INCREASES IN ACCURACY OF FEMALE REPRODUCTION GENETIC EVALUATIONS FOR BEEF BREEDS IN NORTHERN AUSTRALIA

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SUMMARY

Female reproduction traits influence profitability of beef enterprises, but genetic improvement has been limited. This study assessed the impact of including phenotypic reference data and genotypes on the genetic evaluations for three northern Australian beef breeds with different recording and data structures. For young (2016/17) animals, accuracy for days to calving estimated breeding value (EBV) increased 14.7% for Brahman (BB: well-recorded and genotyped), 6.2% for Santa Gertrudis (SG: limited data and small number of strategic genotypes) and 6.0% for Droughtmaster (DM: limited data and not genotyped). With these accuracy increases there is potential to increase the rates of genetic gain for key female reproduction traits.

INTRODUCTION

Female reproduction is an important driver in the production and profitability of beef enterprises. Genetic progress for these traits is typically limited as reproduction traits are difficult to measure, measured late in life, are sex limited and often have low heritabilities (Cammack *et al*. 2009). These issues make reproduction ideal to benefit from genomic selection and single-step genomic selection is ideal as non-genotyped and genotyped animals can be analysed together. A key female reproduction trait is age at puberty (AP), which can be determined from the age at first corpus luteum (CL). Johnston *et al*. (2009) estimated AP to be highly heritable in both BB ($h^2=0.57$) and Tropical Composite ($h^2=0.52$) heifers. Not only do cows need to reach puberty quickly, but they also need to be able to return to cycling quickly after calving, to produce a calf in the annual management cycle. Using real-time ultrasound ovarian scans to detect the first CL in the mating period, Johnston *et al*. (2014) estimated lactation anoestrous interval (LAI) to be moderate to highly heritable for both BB ($h^2=0.51$) and Tropical Composite ($h^2=0.26$) cows. The aim of this paper was to assess the improvement of EBV accuracies for female reproduction traits (days to calving (DC), AP and LAI) when reference data and single-step genomic selection was included into BREEDPLAN genetic evaluations for three tropically adapted northern Australian beef breeds with different recording and data structures.

MATERIALS AND METHODS

Three breeds (BB, SG and DM) were extensively recorded over five years as part of the Repronomics™ project in northern Australia (Johnston *et al*. 2017). Using real-time ultrasound, regular ovarian scans were undertaken to accurately identify the age that heifers become pubertal (AP) and when lactating cows first cycled after their first calving (LAI). Repronomics herds were fully BREEDPLAN recorded with data submitted for BREEDPLAN genetic evaluations. The reference dataset for this study included records from the Repronomics herds as well as additional BB AP and LAI phenotypes collected as part of the Beef CRC (Johnston *et al*. 2009, 2014).

The BB BREEDPLAN evaluation has recently implemented single-step genomic selection and this will soon be implemented for SG. There were 14,821 BB and 3,464 SG animals genotyped with approximately 40K SNPs available for single-step analysis, see Connors *et al*. (2017) for details of

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the genomic pipeline. To evaluate the benefits of including the fertility reference data and single-step genomic selection, BREEDPLAN data from February 2019 extracts for each breed was used in three separate genetic evaluations using the BREEDPLAN methodology (Johnston *et al*. 2018). All evaluations were multi-trait and provided EBVs and accuracies for all traits, with results for three female reproduction EBVs reported in this study; DC, AP and LAI. In all analyses the number of animals remained the same with only the level of recording and inclusion of genomic information changing across runs. Table 1 outlines the information available for the three genetic evaluations considered.

Table 1. Number of days to calving (DC, days), age at puberty (AP, days) and lactation anoestrous interval (LAI, days) records available for genetic evaluations with different levels (GE1, GE2, GE3) of data included for Brahman, Santa Gertrudis and Droughtmaster

Breed	Brahman			Santa Gertrudis			Droughtmaster		
Trait	DC	AP	LAI	DC	AP	LAI	DC	AP	LAI
GE1#	54,154	0	0	34,704	0	0	1,682	0	0
GE2/GE3	1,398	2,020	1,403	238	216	115	808	627	481

[#] GE1 = no phenotypic reference data or genomic selection included; GE2 = phenotypic reference data included but no genomics; GE3 = both the phenotypic reference data and single-step genomics included

RESULTS AND DISCUSSION

The breeds considered represent three different recording and data structures. BB was the largest breed numerically with 449,620 animals included in genetic evaluations and had the highest level of recording and genotyping in the study. For all subsets of animals and traits, increasing the information in the genetic evaluation increased EBV accuracy. Table 2 records the average accuracy for reproduction traits for three data scenarios and three subsets of animals. Despite AP and LAI having substantially fewer records available, the average accuracy was not much lower than the DC accuracy and this was due to the higher heritabilities for AP and LAI.

Table 2. Average accuracy of days to calving (DC, days), age at puberty (AP, days) and lactation anoestrous interval (LAI, days) from genetic evaluations with different levels (GE1, GE2, GE3) of data included for Brahman

Animal subset	Genotyped n=14,821			16/17 born n=24,555			Genotyped 16/17 born n=3,062		
Dataset	GE1#	GE2	GE3	GE1	GE2	GE3	GE1	GE2	GE3
DC	35.4	41.2	49.7	25.7	28.4	33.3	30.1	35.1	44.8
AP	18.2	34.3	44.9	13.1	20.2	26.8	14.5	28.9	41.3
LAI	24.4	32.6	40.9	17.6	20.8	25.7	19.5	25.4	35.2

[#] See Table 1 for descriptions

Including phenotypic reference data and genomic selection (GE3, Table 2) significantly increased accuracy for AP and LAI. Despite only a small increase in the number of DC records, DC accuracy increased by 14.3% for genotyped animals. AP and LAI are both highly heritable and strongly correlated with DC (Johnston *et al*. 2019), and 41% of the increase in DC accuracy of genotyped animals was attributed to correlated responses with AP and LAI, and the remaining increase the result of genomic selection. Approximately 20% of the genotyped animals were also young animals born in 2016/2017. With smaller numbers and no phenotypes themselves at the time of analysis, the average accuracy for these animals were lower than other subsets. However, the increase in accuracy

observed after including the reference data and genomics was similar to that for all genotyped animals. Compared to all young animals, the genotyped young animals tended to have slightly higher accuracy in the base evaluation (likely due to selective genotyping) but they also had approximately twice the improvement in accuracy when phenotypic reference data and genotypes were added to the genetic evaluation; with EBV accuracy for genotyped young animals increased by 14.7% (GE3) compared to the base genetic evaluation (GE1).

Both SG and DM had similar sized evaluations, with 280,596 and 232,551 animals, respectively. However, they have different levels of recording and genotyping for the female reproduction traits analysed for this study. SG have relatively few AP and LAI records available in the reference dataset but were well-recorded for DC. DC is currently a research EBV for DM and has smaller numbers of industry records available, with Repronomics DC records contributing significantly to the total number of DC records for the breed. For the SG breed, the genotyping strategy has focused on genotyping well-recorded and influential industry animals, particularly those with high DC EBV accuracy. This targeted genotyping strategy was evident with genotyped animals having higher EBV accuracies compared to BB in the base evaluation (Table 3). With the smaller genotyped reference population the impact of including reference phenotypic data and genomic selection was smaller for SG than BB, with a 2.7% increase in DC accuracy for genotyped animals. Similar trends were found for the accuracy of sires in the evaluation with DC accuracy increasing by 1.9% when reference data and genotypes were added. The greatest increases in accuracy for the breed were observed for the young 2016/2017 animals; DC accuracy increased 6.2% when reference data and genotypes were included but only 9% of this was due to genomic selection. Despite having small numbers of records in the reference data, non-trivial increases were observed for these young animals as the reference animals were highly influential and well connected to the wider SG population. Across all subsets of SG animals the impact of including genomic selection was small. For genomic selection to have an impact on female reproduction traits more animals need to be genotyped that also have female reproduction traits recorded, as well as increasing the number of AP and LAI phenotypes in the reference population.

Table 3. Average accuracy of days to calving (DC, days), age at puberty (AP, days) and lactation anoestrous interval (LAI, days) from genetic evaluations with different levels (GE1, GE2, GE3) of data included for Santa Gertrudis

Animal subset	Genotyped n=3,464			Sires n=5,211			16/17 born n=12,282		
Dataset	GE1[#]	GE2	GE3	GE1	GE2	GE3	GE1	GE2	GE3
DC	55.6	57.5	58.3	44.6	46.4	46.5	31.7	37.4	37.9
AP	28.6	33.6	35.0	16.7	19.6	19.8	13.1	21.9	22.7
LAI	32.7	35.4	36.5	19.2	21.2	21.4	15.1	20.4	21.0

[#] See Table 1 for descriptions

DC is currently a research trait for DM and there are fewer records. With no CRC data, all AP and LAI records came from the Repronomics project. There are insufficient genotypes to date to enable single-step to be implemented. Although, comparable in overall size to the SG breed, DM's have limited phenotypic recording for female reproduction, and this was evident in the lower trait accuracies (Table 4) compared to other breeds. Including the reference phenotypic data resulted in large increases in accuracy for Repronomics animals where the data was collected, showing the power of recording to lift EBV accuracy for high heritability traits. The DC accuracy for sires increased by 4% and 6% for young 2016/17 born animals when the reference data was added. Despite having lower starting accuracies in the base evaluation, the increase in accuracy as a result of including reference data was comparable to the other breeds.

Table 4. Average accuracy of days to calving (DC, days), age at puberty (AP, days) and lactation anoestrous interval (LAI, days) from genetic evaluations with different levels (GE1, GE2, GE3) of data included for Droughtmaster

Animal subset	'Repronomics' n=2,846		Sires n=2,534		16/17 born n=11,347	
Dataset	GE1[#]	GE2	GE1[#]	GE2	GE1[#]	GE2
DC	18.8	45.5	32.3	36.3	15.0	21.0
AP	3.0	46.4	4.2	15.6	1.4	15.5
LAI	3.0	37.3	4.2	12.1	1.4	10.6

[#] See Table 1 for descriptions

Including the reference phenotypic data and single-step increased the number of animals with accuracies ≥40%. For DC in the base evaluation, 13.8, 37.0 and 3.1% of animals had DC accuracy ≥40% for BB, SG and DM, respectively. In the evaluations including all the available information this increased to 29.5, 47.0 and 12.9% of animals, respectively for BB, SG and DM.

CONCLUSIONS

The inclusion of intensively recorded female reproduction reference phenotypic data and genotypes increased the accuracies for DC, AP and LAI. Only DC is reported to industry, but the new traits are highly heritable and correlated to DC and results showed they contributed significantly to the increase in DC EBV accuracy. The magnitude of accuracy increase depended on the volume of records and the data structure. Results for SG showed that where industry and reference data are closely related, the increase in EBV accuracy from a small reference data set can still be beneficial. The increase in accuracy for genotyped SG was smaller than that for genotyped BB animals. This was due to the smaller number of genotypes and small phenotypic reference dataset but also because the genotyped animals were from industry and had DC recorded, so they already had higher levels of accuracy. The increase in accuracy when selecting young bulls has the potential to significantly increase the rates of genetic improvement for female reproduction traits and thus improve the overall production and profitability of the beef industry.

ACKNOWLEDGEMENTS

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