DEVELOPMENT OF FEMALE FERTILITY INDICATOR TRAITS FOR THE ANGUS HeiferSELECT GENOMIC TOOL

P.A. Alexandre[1], L.R. Porto-Neto[1], B.C. Hine[2], A.M. Samaraweera[3], A.I. Byrne[3], A.B. Ingham[1], C.J. Duff[3] and A. Reverter[1]

[1]CSIRO, Agriculture and Food, Queensland Bioscience Precinct, St Lucia, QLD, Australia.
[2]CSIRO, Agriculture and Food, F.D. McMaster Laboratory, Armidale, NSW, Australia.
[3]Angus Australia, Armidale, NSW, Australia

SUMMARY

Angus HeiferSELECT is a genomic tool designed to inform the selection of replacement heifers by providing genomic estimated breeding values (GEBV) for traits related to cow-calf production, feedlot performance, carcase quality, and resilience. Here, we explore the incorporation of fertility indicator measures into the gamut of traits using data from 9,155 heifers in the Angus Australia database. The heritability of age at first calving (AFC), days to calving (DC), and pregnancy test measured in weeks (PREG) were 0.25, 0.26 and 0.32, respectively. The three traits were favourably correlated. AFC and DC presented a genetic correlation of 0.45, while PREG presented negative correlations to the other traits (-0.23 and -0.45, respectively). The accuracy of the GEBVs varied from 0.24 for DC to 0.34 for PREG. Although the three traits showed low to moderate heritability and prediction accuracy, phenotypic differences between animals at the top and bottom quartiles when ranking animals based on GEBV demonstrate the positive impact that could be achieved by selecting for improved female fertility in commercial enterprises. The findings from this study have demonstrated that DC, AFC and PREG would all be suitable traits for inclusion in the Angus HeiferSELECT tool.

INTRODUCTION

Targeted selection of replacement females is crucial for optimising genetic gain in commercial beef enterprises. The decision of which heifers to keep in the operation, and which to sell, potentially affects the profitability of the herd for years to come (Wathes *et al.* 2014). Angus HeiferSELECT is an advanced genomic tool developed to inform the selection of replacement heifers in commercial beef breeding operations. It includes GEBV for thirteen maternal, growth, feed intake, carcase, and resilience traits. Recently, genomic predictions for birth weight, weaning weight, yearling weight and mature cow weight have been validated based on the animal's self-performance as well as the average performance of their progeny (Alexandre *et al.* 2022). However, worldwide there is an increasing effort to include fertility traits in genetic evaluations (Brzáková *et al.* 2020).

Fertility traits are notorious for having low heritability and some, such as the result of a pregnancy test (PREG), are particularly difficult to measure in beef cattle since it requires a qualified technician. In addition, traits such as age at first calving (AFC) and days to calving (DC) are complex because they involve the steps required to conceive, gestate, and deliver a calf (Minick Bormann and Wilson 2010). Yet, these traits not only allow the identification of animals that are more likely to conceive, but also those who will conceive early in the breeding season, which has implications on calf performance, the heifer's successive re-breeding, and overall herd productivity (Moorey and Biase 2020). For instance, shortening the AFC has been shown to decrease replacement rates, decrease production costs and consequently increase profit (López-Paredes *et al.* 2018).

In the present study, we investigate an opportunity to include fertility indicator traits in the Angus HeiferSELECT trait repertoire. Using data from heifers in the Angus Australia database we investigate the heritability of AFC, DC and PREG, the accuracy of genomic predictions and the possible phenotypic impacts of selecting for these traits.

MATERIALS AND METHODS

Data for the 9,155 heifers were retrieved from the Angus Australia database. It included genomic information for 45,364 autosomal SNPs and three fertility indicator traits (Figure 1A): AFC (n=6,806, 734.4±50.9 days), DC calculated from the start of the joining period (n=2,883, 364.4±197.4 days), and PREG (n=6,070, 13±7.4 weeks). Heifers that failed to calve were penalized with a DC value of 980 days. Records for PREG included N for "non-pregnant" (n=819), P for "pregnant" if the number of weeks pregnant was unknown or over 20 weeks (n=1,668), or a number between 3-20 for the number of weeks pregnant at the time of assessment as advised by a qualified technician (n=3,583). To transform PREG into a numerical trait, we assigned a random 0 to 1 to the "N"s and a random 21 to 25 to the "P"s. We reached this decision after comparing the average age of the heifers at the time of assessment for animals with an N, a P, and four groups based on the number of weeks pregnant (Figure 1B).
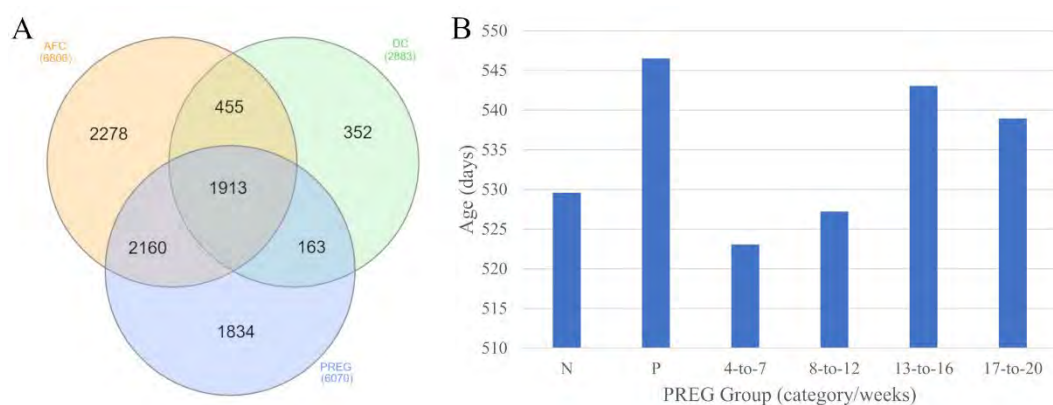

Figure 1. Number of animals with records for age at first calving (AFC), days to calving (DC) and pregnancy test (PREG) (A) and the average age at pregnancy test per category (B)

Heritabilities and genetic correlations were estimated using Qxpak5 (Pérez-Enciso and Misztal 2011). The linear mixed model used to analyse all traits (n=9,155) contained the fixed effects of contemporary group (CG), including mating program type and a minimum CG size of five, and the linear covariate of age at measurement for DC and PREG. The random additive polygenic and residual effects were fitted with assumed distributions $N(\mathbf{0}, \mathbf{G} \otimes \mathbf{V_G})$ and $N(\mathbf{0}, \mathbf{I} \otimes \mathbf{V_R})$, respectively, where $\mathbf{G}$ represents the genomic relationship matrix (GRM) generated using the first method of VanRaden (2008), $\mathbf{V_G}$ is the genetic covariance matrix, $\mathbf{I}$ is an identity matrix, $\mathbf{V_R}$ is the residual covariance matrix and $\otimes$ represents the Kronecker product.

To ascertain the quality of the resulting GEBVs we used the LR Method following Legarra and Reverter (2018). The method compares predictions based on partial and whole data, resulting in accuracy, dispersion, and bias estimates. For that, a series of univariate analyses were undertaken using adjusted phenotypes, first using the whole dataset (calibration), and then using a partial dataset in which data from a random 20% of records were treated as missing (validation). Finally, animals in the validation population were ranked based on their GEBVs from the analyses of the partial dataset and the difference between the average adjusted phenotype of animals in the top and the bottom quartile was calculated (Q1Q4 measure).

RESULTS AND DISCUSSION

Among the fertility indicators, AFC is the most studied trait. Our estimate of heritability for AFC (0.25, Table 1) is well within the values reported in the literature for black Angus, which range from 0.17 to 0.35 (Brzáková *et al.* 2020; Minick Bormann and Wilson 2010). In contrast, studies report a lower heritability for DC compared to our results (0.26), varying between 0.06 and 0.12 for Angus and Nellore (Donoghue *et al*. 2004; Ferreira Júnior *et al.* 2018). The literature is scarce for PREG, particularly when recorded as a continuous trait. When recorded as a binary trait, pregnancy shows low heritability, around 0.13 to 0.17 for heifers (Bormann *et al.* 2006; Buddenberg *et al.* 1989). In this study, PREG showed the highest heritability (0.32) suggesting that our strategy to transform PREG records into a continuous trait was reasonable and perhaps more suitable for genomic selection than binary pregnancy.

As expected, we found a positive genetic correlation between AFC and DC (0.45, Table 1) although not as high as reported in the literature for Nellore (Forni and Albuquerque 2005). While lower values for AFC and DC are indicative of early conception and are therefore desirable, the opposite is true for PREG. This is reflected in the negative genetic correlation between PREG and the other traits, which was stronger for DC (-0.45).

Table 1. Heritabilities (diagonal), genetic correlations (above diagonal) and residual correlations (below diagonal)

	AFC	DC	PREG
AFC	0.25±0.04	0.45±0.31	-0.23±0.36
DC	0.88±0.01	0.26±0.03	-0.45±0.39
PREG	-0.80±0.02	-0.85±0.01	0.32±0.02

The metrics of GEBV quality are presented in Table 2. The GEBV accuracy varied from 0.24 for AFC to 0.34 for PREG. Indeed, increased accuracy is expected for traits with a higher heritability (Fernandes Júnior *et al.* 2016). There were no signs of bias given the high standard errors, but there could be an indication of overdispersion, particularly for AFC, which is not uncommon (Legarra and Reverter 2018) and can be related to the low heritability of the traits.

Table 2. **Method LR accuracy, bias, and dispersion of GEBV for age at first calving (AFC), days to calving (DC) and pregnancy test (PREG)**

	AFC	DC	PREG
Accuracy	0.27	0.24	0.34
Bias	-0.17±0.20	-0.64±0.48	0.03±0.02
Dispersion	0.53±0.01	0.06±0.04	0.26±0.02

The Q1Q4 measure for AFC, DC and PREG were respectively 11.4 days, 25.0 days, and 1.7 weeks. Although one can expect the low to moderate heritabilities and GEBV accuracies to be reflected in the size of phenotypic differences between animals in the highest and lowest GEBV quartile, there are still gains that can be anticipated based on genomic selection.

CONCLUSION

This study has demonstrated that DC, AFC and PREG would all be suitable traits for inclusion in the Angus HeiferSELECT tool, with selection based on either trait resulting in gains in female sexual precocity. The phenotypic differences between animals at the top and bottom of the ranks

demonstrate the positive impact that could be achieved by selecting for improved female fertility in commercial enterprises using the Angus HeiferSELECT tool.

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