Contributed paper

GENOMIC PREDICTION OF LIFETIME PRODUCTIVITY IN BRAHMAN COWS

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SUMMARY

A cow's ability to raise and wean a calf year after year is a primary determinant of profitability in beef production. This lowly heritable trait is impacted by environmental conditions, making it difficult to improve through genetic selection. Given this, there is a heightened interest from industry to develop selection tools that may assist the selection of breeding animals for improved lifetime fertility. The objective of this study was to assess the feasibility and accuracy of a genomic breeding value to capture a cow's potential for lifetime productivity. In this study, yearly mating and calving records were collected from Brahman cows born between 1988-2010. These were used to classify animals based upon whether or not they met a stayability threshold of raising four calves by six years of age (n = 5,516). Relationships between animals was estimated by combining genomic (n = 3,759) and pedigree (n = 11,578) information into an H matrix, and variance components and breeding values were estimated using the blupf90 program suite. Stayability at six years of age was found to be lowly heritable, $h^2 = 0.13$. Despite this, when breeding values were estimated using single step best linear unbiased prediction, a reasonable prediction accuracy was achieved (0.35). This work demonstrates both the potential and limitations of a breeding value for a cow's potential for lifetime productivity, using the intermediate trait, stayability at six years of age.

INTRODUCTION

A cow's ability to raise and wean a calf year after year is a primary determinant of profitability in beef production. A cow's lifetime productivity, measured in number of calves weaned, is the ultimate female fertility trait representing the cumulative effects of puberty with yearly joining, pregnancy, calving, weaning, and rebreed for as long as a cow remains productive in her given production system. A cow must produce enough offspring to offset the cost of heifer development and yearly maintenance, and generate a profit. Within intensive, temperate production systems common in the United States, this breakeven point is generally considered to be five calves by six years of age (Snelling *et al*. 1995). However, this threshold is likely to be earlier within the more extensive, low-input systems common in Australia's north.

Like many other reproductive traits, this lowly heritable phenotype is greatly affected by variable environmental conditions. For example, (rectal) temperature is unfavourably correlated with both pregnancy rate and days to calving, whereas temperature increases fertility decreases (Burrow 2001). This relationship is exacerbated by the increasingly difficult production environments brought about by climate change and is particularly felt by beef cattle producers throughout Queensland and northern Australia. Consequently, there is a heightened interest from the northern beef industry to develop selection tools that may assist the selection of breeding animals for improved lifetime fertility, especially in tropically adapted beef breeds. However, it is a difficult and expensive trait to measure, as cows must have fully reached maturity and be leaving the herd before their lifetime productivity may be fully characterised.

Assessing stayability, or a cow's probability of surviving to a specific age given the opportunity to first reach that age, is often a viable alternative. Previous work to genomically select for lifetime cow productivity in tropically adapted cattle have focused on intermediate life traits as a proxy for lifelong reproduction, such as weaning rate up to six years of age in Brahman (Johnston *et al*. 2014;

Zhang *et al*. 2014) or ability to produce 4 or more calves by 76 months of age in Nellore cattle (Ramos *et al*. 2020).

Tropically adapted cattle raised in Queensland and northern Australia often have a high *Bos indicus* content, are older at the onset of puberty, and are therefore commonly bred as heifers at approximately two years of age. If a cow were to successfully wean a calf every year within this system, she should raise four calves by six years of age. This is milestone is likely the breakeven point within extensive, low input productions systems, with any calves produced after this point generating net profit. Therefore, the objective of this study was to assess the feasibility and accuracy of a genomic breeding value for a cow's potential for lifetime productivity, or stayability to six years of age.

MATERIALS AND METHODS

This project used data and samples collected during the course of the commercial management of the herd and before the commencement of the project. Animal ethics approval was not required for these analyses.

For this study, lifetime productivity of a Central Queensland Brahman cow herd was assessed. Born between 1988 and 2010, these cows were part of a stud herd that has been developed with a heavy emphasis on fertility, where failure to produce a calf was the primary culling criterion. As heifers, these cows were first exposed to a natural service bull at approximately 2 years of age and given a 4-5 month joining window. After which, they are expected to maintain a 365-day calving interval, year after year. This is a long joining period, creating significant variation with respect to when cows calve. This may impact a cow's ability to get back in calf within a year, that is those with the younger calves will find it harder to get back in calf. However, this is a typical situation in northern Australia. Stayability to six years of age was measured as a binary threshold trait (n = 5,516), where cows that successfully gave birth to four calves by six years of age were scored as '1' and those that did not reach this milestone were scored as '0', provided that she was given the chance to calve as a heifer with record of bull exposure at two years of age. Only cohorts that included animals that had reached six years of age were considered.

Starting in 2016, all bulls, cows and calves were genotyped. Genotypes on 3,759 animals were generated using the Geneseek TropBeef V2 array, with 50,045 SNP (after quality control, with genotypes with QC score <0.6 set to missing, monomorphic SNP excluded and SNP with all heterozygous calls excluded). All genotypes were imputed to 709,000 SNP from the Bovine HD array (following further QC) using 4,506 cattle genotyped with the Bovine HD array (including a large number of Brahman, Droughtmaster and Santa Gertrudis cattle). Eagle (Loh *et al*. 2016) was used for phasing, and Minimach3 (Das *et al*. 2016) was used for imputation.

In order to incorporate all available stayability phenotypic records, including those that were ungenotyped, a single-step approach was taken. Genomic relationship was estimated by combining all of the available genomic and ten generations of pedigree information (n = 11,578) into an H matrix, using single step procedures in the blupf90 program suite (Legarra *et al*. 2009). Variance components for stayability at six years of age was estimated using restricted maximum likelihood algorithms in the program remlf90, and genomic breeding values were estimated using single-step genomic best linear unbiased predictions in blupf90. Contemporary group was defined by the cow's year and month of birth, the cow's management cohort. Contemporary group was fitted as a random effect in the model as many cohorts were small (range of 9-175 animals per cohort).

The predictive ability of the breeding values were investigated using a forward validation where data from the youngest cohort of cows with stayability phenotypes (born in 2010, n = 246) was dropped from the model and used as the validation population while the remaining, older cows served as the reference set (n = 5,270). Validation accuracy was calculated as the correlation between the estimated breeding value and the actual phenotype, divided by the square root of the heritability.

RESULTS AND DISCUSSION

In this particular Brahman herd, approximately 71% of all females successfully calved as heifers (Figure 1). This was slightly lower than the median heifer pregnancy rates reported by McGowan *et al*. (2014) of 80% across northern Australia, but in line with rates observed in the Northern Genomics project of 70% (Copley *et al. submitted for review).* Of those females that successfully calved as heifers, 63% were successfully rebred the subsequent joining season. However, of the cows that successfully calved as heifers, only 41% had three consecutive calves and only 29% gave birth to four consecutive calves. This is higher than the success rate reported by Ramos *et al*. (2020) in Brazilian Nellore cattle, where only 19% of females achieved four calvings by six years of age.
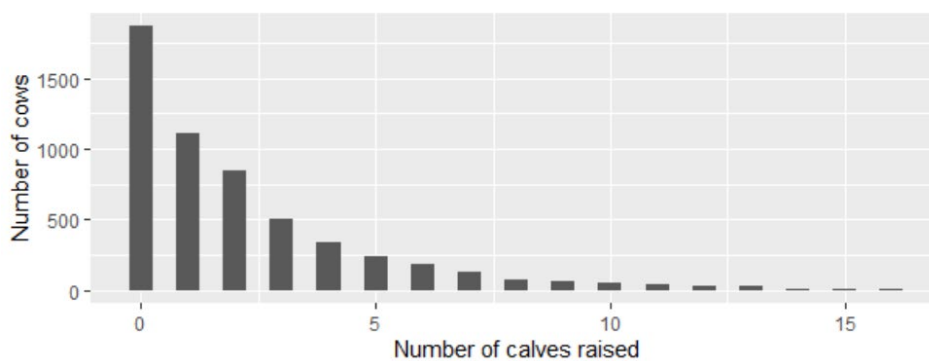
Figure 1. Distribution of lifetime number of calves produced in this population of Brahman females

Heritability for stayability to six years of age was low, $h^2 = 0.13$ ($\sigma_a^2 = 0.023$), but expected given the complexity of this trait and the large role environment and management decisions play on longitudinal fertility. This is comparable to heritabilities of similar traits in Brahman, such as average weaning rate up to 6 years of age ($h^2 = 0.11$; Johnston *et al*. 2014). This estimate is higher than the non-genomic heritability for stayability to six years (raised five calves) in American taurine cattle ($h^2 = 0.11$; Snelling *et al*. 1995). However, this result is lower than the heritability for binary stayability at 76 months reported by Ramos *et al*. (2020) in Nellore cattle ($h^2 = 0.14$)

Predictive ability of the estimated breeding values was tested using a forward validation. The forward validation predicted the performance of the youngest cohort of cows with an accuracy of 0.35, adjusting for heritability. The relatively low, but reasonable predictive accuracy of the breeding values highlights the difficulty of creating a single measure for a longitudinal, lifetime trait. Previous efforts to genomically predict lifetime performance in tropically adapted cattle also had reasonable accuracies, with predictions for average weaning rate up to six years of age achieving an accuracy of 0.39 (Zhang *et al*. 2014) and binary stayability at 76 months of age predicting with an accuracy of 0.55 (Ramos *et al*. 2020). As this cohort ages, increasing the number of phenotypic records available, it is expected that the accuracy should improve with the increase in reference size.

Previous efforts to genetically characterise and develop selection tools for lifetime cow productivity have largely focused on intermediate or component traits, such as stayability (Ramos *et al*. 2020) or productivity up to a set age (Zhang *et al*. 2014). Others have focused on maximizing early in life information by including all yearly production records in a random regression analysis (Snelling *et al*. 2018). These approaches tend to result in higher intermediate heritabilities and are more practical than directly selecting for lifetime productivity; phenotypes may be collected earlier in life, making it easier to develop large reference populations for stayability. However, measuring

stayability does not provide as much information and will not fully characterise the genetic potential of those cows that may produce above and beyond a set age.

CONCLUSIONS

This study demonstrated the potential for a genomic breeding value capturing a cow's potential for lifetime productivity, using the intermediate trait, stayability at six years of age. As a lowly heritable trait, the predictive ability of the estimated breeding values was reasonable but low. However, utilising intermediate component traits is a more practical way to genetically select for lifetime productivity than direct selection, increasing the potential for application within commercial production. As the reference population continues to grow, it is expected that the accuracy of these predictions should improve.

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