GENETIC CORRELATIONS BETWEEN DAYS TO CALVING AND OTHER MALE AND FEMALE REPRODUCTION TRAITS IN BRAHMAN CATTLE

D.J. Johnston and K.L. Moore

Animal Genetics & Breeding Unit*, University of New England, Armidale, NSW, 2351 Australia

SUMMARY

Heritabilities and genetic correlations for male and female reproduction traits were estimated for Brahman cattle raised in northern Australia. The traits included the female reproduction traits of days to calving (DC), age at puberty (AP) and lactation anoestrous interval (LAI). Days to calving using repeat records (DCr) was further considered as separate DC traits for first (DC1) and second parity (DC2) records, as well as a simple binary trait for calving rate (CR). Male reproduction traits included scrotal circumference (SC) and percent normal sperm (PNS) measured in young bulls. The heritability estimates for DCr, CR, DC1, DC2, AP, LAI, SC and PNS, were 0.09, 0.10, 0.09, 0.15, 0.47, 0.40, 0.44 and 0.15, respectively. Genetic correlations between DC1 and AP, LAI, SC and PNS were 0.62, 0.52, -0.32 and -0.66, respectively. For DC2, the genetic correlation with DC1, AP, LAI, SC and PNS were 0.46, 0.56, 1.0, -0.29 and -0.71, respectively. The study has shown that the various reproduction traits were heritable. The 0.46 genetic correlation between DC1 and DC2 suggests they should be considered as separate traits in genetic evaluation and this would allow fitting different genetic correlations with important component traits. Improvement of the genetic evaluation will increase accuracies of female reproduction EBVs and allow more genetic progress in tropical beef breeds in northern Australia.

INTRODUCTION

Reproduction is a key profit driver in many northern production systems. However little or no genetic progress has occurred in the tropical beef breeds due to low levels of recording and difficulty in recording the traits. Days to calving EBV has been used in BREEDPLAN since the 1990s and several breeds and individual breeders have shown significant improvements. Research by Beef CRC showed early-in-life female reproduction traits were moderately heritable (Johnston *et al.* 2009) and could be used in selection to improve lifetime reproductive performance. These new traits have recently been included in BREEDPLAN multiple-trait evaluations of northern breeds. The recently completed Repronomics project (Johnston *et al.* 2017) measured large numbers of Brahman females for these key traits and therefore the aim of this work is to re-estimate the genetic parameters from the additional records to inform the genetic evaluation systems and industry recording.

MATERIALS AND METHODS

Data used were from a February 2019 extract of Australia Brahman Breeders' Association database and included a large amount of female reproduction data submitted from the Repronomics project. Traits used in the study included female reproduction traits: days to calving (DC), heifer age at puberty (AP) and 1st calf-cow lactation anoestrous interval (LAI), and male traits: scrotal circumference (SC) and percent normal sperm (PNS). For this study the days to calving (repeat records, DCr) were separated into traits for first (DC1) and second parity (DC2) records and were further simplified into a binary trait for calving rate (CR).

Adjusted phenotypes and contemporary groups (CG) were obtained from a full BREEDPLAN evaluation for each of the traits. Adjustment methods, DC and CG definitions were as defined by

---

[*] A joint venture of NSW Department of Primary Industries and the University of New England

Graser *et al.* (2005), and for PNS by Jeyaruban and Johnston (2017). AP and LAI were adjusted for significant experimental design effects. The CR phenotype for individuals was constructed from the DC records by assigning a value of 0 for those females that did not calve (i.e. received a penalty DC record) and 1 for those that calved (i.e. valid DC record).

Statistical analyses. Univariate REML analyses were performed for each trait using linear animal model (ASReml, Gilmour *et al.* 2009) and included 3 generations of pedigree where available. The exception was CR, it was analysed using the logit model and EBVs predicted from the underlying scale (CR_{under}) were transformed to the observed calving percent scale (CP_{obs}) using the following equation:

$$CP_{obs} = (\Phi(\tau 1 + CR_{under}) - \Phi(\tau 1))*100$$

where, Φ is the cumulative density function, $\tau 1$ is a threshold (-0.553). The CP_{obs} EBV were regressed against DC EBV to obtain the linear relationship.

A bivariate analysis was used to estimate the genetic correlation between DC1 and DC2. The resultant genetic correlation was significantly less than 1 (see Table 2), so DC was considered as the two separate traits for estimation of correlations with the other male and female reproduction traits. Estimates of genetic correlations for DC2 with other traits resulted in variances and heritabilities that were close to the univariate estimates of DC2 (not presented) and as such there was no need to include DC1 in the estimation of DC2 with other traits.

RESULTS AND DISCUSSION

Number of records and raw trait statistics are presented in Table 1. Days to calving from repeat records (DCr) totalled 29,269 records and for the two separate traits of DC1 (N=19,668) and DC2 (9,601).

Variance components and heritabilities from univariate analyses are presented in Table 1. Heritabilities for DC were low as expected, whereas the component traits were moderately heritable, and in agreement with previous estimates using sub-sets of these data (Johnston *et al.* 2009, 2014a, Corbet *et al.* 2013, Jeyaruban and Johnston 2017).

Table 1. Numbers of records, raw statistics for adjusted phenotypes, variance components (V_a=additive genetic, V_e=residual, V_{pe}=permanent environment, V_p=phenotypic) and estimated heritability (h^2) and standard error (in brackets) for days to calving (DCr, DC1, DC2), calving rate (CR), heifer age at puberty (AP), anoestrous interval in first-calf cows (LAI), scrotal circumference (SC) and percent normal sperm (PNS) in Brahman

Trait	N	Mean	std	V_a	V_e	V_{pe}	V_p	h^2
DCr (d)	29,269	368.1	58.2	222.5	1,216.2	1,120.8	2,562.2	0.09 (0.01)
CR	29,269	0.72	0.45	0.39#	3.29	0.08	3.76	0.10 (0.02)
DC1 (d)	19,668	366.4	63.1	231.2	2,403.0	-	2,634.2	0.09 (0.01)
DC2 (d)	9,601	371.5	48.2	268.2	1,472.8	-	1,741.0	0.15 (0.02)
AP (d)	2,021	632.0	112.4	5,462.0	6,120.5	-	11,582.0	0.47 (0.06)
LAI (d)	1,420	126.1	90.6	2,763.1	4,176.5	-	6,939.5	0.40 (0.07)
SC (cm)	33,983	26.9	4.2	2.90	3.68	-	6.59	0.44 (0.02)
PNS (%)	3,023	67.7	25.3	86.1	480.0	-	566.1	0.15 (0.05)

on underlying scale and repeat records

The relationship between the EBVs of DCr and CP on the observed scale for 672 sires with 10 or more daughters are plotted in Figure 1. The linear relationship was significant (P<0.0001) with a regression coefficient of b = -1.098 %/d and an $R^2 = 0.73$. This simple analysis and Figure 1 suggests these are highly correlated traits but not exactly the same trait. This is not surprising because the DC trait not only captures all of the CR trait but also includes differences in calving date.

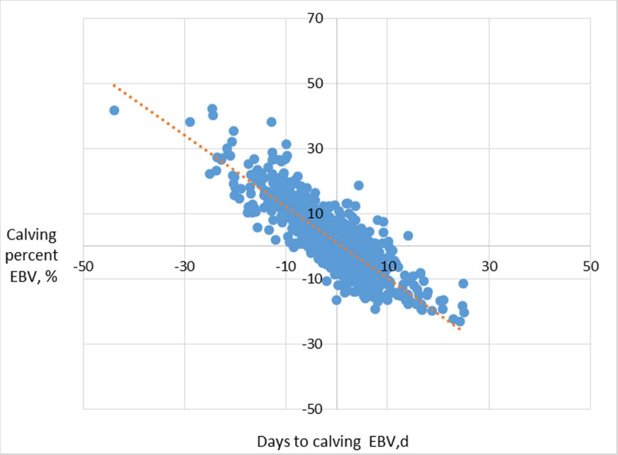

Figure 1. Calving percent EBV (observed scale) versus days to calving EBV for Brahman sires (N=672) with 10 or more daughters with records

Genetic correlations from bivariate analyses are presented in Table 2. The estimate of the genetic correlation between DC1 and DC2 was 0.46. This shows these are not the same trait and re-ranking of sires could occur for daughter's reproduction performance at these two stages. This estimate is not surprising given the different physiological state of the females with regard to lactation status at the two measurement times, and it suggests a repeatability model is not the most suitable method for handling these records.

Genetic correlations between DC1 and the other female traits were positive for AP and LAI, showing shorter DC1 was genetically related to younger AP and shorter LAI. Likewise, the negative correlations for the male traits indicate a shorter DC1 was associated with larger SC and higher PNS. These estimates reflect the -0.71 genetic correlation between AP and PNS. Correlations are similar to earlier estimates from Johnston *et al.* (2014b).

Table 2. Estimated genetic correlations (standard error) between DC1 and DC2 and other reproduction traits in Brahman

Traits#	DC2	AP	LAI	SC	PNS
DC1	0.46 (0.10)	0.62 (0.14)	0.52 (0.19)	-0.32 (0.07)	-0.66 (0.22)
DC2		0.56 (0.14)	1.0*(0.06)	-0.29 (0.07)	-0.71 (0.22)
AP			0.29 (0.12)	-0.48 (0.10)	-0.71 (0.23)
LAI				-0.29 (0.11)	-0.64 (0.23)

see Table 1 for trait names *estimate at bounds

The same pattern of correlations existed between DC2 and the traits, however LAI was larger in magnitude with the correlation going to the bounds, showing this is essentially the same trait, but more heritable. This is likely due to more precision of measurement of LAI compared to DC. PNS was also highly correlated with DC2 and is in agreement with estimates using subset of the data reported by Jeyaruban and Johnston (2017) and reflects the -0.64 between LAI and PNS.

DC1 was most associated with traits related to puberty (e.g. AP), whereas DC2, where the cows are lactating at mating, was very highly correlated with LAI. Male traits offer advantage to genetic evaluation of female reproduction traits, if they are genetically correlated, because they can be measured at a young age in bulls (i.e. before selection) and provide an early prediction of genetic differences in future daughters. Results show PNS was highly correlated with both DC1 and DC2. SC showed similar correlations but at much lower in magnitude but the trait was much more heritable than PNS.

CONCLUSIONS

Improving the genetic evaluation of reproduction traits, especially in northern Australia breeds will have large payoffs for commercial production. DC has been used as an easy to record trait in the genetic evaluation of several tropical beef breeds. However these results confirm that more heritable measures in both males and females can be used as correlated traits in the genetic evaluation of female reproduction. DC is strongly associated with CR and the regression coefficient of -1d DC EBV = +1% CP EBV provides easy to use benchmark.

Changes should be considered to the definition of traits used in BREEDPLAN. The current DC trait could be easily modified to separate it into two traits for DC1 and DC2, and this would provide the added benefit of being able to include the appropriate genetic correlations with correlated traits. However consideration is needed on how these changes would impact on traits in the breeding objective. Also the correlated traits are more costly to record and therefore should be the focus of recording in genomic reference populations to ensure the added value is fully captured. Additional records are required for AP, LAI, and PNS to further reduce the standard errors of these correlation estimates, and to allow the development of genetic evaluation of reproduction traits in other tropical breeds.

ACKNOWLEDGEMENTS

The authors thanks MLA for funding the study under MLA L.GEN.0174 and data from MLA B.NBP.0759. Thanks to the collaborating organisations in Repronomics project and the large team of people involved in designing, running and collecting data in the project. We acknowledge Australian Brahman Breeders' Association and their members for providing access to their database.

REFERENCES

Corbet N.J., Burns B.M., Johnston D.J., Wolcott M.L., Corbet D.H., Venus B.K., Li Y., McGowan M.R. and Holroyd R.G. (2013) *Anim. Prod. Sci.* **53**: 101.

Gilmour A.R., Gogel B.J., Cullis B.R., Thompson R. (2009) ASReml user guide, release 3.0. VSN International Ltd, Hemel Hempstead, UK.

Graser H.U., Tier B., Johnston D.J., Barwick S.A. (2005) *Aust. J. Expt. Ag.* **45**: 913.

Jeyaruban M.G. and Johnston, D.J. (2017) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **22**: 305.

Johnston D.J., Barwick S.A., Corbet N.J., Fordyce G., Holroyd R.G., Williams P.J., Burrow H.M. (2009) *Anim. Prod. Sci.* **49**: 399.

Johnston D.J., Barwick S.A., Fordyce G., Holroyd R.G., Williams P.J., Corbet N.J. (2014a) *Anim. Prod. Sci.***54**: 1.

Johnston D.J., Corbet N.J., Barwick S.A., Wolcott M.L., Holroyd R.G. (2014b) *Anim. Prod. Sci*. **54**: 74.

Johnston D.J., Grant T.P., Schatz T.J., Burns B.M., Fordyce G., and Lyons R.E. (2017) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **22**: 385.