

New Approaches to Fertility Evaluation in a Seasonal Calving System

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Abstract

This paper describes the investigation of possible new approaches for fertility genetic evaluation in the New Zealand seasonal calving system. An earlier study using data from the National Herds Fertility Study database indicated that redefining the 0/1 binary trait for calving rate in the first 42 days of calving (CR42) to a continuous trait expressed as calving day relative to the calving start day (CSD) could significantly increase the accuracy of fertility traits estimates. This paper investigates alternative fertility trait definitions (calving rate and percentage mated), as well as alternative definitions of planned start of mating and calving using a much larger industry dataset than used in the earlier study. Variance components were estimated for fertility traits, including heifer fertility, and genetic correlations estimated, including correlations with production and conformation traits. The results confirm the findings from the previous study - that is, redefinition of CR42 to CSD resulted in improved use of the phenotypic information for genetic prediction. Heifer calving season day was also found to be highly genetically correlated with later cow calving traits, meaning it is a potentially valuable early predictor of daughter fertility in AI bulls. Modest genetic correlations between cow fertility traits and body condition score were found. Results also indicate that the current use of first lactation milk volume yield in the CR42 prediction might be better replaced with protein percentage in CSD. Further work is required using selection index theory to determine if a major revision to the national genetic evaluation for fertility is justified.

Key words: fertility, dairy cows, genetic evaluation, genetic parameters

Introduction

The reproductive performance of dairy cows in New Zealand is superior to many other countries, however, selection for production traits has resulted in a decline in fertility over the last 40 years (Burke and Fowler, 2007). More recently, this has resulted in a shift of focus to ensure that fertility doesn't decline further by including fertility in the national breeding objective (Harris and Montgomerie, 2001). This is particularly important in the New Zealand seasonal calving system, where there is the requirement that cows calve once every 365 days.

An earlier study using data from a moderate sized database of a one hundred and fifty herds (Bowley *et al.*, 2014) has demonstrated that redefining fertility traits as continuous calving traits instead of using binary 0/1 scores as per the current trait definition could significantly increase the accuracy of fertility trait estimates.

Studies in other dairy populations have shown moderate to high genetic correlations between measures of heifer and cow fertility (Jamrozik *et al.*, 2005; Liu *et al.*, 2008; Pryce *et al.*, 2007; Tiezzi *et al.*, 2012), however, the relationship between heifer and cow fertility in the NZ dairy industry has been less well quantified. Initial work by Bowley *et al.* (2014) showed that the heifer calving trait had similar heritability estimates to cow fertility traits. In addition, there was a high genetic correlation between heifer and cow fertility (0.7) which means that the genes underlying cow fertility are similar to those underlying heifer fertility. Hence, heifer fertility traits may be a useful tool in predicting cow and young bulls' fertility estimated breeding values EBVs (Pryce *et al.*, 2007).

The objective of this study was to evaluate the initial findings of Bowley *et al.* (2014) using national fertility data. First, this paper addresses the issue of the impact of alternative planned start of mating (PSM) and planned

start of calving (PSC) definitions on heritability estimates of fertility traits. Second, the genetic parameters for percentage mated at 21 days post-PSM (PM21) and calving rate at 42 days (CR42) were estimated using alternative trait definitions (continuous vs. binary vs. a scoring system) to determine the best fertility traits for subsequent work. Third, genetic correlations of the best fertility traits with other fertility, production and conformation traits were estimated with the aim of identifying possible predictor traits for fertility. Finally, the heritability of heifer calving season day (CSD) was estimated, as well as its genetic correlations with cow fertility traits.

Materials and Methods

Data

The fertility data were extracted from the New Zealand national dairy database. They included records from 1989 to 2013 for cows with records for their first three lactations. All fertility traits used in New Zealand are derived from calving date and first mating date. The date of last mating was also available for this study. Only seasonal matings and calvings were used: matings between September and January and calvings between June and November.

There were no mating or calving records for maiden heifers in the fertility data file. Calving dates for heifers were calculated based on pedigree birthdates and age at first calving (i.e. age at calving as a maiden heifer). Using these dates introduces a degree of ascertainment bias into the dataset because calving records for heifers that were mated but did not calve are not included. Additionally, contemporary groups for maiden heifers were not supplied as part of the data extract. Instead contemporary groups in their subsequent parity were used, where contemporary group consisted of herd and season.

Data for 270 day lactation yield for milk, fat and protein as well as fat and protein percentage and fat to protein ratio in the first lactation were also used in this study. Live weight measurements and body condition

score (BCS) records were also available. BCS was treated as 3 separate traits for days in milk 1-50, 50-90 and 90-140.

Planned start of mating (PSM) and planned start of calving (PSC) definitions

PSM: definitions were used based on first mating date data for cows within each herd:

1. The average mating date of the first 10% of matings observed within herd and season, minus 1 day (Bowley *et al.*, 2014).
2. The first date of a mating period where there are four mating dates within a 7 day window, where the first two dates are on consecutive days. The first of these two consecutive days is set as the PSM (Creagh *et al.*, 2013).
3. The first date of a mating period where there are four mating dates within a 7 day window (DairyNZ, 2008).

PSC: definitions were used based on calving date data for cows within each herd:

1. The average calving date of the first 3-10% of calvings observed within herd and season, minus 3 days (Bowley *et al.*, 2014).
2. Where there are two consecutive weeks with calving data and the previous week contains no calvings, the InCalf method (Burke *et al.*, 2007) sets PSC to either:
 - a. PSC = 3rd day of 1st week, when the number of calvings in the 1st week is greater than that in the 2nd week,
 - b. PSC = 1st day of 2nd week, when the number of calvings in the 2nd week is greater than that in the 1st week.
3. As defined in PSM 1 + 282 days (average gestation length).
4. As defined in PSM 2 + 282 days.

Fertility trait definitions

There were two alternative mating traits used. The difference in days between PSM for a given herd and first recorded mating date was used to define mating season day (MSD). Alternatively, for the proportion of cows mated within the first 21 days of mating (PM21), each cow was scored 1 if she was presented for

mating within the first 21 days of mating within her contemporary group and 0 if she was mated later. Four alternative definitions of PSM were used to derive these traits.

Calving dates and PSC dates were used to derive the calving rate trait (CR42), which is defined in the current genetic evaluation (Harris *et al.*, 2006a) as success or failure of calving in the first 42 days after PSC for a given contemporary group. Three alternative versions of CR42 were used:

1. Calving season day (CSD; continuous) – calculated as the difference in days between PSC and the cow’s calving date,
2. CR42 binary – as in current genetic evaluation, a cow was given a score of 1 if she calved within first 42 days after PSC, and a score of 0 if she calved later,
3. CR42 score – a cow was scored 0 if she calved before PSC, 1 if she calved in first 21 days, 2 if in the next 21 days, 3 for following 21 days, and 4 if she calved after 63 days from PSC.

Three alternative definitions of PSC were used to derive these calving traits.

Additionally, calving interval (difference in days between consecutive calvings), mating interval (difference in days between first and last recorded mating), non-return rate (binary trait where cow was scored 1 if she conceived after first mating and 0 if more than one insemination was required), and calved/not-calved (cow was scored one if she was mated and then calved successfully and 0 if matings didn’t result in pregnancy) were evaluated.

Genetic evaluation model

Genetic analysis was carried out using ASReml software (Gilmour *et al.*, 2009). All fertility traits were analyzed with the same model which corresponds to the one used in national genetic evaluations of fertility traits (Harris *et al.*, 2006a):

$$y = CG + Age*Breed + HF_{FR} + HF_{NZ} + HET_{JExNZ} + HET_{JExFR} + HET_{NZxFR} + REC_{JExNZ} + REC_{JExFR} + REC_{NZxFR} + a + e$$

where:

- y was the phenotypic record
- CG was the fixed contemporary group (herd-year) effect
- $Age*Breed$ was the fixed linear regression of age at calving in days nested within breed (for heifers the Julian day of the year when the cow was born was used)
- HF_{NZ} and HF_{FR} were fixed linear regression of New Zealand and foreign Holstein-Friesian breed composition
- HET and REC were fixed linear regression of breed specific heterosis and recombination effects (Dickerson, 1973)
- a was random animal effect
- e was random error term.

Additionally, bivariate models were utilized to estimate genetic correlations between the best mating and calving traits and production traits (milk, fat, and protein yields, fat and protein percentage and fat to protein ratio), as well as live weight and body condition score. Models used for those additional traits corresponded with those used in national genetic evaluation in New Zealand (Harris, *et al.*, 2006b; Pryce and Harris, 2006).

Results & Discussion

The heritability estimates from single-trait analysis for different mating trait definitions and alternative PSM date definitions are presented in Table 1. While the continuous trait was found to be less sensitive to differences in PSM definitions, the heritability estimates for the binary trait were higher. Therefore, the binary trait should be used in further analysis.

The heritability estimates from single-trait analysis for different calving trait definitions and alternative PSC date definitions are presented in Table 2. Heritabilities were highest for the continuous trait, only slightly lower for the score trait and significantly lower for the binary trait. The continuous trait is therefore able to capture more of the additive genetic variance compared to the binary trait and would be more beneficial for use in genetic evaluations of cow fertility.

While little difference was found between heritability estimates for different PSC definitions, the relative differences between them demonstrates that the continuous trait is most robust to errors in PSC date estimation (Table 2), while the score trait is more sensitive. Therefore, the continuous trait is likely to be slightly more robust than the score trait in situations where the PSC cannot be clearly defined. The score trait can be more easily adapted to include failed fertility of cows that do not successfully calve, but which were presented for mating in the previous season.

Heritability estimates for the remaining evaluated traits were:

- Calving interval – 0.03
- Interval between first and last mating – 0.01
- Non-return rate – 0.01
- Calved/not-calved – 0.01

Calving interval heritability was lower than what can be found in the literature, which is most likely due to the fact that cows in New Zealand are subjected to long involuntary withholding periods due to the seasonal production system. The heritability estimate for the interval between first and last mating was also very low. This could be the result of the fact that last mating dates are not properly recorded for all cows and, therefore, this trait did not capture the true genetic variation underlying this trait.

Genetic correlations between proportion of cows mated within the first 21 days of mating (PM21, binary trait) and calving season day (CSD) and other fertility, production and conformation traits are presented in Table 3. Correlations with milk production traits were lower than those typically found in the literature, which could be due to the fact that in New Zealand, under the seasonal system, cows are not fed so as to meet their full genetic production potential, and so the underlying physiological relationship between traits could be different. For the calving trait, protein percentage could potentially be used as a better predictor trait than milk yield, which is used currently. Genetic correlations with BCS suggest that BCS recorded in early lactation is

sufficient enough as a predictor of cow fertility.

The heritability estimate for heifer calving season was found to be 0.025, which is comparable to cow CSD heritability estimates. The phenotypic correlation between heifer and cow (parity 1) CSD was 0.105 and the genetic correlation was 0.79. This indicates that while phenotypically the traits appear to be quite distinct, genetically they are very similar traits. This provides the opportunity to select for cow fertility at an earlier age of bulls by including heifer calving season day in the national herd genetic evaluation.

Conclusions

Alternative definitions for planned start of mating and planned start of calving were evaluated and minimal differences in heritability estimates were found.

Alternative trait definitions were used for calving (continuous, binary, and score) and mating (continuous and binary) traits. Estimated variance components suggest that the continuous calving trait (CSD) and binary mating trait (PM21) should be used in further analyses.

Heritabilities of other fertility traits (calving interval, mating interval, non-return rate, and calved/not-calved) were low, however, their high genetic correlations with mating and calving traits suggest that they could potentially be useful as predictor traits.

Progress on defining heifer calving traits is well advanced and correlations between heifer calving traits and cow calving traits was found to be high. Therefore, including the heifer calving day trait in fertility evaluations would be beneficial in the national genetic evaluation.

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Table 1. Heritability estimates for proportion of cows mated within first 21 days (PM21) and mating season day (MSD) for alternative planned start of mating (PSM) definitions.

PSM definition	PM21	MSD
1	0.028	0.028
2	0.030	0.028
3	0.029	0.028

Table 2. Heritability estimates for calving rate (CR42) binary and score traits and calving season day (CSD) for alternative planned start of calving (PSC) definitions.

PSM definition	CR42 binary	CR42 score	CSD
1	0.010	0.023	0.026
2	0.010	0.025	0.026
3	0.010	0.023	0.026
4	0.010	0.022	0.026

Table 3. Genetic correlations between proportion of cows mated within first 21 days (PM21) and calving season day (CSD) and other traits.

Trait	PM21	CSD
PM21	---	-0.82
Milk	-0.09	0.13
Fat	0.03	-0.05
Protein	-0.08	0.02
Fat %	0.08	-0.14
Protein %	0.04	-0.22
F/P ratio	0.09	-0.03
Live weight	0.03	0.15
BCS (1-50 DIM)	0.31	-0.27
BCS (50-90 DIM)	0.24	-0.19
BCS (90-140 DIM)	0.34	-0.18
Calving interval	-0.77	-0.05
Interval between first and last mating	-0.40	0.63
Non-return rate	-0.27	0.58
Calved/not-calved	0.16	0.02