NEW MODEL FOR GENETIC EVALUATION OF FERTILITY IN NEW ZEALAND DAIRY CATTLE

K. Stachowicz[1], P.R. Amer[1], B. Falconer[2] and D.P. Garrick[3,4]

[1]AbacusBio Limited, PO Box 5585, Dunedin 9058, New Zealand
[2]DairyNZ Limited, Private Bag 3221, Hamilton 3240, New Zealand
[3]Theta Solutions LLC, Lacey, WA 98516, USA
[4]A.L. Rae Centre for Genetics and Breeding, Massey University, New Zealand

SUMMARY

The current genetic evaluation of female fertility in New Zealand (NZAEL2.0) is based on the binary phenotype of calving rate in the first 6 weeks of the calving season. Recent research suggests that using a continuous phenotype and including a heifer calving trait would increase the accuracy of fertility breeding values. This paper describes and investigates these factors in the context of a new fertility model proposed for New Zealand (NZAEL3.0). Industry implementation steps and results and comparisons of the validation work undertaken on NZAEL2.0 and NZAEL3.0 are presented. The results of the validation undertaken show that NZAEL3.0 is substantially better at predicting future fertility phenotypes compared to NZAEL2.0.

INTRODUCTION

In New Zealand, fertility is currently evaluated in NZAEL2.0 using two binary traits measured in first parity: calving rate within 6 weeks (CR) from planned start of calving (PSC) and percentage mated within 3 weeks (PM) from planned start of mating (PSM). This model has been substantially reduced compared to the previous model (NZAEL1.0) which used data across parities 1 to 3 (Harris *et al.* 2005). The reduction was to enable computational feasibility of the model when used in conjunction with genomic data. Research undertaken since 2013 indicated that redefining fertility as a continuous calving season day trait (CSD, Table 1) instead of using binary scores as per the current trait definition would increase the accuracy of the fertility evaluation (Bowley *et al.* 2015; Stachowicz *et al.* 2014a; Stachowicz *et al.* 2014b). This research has been summarised by Stachowicz *et al.* (2015), where rationale and recommendations for the proposed changes have been provided. The proposed model would consist of seven traits: four CSD and three PM traits. However, with application of genomic methodology such a model would not be computationally feasible. Therefore, a number of reduced models were tested (data not shown) and a seven-trait three breeding value model, where CSD or PM traits in parities 1 to 3 are modelled with the same breeding value, was selected for further assessment. Variance components estimated for this selected model as well as validation of the NZAEL2.0 and NZAEL3.0 models are presented in this paper.

MATERIALS AND METHODS

The proposed model for genetic evaluation of fertility consists of seven traits: CSD0, CSD1, CSD2, CSD3, PM1, PM2, and PM3, and three breeding values (EBVs): CSD0, CSD123, and PM123 (Table 1), where CSD1-3 and PM1-3 are records for 2nd to 4th calvings and matings leading to those calvings. For the purposes of variance component estimation, the data and the model described by Amer *et al.* (2016) and Stachowicz *et al.* (2015) was employed but fit with a repeated records model for CSD123 and PM123. Variance component estimation was carried out using ASReml software (Gilmour *et al.* 2009). NZAEL3.0 evaluations were carried out using BOLT software (Garrick *et al.* 2018) where the required 7x7 residual covariance matrix was derived from the estimated residual and permanent environment variance components estimated by the repeatability model fit in ASReml. The 3x3 additive genetic covariance matrix remained unchanged.

Current testing has focused on a lifetime fertility estimated breeding value:

$$\text{Fert EBV} = -1*(0.28*\text{CSD0} + 1.32*\text{CSD123})$$

where the coefficients applied to CSD0 and CSD123 are based on a relativity determined by the number of discounted expressions, and a scale based on conversion of CSD to CR scale.

The following validation approach was used. The genetic evaluation model was run on national data but with the last four seasons of phenotypic data removed (2016-2019). The full pedigree of ~26.7 million animals including those for cows with removed phenotypes was retained. Fertility records were extracted for 200 herds (approximately 19,000 cows). These cows were all born in 2014 and were sourced from 100 sire proving scheme herds of two breeding companies (CRV & LIC) and a further 100 herds identified as having high data quality scores. Table 1 describes in detail the phenotypes that were derived for these animals.

The validation approach involved classifying these ~19,000 cows into quintiles (5 groups of equal size) based on a specific genetic evaluation option where records from 2016 onwards are excluded (set to missing). Thus, we have 5 groups of animals ranging from high parent average prediction for fertility to low parent average prediction for fertility. We then fit each of the validation phenotypes (Table 1) from the 19,000 cows as a dependent variable in a model with quintile, contemporary group associated with the validation phenotype, and age at corresponding calving also fitted as independent variables. Least Squares Means (LSM) for quintile groups are then compared. A higher separation between the 1st and the 5th quintile group LSMs of validation phenotype values indicates a better performing genetic evaluation system for the target traits of interest.

Table 1. Abbreviations and trait definitions of validation phenotypes

Abbreviation	Trait definition
CR0	Calving rate for heifers, =1 (success) if calved in the first 6 weeks from PSC (binary)
CR1-3	As above but for cows' 2nd to 4th calving
TCD1-3	Timing of conception, days from PSM until the last recorded (successful) mating date after 1st to 3rd calving
3wICR1-3	3 week in-calf rate, =1 (success) if conceived within 3 weeks from PSM after 1st to 3rd calving (binary)
6wICR1-3	6 week in calf rate, =1 (success) if conceived within 6 weeks from PSM after 1st to 3rd calving (binary)
CSD0	Calving season day for heifers, days from PSC to 1st calving
CSD1-3	Calving season day for cows, days from PSC to calving for 2nd to 4th calving
PM1-3	Presented for mating in the 1st 3 weeks from PSM (binary, 1=success) after calvings 1 to 3
GL1-3	Gestation length culminating at 2nd to 4th calving

RESULTS AND DISCUSSION

The estimated variance components for the proposed model are presented in Table 2. Heritabilities and genetic correlations from the repeated records model tended to be higher than corresponding values from the multiple trait model (Stachowicz *et al.* 2015).

Table 2. Heritabilities (repeatabilities; on diagonal) and genetic correlations (off diagonal) for proposed repeated records model for genetic evaluation of fertility

	CSD0	CSD123	PM123
CSD0	0.034		
CSD123	0.686	0.047 (0.272)	
PM123	-0.525	-0.828	0.069 (0.143)

The results of the validation work are presented in Tables 3-5. Table 3 shows the phenotypic

performance contrast between the 1st and 5th quintiles when validation heifers were assigned to these based on alternative parent average genetic predictions. The NZAEL3.0 fertility EBV outperformed the NZAEL2.0 fertility EBV for predicting 6-week in-calf rate, with the difference being substantial (i.e. roughly twice as good) for later parities. Typically, second calving cows constitute a little under 20% of the herd, and so when it comes to predicting whole herd fertility, a paradigm shift in accuracy of fertility genetic merit prediction should be expected with the new approach. There was less difference between the methods for predicting submission rate than there was for in-calf rate after three weeks (Table 4). The NZAEL3.0 fertility EBV was substantially better than the NZAEL2.0 EBV for predicting the ability of cows to calve earlier in the season (Table 5), and also to conceive earlier in the season.

Table 3. Phenotypic performance difference between animals assigned to their 1st versus 5th quintile based on alternative parent average (PA) EBVs taken from alternative evaluation validation runs – Six week in calf rate (6wICR) and gestation length (GL)

Fertility EBV	PA Spread[1] Proposed	PA Spread[1] Current	6wICR1	6wICR2	6wICR3	GL1	GL2	GL3
NZAEL 3.0	10.63	2.92	0.076	0.070	0.070	-0.9	-1.2	-1.2
NZAEL 2.0	6.41	4.57	0.068	0.048	0.031	-0.7	-0.6	-0.5
CSD0	-7.24	-1.81	-0.048	-0.041	-0.035	1.3	1.1	1.3

[1]PA spread for current and proposed EBV indicate the predicted differences in parent average based spread between the first and 5th quintiles of validation animals for the proposed new fertility breeding value, and for the current fertility breeding value, respectively.

The NZAEL3.0 fertility EBV will be expected to bring heifer calving forward (e.g. 1.5 day difference and 1.5% more calving in the first 6 weeks between the 1st and 5th quintiles when compared with the NZAEL2.0 EBV in Table 4), with about 1/3 of the difference (i.e. about 0.5 days when weighted across parities) attributable to shorter gestation length (Table 3). In general, the relationship between fertility EBV and gestation length is only slightly stronger for NZAEL3.0 than for NZAEL2.0 EBV. For example, NZAEL3.0 gives a 66% increase in separation for 6-week in calf rate weighted across parities, and this corresponds to a 100% increase in separation for gestation length (Table 3). In general, it seems likely that farmers would accept a 1.2 day shorter average gestation length as part of a genetic package that gives a 7% gain in 6-week in calf rate. Further, a comprehensive analysis of NZ data by Jenkins *et al.* (2016) indicated that the disadvantages at the extreme short end of the gestation length scale from shortening population average gestation length are more than offset by the gains from reduction in calvings at the extreme long gestation length end of the scale. While earlier born heifer calves have one less day in utero, they have one more day post-partum before the commencement of the heifer mating season.

Table 4. Phenotypic performance difference between animals assigned to their 1st versus 5th quintile based on alternative parent average EBVs taken from alternative evaluation validation runs – Three week in calf (3wICR) and three week submission rates (PM)

Fertility EBV	3wICR1	3wICR2	3wICR3	PM1	PM2	PM3
NZAEL 3.0	0.114	0.134	0.103	0.107	0.119	0.102
NZAEL 2.0	0.074	0.091	0.063	0.092	0.101	0.094
CSD0	-0.069	-0.071	-0.058	-0.042	-0.058	-0.043

The alignment between the difference in EBVs between quintiles, and the difference in

phenotypic performance for calving by 6 weeks was approximately 1:1 for the NZAEL3.0 EBV (compare 10.63% difference in PA in Table 3 with .104 to .125 proportional differences observed in CR1, CR2 and CR3 in Table 4). In comparison, the 6.41% difference in PA from the NZAEL2.0 EBV in Table 3 under predicted the .07 to .09 differences in CR1 observed phenotypically).

Results for a univariate prediction of breeding values for calving season day for first calving heifers have been included in Tables 3 to 5. Low values (earlier calving) are better for this trait, so the signs of the phenotypic differences between the 1st and the 5th quintiles is negative for validation phenotypes where positive is favourable. These roughly reflect the likely outcome of evaluating bulls based on the first calving dates of their first crop of daughters at their first calving using the proposed fertility evaluation. This would give an indication of fertility approximately 3 months earlier than evaluations based on submission rate after 1st calving. The degree of separation in validation phenotypes with selection on CSD0 EBVs from the NZAEL3.0 model is very encouraging, albeit not quite as good as the NZAEL2.0 model, and only 50 to 60% as effective as when using the full evaluation that incorporates all phenotypes. While these evaluations, based on first calving date records only, will have a stronger association with shorter gestation length (Table 3), the values are not of sufficient magnitude to be of concern.

Table 5. Phenotypic performance difference between animals assigned to their 1st versus 5th quintile based on alternative parent average EBVs taken from alternative evaluation validation runs – Calving traits (CR and CSD)

Fertility EBV	CR0	CR1	CR2	CR3	CSD0	CSD1	CSD2	CSD3
NZAEL 3.0	0.047	0.116	0.104	0.125	-4.13	-6.93	-6.89	-5.97
NZAEL 2.0	0.032	0.091	0.084	0.074	-2.58	-5.66	-5.27	-3.95
CSD0	-0.041	-0.083	-0.071	-0.073	3.65	5.04	4.86	4.19

CONCLUSIONS

This study shows that the proposed NZAEL3.0 model for genetic evaluation of fertility outperforms the current NZAEL2.0 model for all of the phenotypes tested. Higher accuracies of fertility breeding values would be expected with the NZAEL3.0 model as well as the improvement in early predictions due to the inclusion of the heifer calving trait into the evaluation. The increased indirect response in shortening of gestation length could become a concern over time, and future work is planned to identify a new phenotype for evaluation based on pregnancy diagnosis, which targets earlier conception and is independent from gestation length.

REFERENCES

Amer P.R., Stachowicz, K., Jenkins, G.M. and Meier S. (2016) *J. Dairy Sci.* **99**: 8227.

Bowley F.E., Green R.E., Amer P.R. and Meier S. (2015) *J. Dairy Sci.* **98**: 2005.

Garrick D.J., Garrick D.P. and Golden B.L. (2018) *Proceedings of the 11th World Congress on Genetics Applied to Livestock Production,* **11**: 973.

Gilmour A.R., Gogel B.J., Cullis B.R. and Thompson R. (2009) VSN International Ltd, Hemel Hempstead, HP1 1ES, UK. www.vsni.co.uk.

Harris B.L., Pryce J.E., Xu Z.Z. and Montgomerie W.A. (2005) *Interbull Bull.* **33**: 47.

Jenkins G.M., Amer P., Stachowicz K. and Meier S. (2015) *J. Dairy Sci.* **98**: 418.

Stachowicz K., Jenkins G.M., Amer P.R. and Meier S. (2014a) *Interbull Bull.* **48**: 89.

Stachowicz K., Jenkins G.M., Dennis N.A., Amer P.R., Bryant J. and Meier S. (2014b) *Proc. of the 5th Australasian Dairy Science Symposium*, pp 65.

Stachowicz K., Jenkins G.M., Amer P.R., Bryant, J.R. and Meier S. (2015) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **21**: 370.