

NEW APPROACHES TO GENETIC ANALYSIS OF FERTILITY TRAITS IN NEW ZEALAND DAIRY CATTLE

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SUMMARY

There is potential for the current New Zealand fertility breeding value (BV) to be improved using additional information and traits. Data from 169 herds were analysed to determine the benefits of utilising alternative phenotypic measures in the calculation of the fertility BV. The heritability of calving season day (CSD; the number of days from the planned start of calving to the actual calving date) and the percentage of cows calving within 42 days of the planned start of calving (CR42) increased modestly (from 0.0206 ± 0.0027 to 0.0213 ± 0.0029 and 0.0087 ± 0.0015 to 0.0092 ± 0.0017 , respectively) after accounting for the use of controlled internal drug release (CIDR) treatments and induced calvings. Incidence of either CIDR use or calving induction as a single binomial trait had a heritability of 0.0223 ± 0.0020 . The use of pregnancy diagnosis data allowed fertility information that would otherwise be discarded to be included in analyses; when used to assign a prolonged CSD and a value of 0 for CR42 to animals that failed to calve, it increased the heritabilities of both of these traits (to 0.0278 and 0.0114, respectively). As CSD was found to be more than twice as heritable as its binary counterpart, it shows potential to replace CR42 as the calving trait used in the fertility BV. Post-partum anoestrous interval (PPAI), derived using incomplete pre-mating oestrous recording in some herds, had a heritability of 0.0813 ± 0.0110 and hence has potential as a trait to be included in genetic improvement programs, but would require more rigorous recording of oestrous during the pre-mating period to be an effective trait. Due to the increasing economic importance of fertility traits, and low heritabilities requiring large numbers of recorded daughters to get accurate BV predictions on sires, data recorded on-farm will become increasingly important in the genetic improvement of fertility. It is recommended that a system of identifying and incentivising herds with robust data-recording systems be designed and implemented to ensure ongoing collection of comprehensive and accurate data.

INTRODUCTION

The reproductive performance of dairy cows in New Zealand is superior to that in many other countries (Harris *et al.* 2002; Griffiths *et al.* 2007). However, fertility has been steadily declining phenotypically over the past 20 years; for example, Harris *et al.* (2006) reported a 10% decline in the proportion of cows re-calving within 42 days of the subsequent calving period between 1990 and 2004. While the estimated heritabilities of fertility traits are small (often less than 0.05), large additive genetic variation exists, meaning that improvement through genetic selection is possible (Harris and Montgomerie 2001; Harris *et al.* 2002). Fertility was first added as a breeding value (BV) to the New Zealand economic selection index, Breeding Worth (BW), in 2001 (Harris and Montgomerie 2001), and is currently largely based on the percentage of calvings within 42 days of the planned start of calving (CR42; Harris *et al.* 2006). BVs may be improved by re-defining current traits and through the inclusion of new traits. Therefore, potential for further improvement may exist through the use of alternative phenotypic measures in the calculation of the fertility BV.

The purpose of this study was to assess methods of data filtering and modification to improve fertility trait heritabilities, and investigate novel ways of measuring fertility to improve the current New Zealand fertility BV.

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MATERIALS AND METHODS

Data and fertility traits analysed. Up to 259,651 records (depending on the trait; Table 1) from 139,134 animals (cows and heifers) in 169 herds participating in a fertility monitoring project across New Zealand were available for analysis (Brownlie *et al.* 2011). SAS (version 9.2) was used to handle, filter and manipulate the data.

Table 1. Fertility traits analysed, their acronyms and descriptions

Trait	Acronym	Description
Post-partum anoestrous interval	PPAI	Days from previous parturition to first observed oestrous (or first mating if oestrous not observed)
Percentage mated 21 days	PM21	1 if first mating occurred within 21 days of start of mating date, 0 if first mating occurred after 21 days, and missing if not mated
Mating season day	MSD	Days from start of mating date to first mating (similar to PM21, but left as a continuous trait instead of being scored 0/1)
Calving rate 42 days	CR42	1 if calved within 42 days of planned start of calving date, 0 if calved after 42 days, and missing if not calved
Calving season day	CSD	Days from planned start of calving date to calving (similar to CR42, but left as a continuous trait instead of being scored 0/1)

Statistical model. Heritabilities were estimated using a univariate animal model in ASReml (version 3), consisting of mean, covariates of age and breed percentage, fixed effects of herd, contemporary group (herd, year and if the animal was a cow or heifer at the time) and interaction between herd and year, and random effects of animal and permanent environmental effect.

Data manipulation and modification.

Data filtering. Various filters were applied to the data to minimise distortion of results. For example, animal records were removed from the dataset used in analyses if the animal was greater than six years old at time of mating, its sire had less than four daughters, there were less than 50 animals in its contemporary group, or it was mated after February or before August (i.e. outside of the normal window for seasonal-calving herds).

Adjustment for fertility treatments. The use of fertility treatments, namely controlled internal drug release (CIDR) and calving induction, results in artificially-altered fertility records. Hence, in order to assess their impact on fertility trait heritabilities, any affected records were set to missing. An additional binomial trait representing the incidence of CIDR use or induction (CIDRIND) was also calculated and analysed. For each record, an animal was scored as 1 if it was treated with a CIDR or induced, 0 if there were records of CIDR use or induction for other animals in that herd-year, and missing if there was no record of CIDR use or induction in that herd-year.

Pregnancy diagnosis data. Some pregnancy diagnosis data, including whether the animal was confirmed pregnant or not, was also available, and was used to test the effect of including knowledge of failed pregnancies on the heritabilities of CR42 and calving season day (CSD). Animals that were diagnosed as not pregnant were given a CR42 record of 0 and a CSD record 10 days later than the last calving day for the year in that herd.

RESULTS AND DISCUSSION

Adjustment for fertility treatments. Accounting for the use of CIDR treatments and induced calvings by setting affected records to missing altered fertility trait heritabilities (Table 2). While the heritabilities of post-partum anoestrous interval (PPAI) and percentage mated 21 days (PM21)

did drop slightly and remained unchanged for mating season day (MSD), this filtering of records modified by fertility treatments had a positive effect on the heritabilities of calving traits. In addition, as the use of such interventions creates fertility records not representative of the true fertility of the animal, removing such records from analyses is the logical option. Attempting to correct records for the effects of these interventions by fitting them as fixed effects in the statistical model did not increase heritabilities.

Table 2. Number of records, adjustments for CIDR use and induction and resulting heritabilities (with standard errors in parentheses) for each of the fertility traits

Trait	Number of records	Heritability (unadjusted)	Set missing if CIDR used?	Set missing if induced?	Heritability (adjusted)
PPAI	31,252	0.0814 (0.0104)	✓	✓	0.0813 (0.0110)
PM21	259,615	0.0335 (0.0035)	✓		0.0352 (0.0037)
MSD	258,854	0.0239 (0.0029)	✓		0.0239 (0.0030)
CR42	218,098	0.0087 (0.0015)	✓	✓	0.0092 (0.0017)
CSD	217,053	0.0206 (0.0027)	✓	✓	0.0213 (0.0029)

CIDRIND was found to have a heritability of 0.0223 ± 0.0020 , and it is recommended that this trait be included in genetic evaluations for fertility, particularly since setting other affected records to missing would mean individuals sub-optimal for fertility would not be adequately penalised unless it is incorporated.

Use of pregnancy diagnosis information. In the absence of pregnancy diagnosis data, when an animal fails to become pregnant or sustain pregnancy, CR42 and CSD are recorded as missing. This is effectively a loss of fertility information, because the associated failure to calve is not accounted for when analysing these calving traits, as missing records are excluded from analyses. Since some pregnancy diagnosis information was available, this was used to test the effect of including knowledge of failed pregnancies on the heritabilities of CR42 and CSD. The result was an increase in the heritability of CR42 from 0.0092 to 0.0114 and CSD from 0.0213 to 0.0278. Hence, recording and use of pregnancy diagnosis data has been confirmed as important in the analysis of calving-based fertility traits.

Replacing CR42 with CSD. CR42 is the calving trait currently used in the fertility BV. However, after adjusting for CIDR use and calving induction, and utilising pregnancy diagnosis information, the heritability for CSD (0.0278) was more than twice that of its binary counterpart, CR42 (0.0114), which suggests that genetic progress for fertility may be made at an increased rate if selection was based on CSD instead. Use of CSD allows differentiation between animals calving in the first versus the second 21-day period of the calving season, allowing more refined selection to ensure a compact calving pattern is maintained. It also alleviates problems associated with not being able to determine the planned start of calving date very accurately because of variation in gestation length. However, further research using a larger dataset is required to verify the benefits of replacing CR42 with CSD as the calving trait in the fertility BV.

Potential for use of PPAI. Of the relatively low number of 31,252 “first oestrous” records, only 1,663 (5%) were actually recorded as an observed oestrous; the remaining were proxies based on the first recorded mating for the season in herd-year groups where some oestrous recording was performed. Despite this, PPAI was the most heritable (0.0813 ± 0.0110 , after adjusting for CIDR use and induction) of all the traits analysed, suggesting that it may be a valuable indicator of fertility. Currently, one of the reasons for poor PPAI measurements is that oestrous detection only begins 3 to 4 weeks prior to the planned start of mating date at the earliest, and many animals cycle before this time. An analysis of the data revealed that, based on an average PPAI of 40 days,

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58% of first oestrous detected would have occurred prior to this and hence not been recorded. Hence, PPAI shows substantial potential as a trait to be included in selection programs for fertility, but it would be necessary to highlight to farmers the benefits of early oestrous recording, both for genetic improvement as well as general herd management.

Collection of farmer-recorded fertility data. Farmer-recorded data are going to become increasingly important in the genetic evaluation of future sires. This importance will be driven by the rapid development of genomic selection methodologies and the associated reduction in the number of progeny-tested sires, as well as the increasing availability of on-farm milk recording and analysis systems reducing the need for herd testing. Currently, data recording on commercial farms is highly fragmented and is not always stringent, particularly in the case of fertility. It is recommended, therefore, that a system of identifying and incentivising selected herds with robust data-recording systems be designed and implemented to ensure ongoing collection of comprehensive and accurate data for use in genetic improvement programs. Ideally, these herds would use a high-proportion of semen from elite young sires identified using genomic information.

CONCLUSION

The results of this study show that there is potential for improvement in the New Zealand fertility BV through the inclusion of additional information. Adjusting for CIDR use and calving induction by setting affected records to missing is not only logical but increased the heritabilities of the calving traits CSD and CR42. Incidence of CIDR use or induction as a binomial trait was also reasonably heritable and should be included in fertility evaluations to ensure animals that are sub-optimal for fertility are adequately penalised. Pregnancy information further increased accuracy of selection for CSD and CR42. As CSD seems to be a more heritable trait than its binary counterpart, further study into replacing CR42 with CSD as the calving trait in the fertility BV is warranted. PPAI shows promise as a fertility trait with relatively high heritability, but would require recording of oestrous during the pre-mating period. In order to facilitate ongoing genetic improvement of fertility, herds with robust data-recording systems need to be identified and used as sources of comprehensive and accurate data to be used in sire genetic evaluations.

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