PROPOSED CHANGES IN THE GENETIC EVALUATION OF DAIRY FERTILITY IN NEW ZEALAND

K. Stachowicz[1], G.M. Jenkins[1], P.R. Amer[1], J.R. Bryant[2] and S. Meier[2]

[1]AbacusBio Limited, PO Box 5585, Dunedin 9058, New Zealand
[2]DairyNZ Limited, Private Bag 3221, Hamilton 3240, New Zealand

SUMMARY

This paper summarises the findings of a number of research projects exploring the genetic evaluation of dairy cattle fertility in New Zealand and describes the proposed changes to the genetic evaluation system. The following recommendations for changes in the national genetic evaluation model of fertility traits were made: 1) replace the binary calving trait with its continuous version measured in days; 2) include records on first calving of heifers in the model; 3) include the information on reproductive interventions like labour inductions and mating hormonal synchronization for evaluating fertility phenotypes; 4) drop milk production traits from the model; 5) retain body condition score as a predictor trait in the model; 6) add gestation length as a new correlated predictor trait to the model; 7) consider the inclusion of a gestation length breeding value (direct) in selection index.

INTRODUCTION

The reproductive performance of dairy cows is a major driver of profit in dairy farming, especially in seasonal, pasture-based systems, where the calving interval is essentially constrained to a short window around 365 days. Herds that achieve high levels of fertility (i.e. meet the industry target of 78% 6-week in-calf rate with minimal use of hormonal intervention) are able to maintain a condensed seasonal calving pattern and minimise the number of cows being culled involuntarily for reproductive reasons. By international standards, reproductive performance of dairy cows in New Zealand is high. It has, however, experienced the global decline in fertility that was associated with selection for high milk yields without the protection of including fertility in the economic selection index, known as Breeding Worth (BW; Harris and Montgomerie 2001).

In New Zealand, fertility is currently evaluated using two binary traits: calving rate at 42 days (CR42; if cow calves within 42 days from the planned start of calving in parities 2 to 4) and percentage mated at 21 days (PM21; if the cow is presented for mating within 21 days from planned start of mating) in parities 1-3, along with two predictor traits: first lactation milk yield and body condition score (BCS). These traits indirectly measure a cow's genetic propensity to return to a fertile state after calving and to become pregnant in a period that will allow her to maintain a 365-day calving interval. Both PM21 and CR42 have low heritability (0.05 and 0.02, respectively; Harris *et al.* 2005).

There are potential benefits of incorporating new fertility traits into the genetic evaluation, particularly if these traits are more accurate measures of true fertility or if they can be measured earlier in the cow's life than current mating and calving traits. A number of research projects were undertaken in order to explore possible improvements to the national genetic evaluation system for fertility.

Bowley *et al.* (2015) analysed data from 169 herds participating in fertility monitoring projects (Brownlie *et al.* 2011) in the 2011 and 2012 seasons and demonstrated that redefining fertility as a continuous calving trait (CSD - calving season day, which is defined as the difference in days between planned start of calving for a given contemporary group and actual cow's calving date) instead of using binary (0/1) scores as per the current trait definition could increase the accuracy of fertility evaluation. A heifer calving trait was also investigated and shown to have similar heritability estimates to cow fertility traits. In addition, there was a relatively high genetic correlation between heifer and cow fertility (0.7) which means that some of the genes underlying cow fertility are similar to those underlying heifer fertility. Hence, the heifer fertility trait may be useful in predicting the estimated breeding value (EBV) for fertility of cows and young bulls (Pryce *et al.* 2007). Adjusting for reproductive interventions by setting affected calving and mating records to missing was also suggested (Bowley *et al.*, 2015). Novel potential fertility traits were investigated and postpartum anoestrous interval was recommended to be considered as a trait with heritability higher than currently evaluated traits (0.08). However, its inclusion on a national scale would require a substantial effort by the industry to record phenotypic data.

Stachowicz *et al.* (2014a) evaluated the initial finding by Bowley *et al.* (2015) using national fertility data. Firstly, this research addressed the issue of the impact of alternative approaches of identifying planned start of mating and planned start of calving dates for each contemporary group on heritability estimates of fertility traits and found minimal differences. Secondly, the genetic parameters PM21 and CR42 were estimated using alternative trait definitions (continuous vs binary vs a scoring system) to determine the best fertility traits for subsequent work. From this, it was recommended that the binary version of the mating trait and the continuous version of the calving traits should be used. Thirdly, genetic correlations of the best fertility traits with other fertility, production and conformation traits were estimated to identify possible predictor traits for fertility. Results indicated that milk yield, the current predictor trait, might be better replaced with protein percentage. Finally, the heritability of heifer calving season day (CSD) was estimated, as well as its genetic correlations with cow fertility traits and this was found to be a valuable early predictor trait of future cow fertility.

Selection index modelling methods were used to investigate the impact of changes in the fertility genetic evaluation model on accuracy of estimated breeding values for fertility traits (Stachowicz *et al.*, 2014b). The binary or continuous equivalents of the current fertility traits were compared, replacing milk yield with protein yield or protein percent as a predictor trait in the fertility model and by considering the impact of inclusion of the heifer fertility trait. The results of this study agreed with previous findings, that: 1) the continuous version of CR42 was a more accurate predictor of true fertility than the currently used binary trait; 2) including milk production traits in the fertility model has minimal impact on accuracy of the prediction for fertility; and, 3) adding the heifer calving trait increased the accuracy of cow fertility trait predictions.

The research reported here continues the work described by Stachowicz *et al.* (2014a & 2014b). Gestation length (GL) expressed as trait of the calf was investigated as a possible predictor trait to be included in the genetic evaluation model for cow fertility. Variance components were estimated and the selection index model was extended to include this trait in order to evaluate the impact it would have on the accuracy of the fertility breeding value prediction.

MATERIALS AND METHODS

Data. The fertility data were extracted from the New Zealand national dairy database. This data included records from 1989 to 2013 for cows having at least heifer calving recorded. Mating and calving records from the first three lactations were considered. Data edits and fertility trait (PM21 and CSD) definitions were described in detail by Stachowicz *et al.* (2014a). Gestation length data were included for the cows that had fertility phenotypes, as well as for all the calves born to those cows. Gestation length was calculated as a difference in days between last recorded mating and calving date. Only artificial insemination matings were included.

Genetic analysis. Genetic analysis was carried out using ASReml software (Gilmour *et al.*, 2009). The fertility traits (PM21 and CSD) were analysed with the same model which corresponds to the one used in national genetic evaluations of fertility traits (Harris *et al.* 2005):

$$PM21 \text{ or } CSD = CG + Age*Breed + HF_{FR} + HF_{NZ}$$

$+ HET_{JExNZ} + HET_{JExFR} + HET_{NZxFR} + REC_{JExNZ} + REC_{JExFR} + REC_{NZxFR} + a + e.$

Gestation length was analysed with the following direct- maternal model:

$$GL = CG + SireCode + AgeD*BreedD + SexC*BreedC + dHF_{FR} + dHF_{NZ} + cHF_{FR} + cHF_{NZ}$$
$$+ dHET_{JExNZ} + dHET_{JExFR} + dHET_{NZxFR} + dREC_{JExNZ} + dREC_{JExFR} + dREC_{NZxFR}$$
$$+ cHET_{JExNZ} + cHET_{JExFR} + cHET_{NZxFR} + cREC_{JExNZ} + cREC_{JExFR} + cREC_{NZxFR}$$
$$+ a + m + mpe + e,$$

where:

- *CG* is the fixed contemporary group effect (herd-year-age for PM21 and CSD; herd-year-age of the dam for GL)
- *SireCode* is the sire official indicator
- *Age*Breed* is 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)
- *AgeD*BreedD* is the fixed linear regression of age of the dam in days nested within breed of the dam
- SexC**BreedC* is the fixed linear regression of sex of the calf nested within breed of the calf
- HF_{NZ} and HF_{FR} are fixed linear regressions of New Zealand and foreign Holstein-Friesian breed composition (*d* for dam; *c* for calf)
- *HET* and *REC* are fixed linear regressions of breed specific heterosis and recombination effects (*d* for dam; *c* for calf)
- *a* is a random animal effect
- *m* is a random maternal effect (model allowed for covariance between *a* and *m*)
- *mpe* is a random maternal permanent environmental effect
- *e* is a random error term.

The multivariate animal model included 8 traits: PM21 in parities 1-3, CSD in parities 0-3 (where 0 denotes heifer calving), and GL.

Selection index modelling. The selection index model, as described by Stachowicz *et al.* (2014b), was extended to predict the effects of including GL as predictor a trait in the fertility genetic evaluation model. It was also used to assess the effects of placing direct selection emphasis on GL (by including it in the BW index) on the rates of genetic change that might be expected in GL, fertility, and the overall annualised profit from dairy cattle genetic improvement in New Zealand. Direct selection emphasis on GL, in addition to using it as a correlated predictor of daughter fertility, may be justified in the future based on the effect the bull has as a service sire on the fertility of the cows to which he is mated.

RESULTS AND DISCUSSION

Genetic parameters. Estimated heritabilities, as well as genetic and residual correlations are presented in Table 1. Gestation length is a trait with very high heritability (0.68) as well as high and favourable genetic correlations with evaluated fertility traits (PM21 and CSD), while corresponding residual correlations remain low, which makes GL a perfect candidate as a predictor trait for fertility traits in a multiple trait evaluation.

Selection index modelling. These results indicate that including direct GL as a predictor trait in the fertility genetic evaluation model, in addition to the changes already considered by Stachowicz *et al.* (2014b), would further increase the accuracy of the fertility breeding value prediction. If GL was to be utilized in the BW index as well as a predictor trait in the fertility genetic evaluation model, then a further increase in the rate of genetic gain would be expected for both female fertility and GL. Including GL as a predictor trait in the fertility model and the BW index could increase annual industry profit by about $7 million. Including GL in the BW index only would allow for capturing around 20% of this amount. The phenotypic effects of GL on future fertility, production, survival and other traits were investigated and discussed by Jenkins *et* *al.* (2015).

Table 1. Residual correlations (below diagonal), genetic correlations (above diagonal) and heritabilities (diagonal) for PM21 in parities 1-3, CSD in parities 0-3 and GL (A=direct animal effect, M=maternal effect)

	CSD_0	CSD_1	CSD_2	CSD_3	PM21_1	PM21_2	PM21_3	GL_A	GL_M
CSD_0	**0.02**	0.66	0.39	0.40	0.07	0.22	0.04	0.57	0.08
CSD_1	0.12	**0.02**	0.30	0.34	-0.25	-0.03	-0.06	0.56	0.09
CSD_2	0.00	0.34	**0.01**	0.70	-0.49	-0.58	-0.42	0.45	0.09
CSD_3	0.03	0.06	0.16	**0.02**	-0.50	-0.47	-0.58	0.38	0.09
PM21_1	-0.12	-0.17	-0.05	-0.01	**0.03**	0.54	0.52	-0.15	-0.07
PM21_2	-0.04	-0.08	-0.16	-0.07	0.10	**0.06**	0.77	-0.21	-0.06
PM21_3	-0.03	-0.06	-0.11	-0.27	0.07	0.14	**0.05**	-0.22	-0.07
GL	0.01	-0.02	0.07	0.07	0.08	0.04	-0.02	**0.68**	-0.26

Recommendations. Based on data from a number of research projects, the following recommendations for changes in the national genetic evaluation model of fertility traits are made: 1) replace the binary CR42 with its continuous version CSD; 2) include heifer CSD in the model; 3) include the information on reproductive interventions in fertility phenotypes; 4) drop milk production traits from the model; 5) retain BCS in the model; 6) add GL as a new predictor trait to the model; 7) consider the inclusion of a direct GL EBV in the BW index to account for the advantage of shorter GL sires to the cows they are mated, over and above the improvements in the fertility of their daughters from shorter GL.

Future work. Variance components for the recommended model are currently being estimated. The next steps include the implementation of a new model for genetic evaluation to be run using the full national fertility data set. New results will be compared with the current genetic evaluation outcomes, prior to releasing new fertility breeding values to industry for consultation.

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