

GENETIC PARAMETERS OF POST-PARTUM REPRODUCTIVE STATUS IN BEEF CATTLE FROM NORTHERN AUSTRALIA

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SUMMARY

Lifetime reproductive performance is a major issue for the Northern Australian beef industry. Delayed cycling of lactating cows after parturition is one of major causes of reproductive inefficiency and impacts on the profitability of beef businesses. In the CRC for Beef Genetic Technologies, genetic markers have been used to develop prediction equations for the improvement of post partum anoestrus interval in tropically adapted beef cattle. An independent cattle population was established to validate these prediction equations. Data were collected at weaning on 4286 cows from 27 herds of 4 breeds in Northern Australia. Using ultrasonic ovarian scans and pregnancy tests, cows were scored for the reproductive status (REP3): 1) being pregnant (P), or 2) having a *corpus luteum* (CL), or 3) having a follicle (F). REP3 was also rescored into two binary traits: PREG2: pregnant (P) or not pregnant (F or CL) and HEAT2: cycling (P or CL) or not cycling (F). A threshold model was fitted to estimate genetic variance for these three traits. Analyses were implemented using both REML (sire model) and Gibbs Sampler (animal model) for the pooled dataset and two large breeds. The heritability estimates for reproductive status, either in REP3 or binary traits (PREG2 and HEAT2) were low to moderate. Results from REML and Gibbs Sampler were similar for REP3 and PREG2. The practical and important trait is PREG2. For this trait, the estimates of heritability in this study ranged from 0.15 to 0.22. These data may provide a useful resource for validating genomic prediction equations.

INTRODUCTION

Female reproductive rate is important to the Northern Australian beef industry, specifically the number of calves produced over the lifetime of breeding females. However, improvement of reproductive rate using traditional selection practices has had limited success because of the long generation interval, the difficulty of collecting phenotypes and low heritabilities of industry measured traits, such as calving rate and days to calving (Meyer *et al.* 1990, Johnston and Bunter 1996). Recently, a large heritability (0.52) of a specific component of reproduction rate - length of *post partum* anoestrous interval (PPAI, measured as the time of the first detected *corpus luteum* (CL) after first calving) - was estimated in 3 years old Brahman (Johnston *et al.* 2010). The high heritability for this component trait, especially in these cattle, suggests there is potential to exploit this genetic variation and improve female reproduction in Brahman.

Genomic selection offers an alternative approach. One of the main goals of the CRC for Beef Genetic Technologies is to develop genomic selection tools that can be used to increase calving rates of cattle, particularly Brahmans, in Northern Australia. Prediction equations based upon data from approximately 1000 Brahman cows and 1000 Tropical composite cows were developed for a number of fertility traits. In commercial herds data such as PPAI are infeasible to collect; however, reproductive status can be collected in commercial herds. To determine the efficacy of these equations a validation dataset was established. This involved collecting the reproductive status of

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thousands of cows in Northern Australia as well as samples for genotyping. This study describes the estimate of genetic parameters for 3 measures of reproductive status.

MATERIALS AND METHODS

Population and phenotypes. In 2010, records of 4286 lactating cows were collected from 27 herds in 4 tropically adapted cattle breeds (11, 7, 7 and 2 herds in Breeds A to D, respectively). Most of cows (60%) were younger than 4 years. Breed names are anonymous because these data do not support the comparison of the reproductive status amongst breeds. In these herds, bulls had generally been moved into mating paddocks a few weeks after cows had calved and remained in the paddocks for on average approximately 4 months. Data recording took place at the time of weaning, about five weeks after bulls had been removed from these paddocks.

Each cow's weight (WT) and reproductive status was measured. Stage of pregnancy and ovarian activity was assessed in cows at weaning by experienced operators using ultrasound imaging. Pregnancy was scored by approximate foetal age down to 1 month. Non-pregnant cows were scored for the presence of a CL or *corpus albicans* (CA) on either ovary. In the absence of CL and CA, non-pregnant cows were scored for the size of the largest follicle on either ovary. As a result, each cow's reproductive status (REP3) was scored as: 1) pregnant (P), or 2) having a CL, or 3) having a follicle (F). This score was rescored into two binary traits: PREG2: pregnant (P) or not pregnant (CL or F), and HEAT2: cycling (P or CL) or not cycling (F). The distribution of reproductive status and average of 3 traits in each breed are shown in Table 1. The differences amongst breeds in reproductive status (in 3 categories) were tested using Fisher's Exact Test. The distribution of sires by numbers of daughters per sire is shown in Table 2. The average number of daughters per sire was 5 with a range from 1 to 65.

Table 1. Distribution and means of reproductive status of cows across breeds

Breed	Distribution				Means		
	F	CL	P	Total	REP3	PREG2	HEAT2
A	408	256	1072	1736	1.38	0.61	0.76
B	166	240	1129	1535	1.63	0.74	0.89
C	100	99	525	724	1.59	0.73	0.86
D	7	18	266	291	1.89	0.91	0.98
Total	681	613	2992	4286	1.59	0.70	0.84

Table 2. Distribution of sires by numbers of daughters in pooled four breeds

Breed	No. of sires	Daughters per sire			Mean*	Max*
		1-10	11- 20	>20		
A	335	290	33	12	5.0	44
B	189	154	22	13	7.0	65
C	145	123	20	2	4.8	31
D	54	47	7		5.1	19

*Average and maximum number of daughters per sire

Statistical Model A model containing the effects of breeder, year of birth, herd, management group and their first order interactions as well as sire (as fixed effect) was used to determine significant effects using the R MASS package (Venables and Ripley 2002). A univariate model, with the significant fixed effects, was used to estimate variance components and heritability. The model was $\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$, with $\text{Var}(\mathbf{u}) = \mathbf{A}\sigma_u^2$ and $\text{Var}(\mathbf{e}) = \mathbf{I}\sigma_e^2$, where \mathbf{y} , \mathbf{b} , \mathbf{u} and \mathbf{e} were

vectors of phenotypic observations, fixed, additive genetic (sire or animal) and residual effects, **A** was the numeric relationship matrix using up to 4 generations of pedigree. **X** and **Z** were incidence matrices relating **b** and **u** to the observations, respectively. The analyses were implemented for REP3, PREG2 and HEAT2 using REML and Gibbs Sampler (in house software) methods for the pooled across breed dataset and for two large breed (A and B) sets separately.

For the REML analyses, the threshold sire model was fitted using the logit as the link function. These analyses were carried out using ASREML V3 package (Gilmour *et al.* 2009). Variance components were used to calculate the heritability as $h^2 = 4*\sigma_s^2 / (\sigma_s^2 + 3.29*\sigma_e^2)$.

For the Gibbs Sampler analyses, an animal model was fitted. The Gibbs sampler was implemented using a Markov chain Monte-Carlo of 5,000,000 cycles with burn-in period of 1,000,000 and thinning interval of 100. The posterior means of genetic additive and residual variance components were used to calculate the heritability as $h^2 = \sigma_u^2 / (\sigma_u^2 + \sigma_e^2)$. The 95% Highest Posterior Density (HPD) interval was estimated using the Coda R package (Plummer *et al.* 2010).

RESULTS AND DISCUSSION

In the complete dataset, 70% of cows were pregnant and 84% showed cycling. The REP3 differed markedly across breeds ($P < 0.001$) except the difference between Breeds B and C. The proportion of pregnant cows for breed A was lower than other breeds, while in the small Breed D dataset, almost all cows were pregnant.

REML Estimates. As shown in Table 3, heritability estimates from the pooled analyses of reproductive status (for categorical trait REP3 and binary traits: HEAT2 and PREG2) were low to modest, ranging from 0.06 to 0.23. Heritability estimates in the Breed A data ranged from 0.13 to 0.19. For all traits, the heritability estimates for Breed B were higher than that from the analysis of all breeds or Breed A; but were associated with large standard errors. Across datasets, heritability estimates for HEAT2 were either low or associated with large standard errors.

Table 3. REML estimates of heritability and its standard error for REP3, PREG2 and HEAT2 from the analysis of all breeds jointly and Breeds A and B separately

Trait	Complete	Breed A	Breed B
	Mean±se	Mean±se	Mean±se
REP3	0.23±0.07	0.16±0.09	0.32±0.13
PREG2	0.13±0.07	0.13±0.09	0.26±0.13
HEAT2	0.06±0.08	0.19±0.11	0.21±0.20

Gibbs Sampler. Heritability estimates derived from the animal threshold model for REP3, HEAT2 and PREG2, using a Gibbs Sampler, are shown in Table 4. For across breed analysis, heritability estimates for REP3 and PREG2 from MCMC were 0.13 and 0.15, respectively, similar to the REML estimates. The estimates for HEAT2 from the Gibbs Sampler analysis were lower than that from the REML method, but the REML results were associated with larger standard errors. The heritability estimates for REP3 for Breeds A and B cows were 0.16 and 0.20, respectively. The estimates for HEAT2 were lower than estimates for REP3 and PREG2 in either joint or single breed analyses.

The 95% HPD estimate for HEAT2 from complete or Breed A datasets and for REP3 from Breed B include zero in the 95% HPD range. Both methods (REML and Gibbs Sampler), using a

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threshold model, generated similar estimates of heritability for REP3 and PREG2, the combination of the Gibbs Sampler method with the animal threshold model had higher precision than the REML estimates based on a sire threshold model. Most of the estimates from Gibbs Sampler were located in the center of 95% HPD interval (Table 4). This dataset comprised a large number of sires with relatively small numbers of daughters, this could penalize analyses based on a sire model. Though PREG2 in this study was derived from REP3, it is easily to measure directly than REP3.

Table 4. Posterior means for heritability estimates, their Monte Carlo standard deviation and 95% high posterior density (95% HPD) for REP3, PREG2 and HEAT2 using the Gibbs Sampler method for the Complete, and Breeds A and B datasets

Trait	Complete		Breed A		Breed B	
	Mean±sd	HPD95%	Mean±sd	HPD95%	Mean±sd	HPD95%
REP3	0.13±0.05	0.03-0.22	0.16±0.07	0.003-0.27	0.20±0.09	0.00-0.34
PREG2	0.15±0.05	0.06-0.25	0.17±0.07	0.03-0.30	0.22±0.08	0.05-0.37
HEAT2	0.05±0.05	0.00-0.14	0.09±0.07	0.00-0.22	0.13±0.08	0.001-0.27

CONCLUSION

In this population heritability estimates for reproductive status, either as a categorical trait (REP3) or as a binary trait (PREG2 and HEAT2) appear to be lowly to moderately heritable. Results from both REML and Gibbs Sampler were similar for REP3 and PREG2. PREG2 is the important trait from a practical perspective – it is easily measurable. Estimates of its heritability in this study ranged from 0.15 to 0.22. These data may be a useful resource for validating prediction equations estimated from genetic marker data.

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