

## NEW MODULE FOR PREDICTION OF REPRODUCTIVE TRAITS EBV IN BREEDPLAN

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### SUMMARY

BREEDPLAN publishes EBVs for days to calving (DTC) from natural mating (NAT) as the key measure of genetic merit for female reproduction. More recently, oestrus synchronization and artificial insemination (AI) have become more widely used in beef cattle in Australia to improve reproductive efficiency. The aim of this study was to develop a reproductive module to predict reproductive performance in beef cattle in Australia by using mating outcomes from AI, NAT from females and scrotal circumference (SC) in males. The study analysed mating and calving data collected on Angus cattle in Australia and New Zealand using the events-based recording system introduced in 2010. Genetic parameters for 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> parities conception rate (CR) to AI and DTC from NAT were estimated. Mean CR from 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> parities of AI were 51.5%, 56.2% and 70.4% and for DTC of NAT were 303, 308 and 305 days, respectively. Estimated heritability for CR from 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> parities were 0.15, 0.12 and 0.10 and for DTC were 0.05, 0.11 and 0.14, respectively. Moderate negative genetic correlations (-0.41 to -0.10) were estimated between CR and DTC of all three parities and were significantly lower than 1 suggesting that they were different traits. Therefore, there are benefits in genetic evaluation from including AI data and modelling parities as different traits.

### INTRODUCTION

Cow reproductive efficiency is important for the productivity and profitability of beef cattle in Australia. DTC has been implemented in the BREEDPLAN genetic evaluation as the key measure of genetic merit for female reproduction in naturally mated (NAT) females (Schneeberger *et al.* 1991). DTC is calculated as the number of days between the first joining date for a cow and its subsequent calving. However, low heritability, low intensity of selection together with repeat observations accumulating relatively late in life limit the capacity to improve female fertility using DTC measures alone. More recently, oestrus synchronization and AI have become more widely used in beef cattle in Australia to improve reproductive efficiency and increase genetic gain, and has now become the dominant mating technique for seedstock breeders in temperate Australia. CR to AI has been proposed as an important trait to describe reproductive performance in heifers (Bormann *et al.* 2006). However, published heritabilities for CR were also low (Bormann *et al.* 2006) and relationship to natural joining traits unknown. Therefore, we combined several measures of male and female traits to increase the accuracy of EBVs for fertility traits in Angus cattle.

### MATERIALS AND METHODS

An enhanced event-based recording system was introduced in 2010 for submission of records for genetic evaluation of reproductive efficiency in BREEDPLAN. This recording system includes all mating events such as mating and pregnancy test outcomes, in addition to culling and disposal dates as well as codes identifying all heifers and cows subjected to synchronization, AI and/or NAT. Mating and calving records for AI and NAT, along with the pedigree data, were obtained for heifers and cows in the BREEDPLAN evaluation for Angus cattle in May 2022. Initial examination of the

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data revealed incomplete data submission for animals from unsuccessful mating. Therefore, 400-days weight management groups were used to eliminate these selective records from AI or NAT. Only contemporary groups with more than 90% of heifers with 400-day weight records also having mating records (either AI or NAT) were included.

Currently in BREEDPLAN, DTC for NAT, was defined as the number of days from “bull in date” to the resultant calving and all non-calving cows were included by assigning a penalty DTC record as described by Johnston and Bunter (1996). Up to 6 DTC records per cow, in a repeatability model, are used to predict EBVs. In this study, for AI mating traits, CR was defined as a binary trait with females, who calved to the first AI sire used, recorded as 1 and those which failed to calve as 0. Records of heifers initially mated by AI, but conceived to subsequent AI or NAT, were analysed as failing (0) to calve to the first AI. Similarly, to DTC, CR to AI for heifers aged between 270 to 625 days at the time of first breeding were identified and their parity records between 270 to 625, 626 to 990 and 991 to 1340 days were defined as 1<sup>st</sup> (CR1), 2<sup>nd</sup> (CR2) and 3<sup>rd</sup> (CR3) CR records, respectively. Scrotal circumference (SC) records of males and their contemporaries measured for DTC and CR, were also included as an extra trait in the analyses. Number of records and descriptive statistics for CR using AI, DTC using NAT and SC are presented in Table 1.

Combined threshold and linear animal models were used to estimate genetic parameters for binary traits (CR) and linear traits (DTC and SC).

$$\text{Model for CR was } l_{ijs} = cg_i + age_j + age_j^2 + a_j + s_s + e_{ijs}$$

Where  $l_{ijs}$  is the liability on the underlying scale for the CR score of animal  $j$  in a fixed contemporary group  $i$  ( $cg_i$ ) and  $age_j$  and  $age_j^2$  are linear and quadratic covariates for age at mating,  $a_j$  is the random additive genetic effect of female  $j$ . The  $s_s$  is an additional random effect of service sires. The random error variance was fixed at 1. The contemporary group included herd of birth, year of birth and date of AI. Bayesian analysis, using Gibbs sampling, was used to estimate the means of marginal posterior distributions for CR. The analysis was carried out using THRGIBBS1F90 (Misztal *et al.* 2002). Single chains of 100,000 iterations were sampled with the first 20,000 samples discarded. Every 20<sup>th</sup> sample was stored and a total of 4,000 were kept to compute posterior means and highest posterior density interval (95%) credible regions.

$$\text{Model for DTC was } Y_{ij} = cg_i + age_j + age_j^2 + a_j + e_{ij}$$

Where  $Y_{ij}$  is the DTC of female  $j$  in a fixed contemporary group  $i$  ( $cg_i$ ),  $age_j$  and  $age_j^2$  are linear and quadratic covariates for age at mating,  $a_j$  is the random additive genetic effect of female  $j$  and  $e_{ij}$  is the random error associated with this observation. The contemporary group included herd of birth, year of birth and service sire as defined in BREEDPLAN (Graser *et al.* 2005). In order to account for the selection of data in the 2<sup>nd</sup> and 3<sup>rd</sup> AI and NAT, a tri-variate analysis using CR and DTC records from all parities was performed.

$$\text{Model for SC was } Y_{ijk} = cg_i + age_j + age_j^2 + age_k + age_k^2 + a_j + e_{ijk}$$

Where  $Y_{ijk}$  is the SC of male  $j$  in a fixed contemporary group  $i$  ( $cg_i$ ),  $age_j$  and  $age_j^2$  are linear and quadratic covariates for age at measurement,  $age_k$  and  $age_k^2$  are linear and quadratic covariates for age of dam at birth in days,  $a_j$  is the random additive genetic effect of male  $j$  and  $e_{ijk}$  is the random error associated with this observation.

Estimates of (co)variance components and solutions for fixed effects of DTC for NAT were obtained by REML using an Average Information algorithm (AI algorithm) and the Expectation-maximisation algorithm (EM algorithm) in WOMBAT (Meyer 2007). Genetic correlations between CR, DTC and SC were estimated in a multivariate animal model by combining the threshold model for CR with linear models for DTC and SC. Models identified for the univariate analysis were used in the multi-variate analysis. Pedigree information from up to six generations was used. All multivariate animal model analyses were carried out using THRGIBBSF90 (Misztal *et al.* 2002).

## RESULTS AND DISCUSSION

Descriptive statistics for the data used in this analysis are presented in Table 1. Mean ages of heifers at first mating were very similar for AI and NAT and were 434 and 439 days, respectively. However; there was a large difference in the mean calving rate for heifers mated by AI as compared to NAT (51.5% for CR1 and 93.4 for DTC1). Expertise of oestrous synchronization, heat detection and AI all influence the CR for AI heifers. Furthermore, NAT heifers may have had more than one exposure to bulls and more than one expression of heat in the natural mating period. Similar mean calving rate of 93% was observed for 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> NAT, as well as for their DTC for 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> parities (303, 308 and 305 days respectively). The percentage of females conceiving to first insemination using AI was similar to the value of 60% reported by Bormann *et al.* (2006) for American Angus heifers. Donoghue *et al.* (2004a) reported 79.3% for first CR of Angus cattle in Australia. The higher rate observed may be due to the incomplete submission of data analysed for that study where some reproductive data from animals with unsuccessful mating outcomes were not recorded or included. Furthermore, the data used in Donoghue *et al.* (2004a) were collected prior to 2003 and the data used in this analysis were collected after 2010.

**Table 1. Descriptive statistics for 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> parity conception rate to artificial insemination (AI) and days to calving to natural mating (NAT) of heifers and cows and scrotal circumference (SC) of bulls**

Variables	AI			NAT (days)			SC (cm)
	1 <sup>st</sup>	2 <sup>nd</sup>	3 <sup>rd</sup>	1 <sup>st</sup>	2 <sup>nd</sup>	3 <sup>rd</sup>	
Number of records	13233	5119	2717	25291	12196	3695	14516
Number of sires	1052	531	357	4014	2275	1112	1274
Number of dams	8805	3778	2148	20684	9357	3347	10083
Number of contemporary groups	165	168	141	2204	1155	850	710
Mean age (days)	434.1	811.8	1174.1	439.4	761.2	1173.7	394.8
(SD)	(22.9)	(31.8)	(24.9)	(37.8)	(38.4)	(34.4)	(45.7)
Mean conception rate (%)	51.5	56.24	70.4	93.4	92.8	93.0	
Trait means				303.4	308.3	305.2	36.6
(SD)				21.4	22.4	20.6	2.97

Estimated posterior means for additive genetic variances, heritabilities and genetic correlations are presented in Table 2. Estimated additive variance and heritabilities for DTC2 and DTC3 were higher than DTC1, supporting the need for splitting the DTC records based on parities. Similar low heritabilities were estimated for CR1, CR2 and CR3. Low to moderate negative genetic correlations were estimated between CR of first three parities using AI and DTC from the first three parities using NAT, illustrating that higher CR is associated with shorter DTC. Overall, the genetic correlations between CR and DTC were lower than 1, suggesting that the CR and DTC were different traits. This is expected for the reasons given in the previous paragraph and in addition, CR is a binary trait and DTC is a continuous trait. Low genetic correlations were estimated between SC with CR and DTC was a continuous trait. Therefore, the data from CR and SC could increase the accuracy of DTC EBVs, enhancing the scope for selection and genetic improvement of female reproduction in Angus heifers.

Additive variance for CR1 was 0.09 and was lower than the value of 0.11 reported by Bormann *et al.* (2006) for American Angus heifers. However, the estimated heritability was slightly higher than the value of 0.03 reported by Donoghue *et al.* (2004b) for Angus heifers in Australia. This may be due to the fact that the herds selected in this study, have minimised the incomplete submission of

data for animals from unsuccessful mating than the above study. Estimated additive genetic variance and heritabilities for DTC1 of NAT heifers were 16.6 and 0.05 ( $\pm 0.02$ ) respectively. Estimated heritability was slightly lower than the value of 0.06 reported by Donoghue *et al.* (2004b). The genetic correlation between CR and DTC of 1<sup>st</sup> NAT was lower in magnitude than the value of -0.66 reported by Donoghue *et al.* (2004b).

**Table 2. Estimated additive genetic variances ( $\sigma^2_a$ ), heritabilities ( $h^2$ ) and genetic correlations for 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> parity conception rate by artificial insemination (AI) and days to calving by natural mating (NAT) and scrotal circumference (SC) in bulls**

Traits <sup>ab</sup>	$\sigma^2_a$	$h^2$	Genetic correlations					
			2 <sup>nd</sup> AI	3 <sup>rd</sup> AI	1 <sup>st</sup> NAT	2 <sup>nd</sup> NAT	3 <sup>rd</sup> NAT	SC
1 <sup>st</sup> AI	0.09	0.08	0.31	0.47	-0.29	-0.14	-0.10	0.10
2 <sup>nd</sup> AI	0.17	0.13		0.44	-0.33	-0.37	-0.34	0.15
3 <sup>rd</sup> AI	0.13	0.12			-0.22	-0.31	-0.41	0.23
1 <sup>st</sup> NAT	16.62	0.05				0.61	0.52	-0.17
2 <sup>nd</sup> NAT	38.21	0.11					0.44	-0.12
3 <sup>rd</sup> NAT	43.73	0.14						-0.10
SC	2.71	0.53						

<sup>a</sup> standard deviation from 4000 iterations from threshold model ranged between 0.04 to 0.06

<sup>b</sup> approximate standard error from linear model evaluation ranged between 0.02 to 0.06.

## CONCLUSIONS

This study has shown AI mating records could be included in genetic evaluation of reproduction traits. Higher estimated additive variance and heritabilities for DTC2 and DTC3 than that of DTC1, suggest that separation of DTC records based on parities also benefits the evaluation. Moderate to high non-zero genetic correlations were estimated between CR from the first three AI and DTC from the first three NATs, suggesting that both CRs from AI mating and DTC from NAT need to be included in the BREEDPLAN evaluation to enhance selection for higher heifer fertility. The CR and DTC traits reported here, together with SC, will form the core of a new reproduction trait analysis for BREEDPLAN.

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