CONCEPTION-BASED FERTILITY TRAIT FOR GENETIC EVALUATION OF NEW ZEALAND DAIRY CATTLE

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SUMMARY

Genetic evaluation of dairy cow fertility in New Zealand is currently based on calving season day, defined as the number of days from planned start of calving for the herd to cow calving date. This phenotype has gestation length embedded in it. Recently, a concern has been raised that shortened gestation lengths are the driving force behind good reproductive performance, as opposed to the cow's ability to conceive in a timely manner. Therefore, the goal of this research was to explore a range of possible alternative fertility phenotypes to find a replacement for calving season day that would be, at least on a phenotypic level, independent from gestation length. Using data from herds with good data quality, alternative conception-based fertility trait definitions were evaluated and compared. Variance components were estimated using ASReml software. Binary six-week in-calf rate was suggested as the best trait definition due to the relatively high genetic variance, desirable genetic and residual correlations with other fertility traits evaluated, and practicality of data recording. Further testing and validation are planned before a new conception-based fertility trait is finalised for inclusion in routine genetic evaluation.

INTRODUCTION

Over the past decade, research into calving date-based approaches to the NZ fertility evaluation has demonstrated a substantial improvement in validation accuracy for a wide range of key fertility metrics of commercial relevance to NZ dairy farmers, relative to previous prediction methods. However, the implementation of the new fertility breeding value has not been fully endorsed by all industry partners. Of particular concern was an increased role of short gestation length (GL) in driving the superior fertility predictions for new animals. When information is scarce or inaccurate on submission and conception rates, fertility breeding value estimates are likely to be dominated by GL. It can be argued that GL is not a true fertility trait, and some concerns exist about deployment of strong selection pressure for short GL. Therefore, it would be advantageous to separate fertility breeding values into three separate components: (1) resumption of cyclicity and oestrous expression (submission rate); (2) probability of getting pregnant (conception rate); and (3) GL. Submission rate (PM21) and GL are currently being evaluated in NZ. The goal of this research was to examine alternative definitions of conception-based fertility traits and recommend one that would be most suited for New Zealand dairy farming systems.

MATERIALS AND METHODS

Data. Fertility phenotypic data were extracted from New Zealand's national dairy database. This data included records from 2005 to 2014 calving seasons. Mating and calving records from the first five parities were considered. Extensive data filters were applied to obtain data from herds with good recording practices and sufficient animals. A random sample of around 30,000 cows with phenotypic records was drawn from herds meeting these criteria. Data edits and current fertility trait (CSD0 - heifer, CSD - cow and PM21) definitions were described in detail by Stachowicz *et al*. (2014). Ten conception-based fertility phenotypes were derived for testing (Table 1). They incorporate a variety of attributes, including the timing of conception (i.e., continuous - CR1 and CR2; binary versions – CR7 to CR10), the number of inseminations required to achieve conception (i.e., CR3), and conception outcomes associated with various categories of insemination (i.e., CR4 to CR6). Two

versions of each phenotype were tested; one as defined as per Table 1, and one which included penalties for 'poor' fertility cows – i.e., carryover cows and cows that had been culled for infertility. For continuous traits, penalties were defined as the maximum value for the contemporary group, plus an additional 21-day oestrus cycle (for interval traits) or insemination (for number of inseminations), whereas cows with a binary trait penalty were set to 0. Conception confirmation is currently defined by non-return and the presence of a subsequent calving rather than the use of pregnancy diagnosis data; this is likely to change in the future because of industry data coordination initiatives.

Table 1. Conception-based fertility traits definitions

Trait	Trait name	Definition	Unit	Min.	Max.
CR1	Time of conception day	Days from PSM to conception	days	-21	100
CR2	Interval from first to last insemination	Days from first insemination to conception	days	0	100
CR3	Number of inseminations	Number of inseminations within season	score	1	10+
CR4	Pregnant to first service	Confirmed pregnant to first service	binary	0	1
CR5	Pregnant to any service	Confirmed pregnant to any service	binary	0	1
CR6	Pregnant to AI	Confirmed pregnant to AI	binary	0	1
CR7	Three-week in-calf rate	Confirmed pregnant within three weeks of PSM	binary	0	1
CR8	Six-week in-calf rate	Confirmed pregnant within six weeks of PSM	binary	0	1
CR9	Three-week in-calf rate	Confirmed pregnant within three weeks of first mating	binary	0	1
CR10	Six-week in-calf rate	Confirmed pregnant within six weeks of first mating	binary	0	1

Genetic analysis. Variance components estimation was carried out using ASReml software (Gilmour *et al.*, 2009). Traits that are currently evaluated in the New Zealand genetic evaluation of fertility traits were analysed using models described by Amer *et al.* (2016) and Stachowicz *et al.* (2015, 2021). Conception-based fertility traits were analysed with a repeated records animal model, which in a simplified linear version can be represented as:

$$CR1\text{-}10 = CG + Age*Breed + Age^2*Breed + TR + FR + HO + Inbr + Het + Rec + a + pe + e$$

where:
- CG is the fixed contemporary group effect of herd-year-parity,
- $Age*Breed$ & $Age^2*Breed$ are the fixed linear and quadratic regressions of age at calving nested within breed,
- TR is the fixed effect of pregnancy termination reason (normal, abortion, induction, premature),
- FR & HO are fixed linear regressions of New Zealand Friesian and foreign Holstein breed composition,
- $Inbr$ is fixed linear regression of inbreeding,
- Het is fixed linear regression of heterosis,
- Rec is fixed linear regression of recombination loss,
- a is a random animal effect,
- pe is a random permanent environmental effect,
- e is a random error term.

Each of the conception-based traits was first analysed with a univariate model. Next, five traits were chosen for further work and were analysed using pairwise bivariate models with traits from the

current evaluation system (CSD0, CSD, PM21). Finally, three traits of interest were analysed in three-trait models with CSD0 and PM21, with these new conception traits considered as alternative potential replacements for CSD.

RESULTS AND DISCUSSION

The results of initial univariate analysis of conception-based fertility traits defined with and without penalties are presented in Table 2. Heritabilities were consistently higher for phenotypes with penalties applied compared to phenotypes without penalties. This is the opposite trend to what was found for calving season day (CSD) in the past (Stachowicz *et al.*, 2014). We hypothesise that using penalties to account for carryovers and cows that were culled due to fertility issues leads to higher estimates of genetic variance. Traits derived using planned start of mating as opposed to using a cow's first mating as a base had higher heritability. This is consistent with observations from seasonal calving herds in Ireland (Stachowicz *et al*., 2022). Based on the univariate results, five traits were chosen for bivariate runs. Genetic correlations were estimated between those traits and traits in the current genetic evaluation of fertility (CSD0 - heifer, CSD - cow, PM21; Table 2). Pregnant to first service (CR4) had the lowest genetic correlations with CSD and PM21, whereas the remaining traits had values ranging from 0.90-0.96. Genetic correlations with CSD0 ranged from 0.45-0.63. Phenotypic correlations (data not shown) between PM21 and conception-based traits were much lower than genetic correlations. This suggests that the extra records from conception phenotypes should add value, over and above submission data, when bulls have lower numbers of daughters.

Table 2. Heritabilities (h^2) and repeatabilities (rep) of conception-based fertility traits with (*) and without penalties, and their genetic correlations (r_G) for a subset of 5 selected traits with calving season rate heifer (CSD0), calving season day cow (CSD) and submission rate (PM21)

Trait	h^2	rep	h^{2*}	rep*	r_GCSD0	r_GCSD	r_GPM21
CR1	0.018	0.089	0.030	0.139	0.56	0.96	-0.90
CR2	0.008	0.054	0.017	0.093			
CR3	0.008	0.060	0.014	0.081			
CR4	0.012	0.047	0.014	0.046	-0.50	-0.86	0.63
CR5	0.007	0.007	0.012	0.054			
CR6	0.013	0.058	0.014	0.068	-0.47	-0.96	0.91
CR7	0.020	0.060	0.028	0.066	-0.63	-0.95	0.95
CR8	0.011	0.064	0.020	0.081	-0.45	-0.96	0.91
CR9	0.008	0.045	0.014	0.053			
CR10	0.006	0.025	0.013	0.042			

Three traits (CR1; timing of conception and CR7/CR8; three- and six-week in-calf rates) were chosen as potential replacements for CSD and included in three-trait variance components estimation with CSD0 and PM21. This decision was based on estimates of genetic and residual (data not shown) correlations as well as on within-season data availability and naming conventions already used by farmers. Results are presented in Table 3. With multiple trait models, estimates of heritabilities tend to increase compared to univariate runs. Genetic correlations between conception-based traits and CSD0 were comparable to current estimates for CSD (Amer *et al*., 2016). Three-week in-calf rate had the highest genetic correlation with PM21 (0.94) compared to timing of conception and six-week in-calf rate (0.91). this indicates that three-week in-calf rate would be least preferred conception-based phenotype as it would provide less additional information on top of three-week submission rate compared to the other definitions. The binary six-week in-calf rate would likely be preferable to the continuous timing of conception trait because as soon as the six-

week period from planned start of mating is complete the entire contemporary group's phenotypes are available and can be used immediately for evaluation. However, there may be a trade-off between timely data availability and potential biases introduced to evaluation if phenotypes of poor fertility contemporaries were not included in evaluation of the binary trait.

Table 3. Heritabilities (repeatabilities; on diagonal) and genetic correlations (off diagonal) for conception-based fertility traits (with penalties (*) with calving season rate heifer (CSD0) and submission rate (PM21)

	CSD0	CR1*	PM21		CSD0	CR7*	PM21		CSD0	CR8*	PM21
CSD0	0.023			CSD0	0.022			CSD0	0.021		
CR1*	0.64	0.048 (0.13)		CR7*	-0.66	0.044 (0.07)		CR8*	-0.59	0.033 (0.09)	
PM21	-0.58	-0.91 (0.16)	0.067	PM21	-0.56	0.94	0.065 (0.16)	PM21	-0.55	0.91	0.063 (0.16)

CONCLUSION

The goal of this research is to construct a more accurate conception-based fertility trait, as well as to determine whether greater overall economic advantage could be achieved with inclusion of this new trait in an economic index. This requires a more comprehensive definition of how the different components of fertility genetics contribute to farm profitability than is available in the current genetic evaluation system so they can be weighted accordingly. Based on our results, the continuous time of conception trait and binary three- and six-week in-calf rates are recommended for further testing in full GE univariate and multivariate runs. Next steps will include validation work, where phenotypes of the validation cow cohort are set to missing in prototype genetic evaluations, with the predictive ability of test models then evaluated across a range of fertility phenotypes, including the impact on GL. High genetic correlations between conception traits and CSD indicate that there might still be GL effects embedded in the new conception-based fertility trait. Correlations between conception-based fertility traits and GL EBVs will be assessed during validation and testing work. After the final conception-based fertility phenotype is chosen, the next step will be to incorporate the new trait in the economic index alongside GL which will have a non-linear economic weight to help ensure that any further shortening trend in GL will not pass the point after which short GL might have negative impacts on calf health and survival.

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