

There is substantial genetic variation in these traits, and important differences in daughter reproductive performance can be reflected in sire breeding values while the sires are still active in the AI industry.

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