

**PREDICTION OF GESTATION LENGTH AND DAYS TO CONCEPTION FROM  
FOETAL AGE SCANS FOR GENETIC IMPROVEMENT OF MATERNAL FERTILITY  
IN BEEF COW HERDS: A SIMULATION STUDY**

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**SUMMARY**

A stochastic simulation model has been used to investigate the potential for combining foetal aging and birth date information to distinguish days to conception (DTCon) from gestation length (GL) under natural mating scenarios. The use of this data in genetic evaluations was assessed, with allowance for the error arising from an allocation to 5- or 10-day increments. The model for genetic evaluation included random additive genetic, permanent environmental and residual effects. Introducing an error associated with foetal aging of animals increased the error variances for DTCon and GL but had little effect on the additive genetic variances, resulting in overall lower heritabilities for both traits. Accounting for the foetal aging error, however, reduced the accuracies for estimated breeding values (EBV) only slightly, and this was true for sires, dams and progeny. The simulation outcomes indicate that foetal aging can be used as a tool to accurately predict the genetic merit of different classes of animals (sires, dams and progeny) for DTCon and to predict GL EBV with improved accuracies due to a larger number of phenotypes from naturally mated beef cow herds so long as the prediction of foetal aging can be done as accurately as 5, or 10 days.

**INTRODUCTION**

Genetic improvement of cow fertility within New Zealand beef cow herds is mainly achieved by selecting on traits such as days to calving (DTC) or gestation length (GL). Currently, DTC phenotypes require knowledge of the start date of mating and calving date records based on natural (unsynchronised) mating, while GL is based on the number of days between artificial insemination (AI) of cows and subsequent calving date (Graser *et al.* 2005). While the main variation in DTC is due to differences in the conception date following bull exposure, the use of birth date data alone does not allow for the separation of effects of conception date and GL under natural mating scenarios. Although evaluating GL includes information on the conception date, this is based on AI rather than natural mating (Graser *et al.* 2005) and is therefore only available on a restricted subset of animals. The use of foetal aging at pregnancy scanning may be a useful tool to separate the effects of days to conception (DTCon) and GL for naturally mated cows, providing an improved estimate of cow fertility (ability to conceive) and enabling GL estimated breeding values (EBV) to be assessed much more accurately on a larger sample of bulls. Foetal aging can be accurate to 5-day increments (Tweedie *et al.* 2019) such that an element of error is associated with the measurement of conception date from foetal age scans (White *et al.* 1985). The aim of this study was to develop a stochastic simulation to evaluate the impact of error associated with DTCon and GL estimated from foetal age scans and the applicability of foetal aging as a tool to separate the effect of DTCon and GL from DTC for the use in genetic evaluations.

**MATERIALS AND METHODS**

**Simulation model overview.** The simulation model was built using R version 4.2.1 (R Core Team 2019). The model simulated a beef cow herd and their progeny from mating to their subsequent calving for twenty consecutive years under New Zealand hill country conditions. The model ran simulations on an individual animal level and produced key production outcomes for the traits DTCon, GL and DTC. The cows simulated in the model were managed in an individual herd

within the same mob, assuming the same environmental conditions and management strategies. The size of the cow herd at the start of the simulation was set to 1,000 animals.

**Annual production cycle.** Cows were mated annually via natural mating for a total of 63 days, allowing them to cycle 3 times based on a 21-day cycling interval. The percentage of bulls used for mating was set to 2 percent of the herd size aligning with typical farming practices within New Zealand beef breeding herds. Each year 50 percent of the bulls were replaced randomly. Cull cows were removed from the breeding herd after weaning of their calf at foot. Culling was conducted firstly due to cows not getting in calf and secondly due to age (cows older than 10 years of age were removed from the breeding herd). The annual replacement rate was set to 20 percent of the herd, such that additional cull cows were selected randomly from the remaining herd if the number of cull cows due to failure to conceive or age were below the threshold to maintain the herd size of 1,000 cows across multiple years. The model simulated a self-replacing herd where female progeny were retained and first mated at 2 years of age. The average number of progeny per sire was 81 ( $\pm 66$ ).

**Simulated phenotypes.** The true phenotype for DTCon (trait of the cow) for each animal  $i$  was calculated annually at time  $t$  as

$$DTCon_{it} = \mu + TBV_i + pe_i + e_{it}$$

and GL (trait of the calf) was calculated as

$$GL_i = \mu + TBV_i + e_i$$

where  $\mu$  was the overall mean of the population for each trait;  $TBV_i$  was the true breeding value of animal  $i$  for DTCon or GL;  $pe$  was a permanent environmental effect due to repeated records of the animal and  $e$  a temporary environmental effect. True breeding values of calves were calculated as  $TBV = 0.5(TBV_{sire} + TBV_{dam}) + ms$  where  $ms$  was a mendelian sampling component. True breeding values of the base population (i.e., sires ( $TBV_{sire}$ ) and dams ( $TBV_{dam}$ )), mendelian sampling components, permanent and temporary environmental effects were simulated from a Log-normal distribution for DTCon or Normal distribution for GL with zero means and variances equal to  $\sigma_a^2$ ,  $0.5\sigma_a^2$ ,  $\sigma_{pe}^2$  and  $\sigma_e^2$ , respectively (Table 1). Genetic correlations between DTCon and GL were set to zero. Phenotypes for DTC were obtained as the sum of DTCon and GL for each cow.

**Table 1. Simulation input parameters for days to conception (DTCon) and gestation length (GL): phenotypic means ( $\mu$ ), heritabilities ( $h^2$ ), additive genetic ( $\sigma_a^2$ ), permanent ( $\sigma_{pe}^2$ ) and temporary ( $\sigma_e^2$ ) environmental variances**

Trait	$\mu$	$h^2$	$\sigma_a^2$	$\sigma_{pe}^2$	$\sigma_e^2$	References
DTCon <sup>1</sup>	2.87	0.21	0.15	0.28	0.28	Weik <i>et al.</i> (2021)
GL	282	0.64	11.83	0.00	6.66	Crews (2006)

<sup>1</sup>Values on the logarithmic scale.

**Simulation of foetal aging error.** A foetal aging error was added to the simulated DTCon phenotypes by rounding values to the nearest 5 (DTCon<sub>5</sub>) or 10 increments (DTCon<sub>10</sub>). This error was introduced to reflect the error associated with foetal aging, which is generally only accurate to 5-day (or 10-day) increments (White *et al.* 1985). Similarly, GL phenotypes were adjusted, aligning with the foetal aging error to obtain GL<sub>5</sub> and GL<sub>10</sub>.

**Genetic evaluation.** Genetic evaluation was performed in ASReml (Gilmour *et al.* 2009) using univariate animal models. The following equation was used for genetic evaluation:

$$y_{ij} = \mu_i + a_{ij} + pe_{ij} + e_{ij}$$

for DTCon, DTCon<sub>5</sub>, DTCon<sub>10</sub> and DTC due to repeated records on the same animal, or

$$y_{ij} = \mu_i + a_{ij} + e_{ij}$$

for GL, GL<sub>5</sub> and GL<sub>10</sub> with no repeated records on the same animal, where  $y_{ij}$  was the phenotype of animal  $i$  for trait  $j$ ;  $\mu_j$  was the mean for trait  $j$ ;  $a_{ij}$  was the random additive genetic effect of animal  $i$

for trait  $j$ ;  $pe_{ij}$  the permanent environmental effect of animal  $i$  for trait  $j$  and  $e_{ij}$  the random residual effect unique to each  $y_{ij}$ . Cows that failed to conceive were included in the analysis by assigning a penalty of 21 days to DTCon, DTCon<sub>5</sub> and DTCon<sub>10</sub> from the last conception date within the herd (Meyer *et al.* 1990).

**Model application.** A total of 10 replicates were simulated, and key outcomes were averaged across replicates to determine the mean and SD for DTCon, GL and DTC EBV. Estimated breeding values were obtained for 3 classes of animals which were sires, dams and animals without progeny of their own (i.e., animals born in the last year of the model run). The accuracies of EBV were assessed within each grouping as the correlations between simulated TBV and EBV.

## RESULTS AND DISCUSSION

Variances and heritabilities from univariate models for each trait are presented in Table 2. For both DTCon and GL the additive genetic variances were similar with or without the error associated with foetal aging, whereas the phenotypic variance increased. This resulted in a decline in heritability estimates from 0.20 to 0.16 for DTCon and from 0.63 to 0.43 for GL.

**Table 2. Simulated additive genetic ( $\sigma^2_a$ ), permanent ( $\sigma^2_{pe}$ ) and temporary ( $\sigma^2_e$ ) environmental variances, heritabilities ( $h^2$ ) and repeatabilities ( $t$ ) with standard errors shown in brackets for all traits considered in the analysis**

	$\sigma^2_a$	$\sigma^2_{pe}$	$\sigma^2_e$	$h^2$	$t$
DTCon <sup>1</sup>	0.14 ( $\pm 0.02$ )	0.28 ( $\pm 0.01$ )	0.28 ( $\pm 0.003$ )	0.20 ( $\pm 0.02$ )	0.60 ( $\pm 0.01$ )
DTCon <sub>5</sub> <sup>1,2</sup>	0.13 ( $\pm 0.01$ )	0.24 ( $\pm 0.01$ )	0.28 ( $\pm 0.003$ )	0.19 ( $\pm 0.02$ )	0.57 ( $\pm 0.01$ )
DTCon <sub>10</sub> <sup>1,2</sup>	0.18 ( $\pm 0.02$ )	0.37 ( $\pm 0.02$ )	0.59 ( $\pm 0.01$ )	0.16 ( $\pm 0.02$ )	0.48 ( $\pm 0.01$ )
GL	11.65 ( $\pm 0.43$ )	-	6.77 ( $\pm 0.23$ )	0.63 ( $\pm 0.02$ )	-
GL <sub>5</sub> <sup>2</sup>	11.60 ( $\pm 0.47$ )	-	8.81 ( $\pm 0.27$ )	0.57 ( $\pm 0.02$ )	-
GL <sub>10</sub> <sup>2</sup>	11.83 ( $\pm 0.58$ )	-	15.46 ( $\pm 0.37$ )	0.43 ( $\pm 0.02$ )	-
DTC <sup>1</sup>	0.00032 ( $\pm 0.00004$ )	0.00062 ( $\pm 0.00004$ )	0.00113 ( $\pm 0.00001$ )	0.15 ( $\pm 0.02$ )	0.45 ( $\pm 0.01$ )

<sup>1</sup>Values on the logarithmic scale.

<sup>2</sup>Error of 5 or 10 days associated with DTCon and GL records due to foetal aging.

Overall, EBV accuracies decreased with an increase in error associated with foetal age scanning of cows, and this was true for both DTCon and GL across all animals considered in the analysis (Table 3). However, the reduction in accuracy was small and decreased for the prediction of sire EBV from 0.73 to 0.71 for DTCon and from 0.97 to 0.95 for GL. Results indicated that the genetic merit of each class of animals may be assessed reasonably accurately for DTCon and GL using foetal age scanning, irrespective of the error associated with the actual measurement.

Although the error arising from foetal age scanning had a more prominent impact on the accuracy of GL EBV compared to DTCon EBV (especially for animals with less information on relatives), outcomes are likely to provide a suitable estimate for the duration of gestation from naturally mated beef cow herds. This would increase the number of phenotypes available independent of AI information, leading to an increase in accuracies for GL EBV. This has potential implications for beef on dairy herds such that a larger number of beef bulls may be identified with shorter GL to use over dairy cows to increase days in milk (Coleman *et al.* 2021).

Outcomes from this study indicate that foetal aging may be used as a tool to determine the ability of cows to conceive following natural mating and may provide a better estimate of cow fertility compared to DTC due to overall higher accuracies for each class of animal. Currently, foetal aging using transrectal ultrasonography is the most common method in New Zealand for estimating conception date under extensive farming systems (Brownlie *et al.* 2016). The highest accuracy may be obtained when cows are scanned between 42 and 90 days of gestation (White *et al.* 1985). The

restricted mating season with seasonal calvings and high pregnancy rates in New Zealand farming systems would allow foetal aging to be estimated across the entire herd on a single day (Brownlie *et al.* 2016). This has the potential for wider use across the New Zealand beef population and may be implemented in a cost-effective and efficient way at pregnancy scanning when animals are yarded together. Future research may consider using other technologies, such as neck collars to measure cycling activity more accurately and provide a prediction of the actual conception day without error.

**Table 3. Distribution of true (TBV) and estimated (EBV) breeding values and their accuracies for days to conception (DTCon), gestation length (GL) and days to calving (DTC) for 3 different classes of animals**

Trait	Estimate	Sires			Dams			Progeny		
		Mean	SD	Acc	Mean	SD	Acc	Mean	SD	Acc
DTCon	TBV	0.00	0.37		-0.03	0.37		-0.04	0.37	
	EBV	0.01	0.27	0.73	-0.03	0.23	0.62	-0.04	0.13	0.32
DTCon <sub>5</sub> <sup>1</sup>	EBV	0.01	0.26	0.73	-0.03	0.22	0.62	-0.04	0.12	0.32
DTCon <sub>10</sub> <sup>1</sup>	EBV	0.01	0.30	0.71	-0.02	0.25	0.60	-0.03	0.14	0.30
GL	TBV	0.00	3.27		0.04	3.40		0.15	3.36	
	EBV	0.03	3.18	0.97	0.05	2.82	0.83	0.16	2.83	0.84
GL <sub>5</sub> <sup>1</sup>	EBV	0.01	3.17	0.96	0.03	2.75	0.81	0.15	2.74	0.81
GL <sub>10</sub> <sup>1</sup>	EBV	-0.01	3.14	0.95	0.02	2.62	0.76	0.11	2.56	0.75
DTC	TBV	0.00	3.29		0.00	3.43		0.11	3.39	
	EBV	0.00	0.01	0.30	0.00	0.01	0.29	0.00	0.01	0.19

<sup>1</sup>Error of 5 or 10 days associated with DTCon and GL records due to foetal aging.

## CONCLUSIONS

The simulation study has demonstrated the value of foetal aging as a tool to separate the effects of DTCon and GL from DTC records for naturally mated beef cows. Foetal aging has the potential to add value to future genetic evaluations by providing an improved estimate of fertility based on the cows' ability to conceive and allowing more bulls from naturally mated beef cow herds to be evaluated for GL EBV with higher accuracies.

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