

LONGEVITY OF REFERENCE POPULATIONS IN A TRANS-TASMAN GENETIC EVALUATION: REVIEW OF THE ANGUS SIRE BENCHMARKING PROGRAM

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SUMMARY

The Angus Sire Benchmarking Program (ASBP) remains the cornerstone genomic reference behind Angus Australia's TransTasman Angus Cattle Evaluation (TACE). The success of industry funded genomic reference populations depends on the ability to maintain a strong relationship of the seedstock population with the sires selected for the reference population. Results from a review of the ASBP show that, for hard to measure traits (eg. feed intake), the ASBP is influencing the accuracy of breeding value estimation across the registered population. However, the evolution of the genetic make-up of the Trans-Tasman herd means that the continued collection of hard to measure phenotypes via the ASBP or similar programs is essential.

INTRODUCTION

In recent decades, Angus breeders in Australia have achieved genetic improvement in profitability through the application of performance-based selection programs, using a highly effective genetic evaluation pipeline underpinned by BREEDPLAN software (Graser *et al.* 1995). Coinciding with the emergence of genomic technology and the foreseen transition to a genomically enhanced evaluation, Angus Australia commenced the Angus Sire Benchmarking Program (ASBP) in 2010 (Parnell *et al.* 2019). Since then 12 cohorts (11 cohorts have provided data to date) of sires have produced progeny to help build a relevant genomic reference for Australian and New Zealand Angus Cattle. To capture all of the potential value genomic selection presents, genomic reference populations should have a low average relationship between the reference animals, while ensuring that the relationship between the reference population and the animals being evaluated is high (Clark *et al.* 2012; Pszczola *et al.* 2012). A key design feature of the ASBP has been the development of a genomic reference of 4,000 – 6,000 animals recorded for hard to measure traits, with reference sires refreshed annually (Parnell *et al.* 2019) to account for the decay in linkage disequilibrium over time (Porto-Neto *et al.* 2014). The Trans-Tasman Angus population is managed by a multitude of breeders predominantly spread across southern Australia and New Zealand, encapsulating a diversity of environments, production systems and breeding objectives. Consequently, without a nucleus breeding program controlling the dissemination of genetic material, the sires represented in the ASBP needs to align with the past and future selection decisions of Angus breeders. Consequently, this paper endeavours to quantify the importance of an evolving reference population which changes to reflect current (and future) genetics each year.

MATERIALS AND METHODS

Angus Sire Benchmarking Program. The key objective of the ASBP was to establish a contemporary reference population, and the associated genotypes and phenotypes for economically important traits to facilitate the application of genomic selection for the Angus breed. Parnell *et al.* (2019) described the initiation of the ASBP, which commenced in 2010, with 35 Angus bulls

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joined by fixed-time AI to 1,640 cows across 5 co-operator herds. Subsequently, between 21 to 47 bulls have been joined to 1,000 to 2,500 cows annually. For each year's matings (subsequently referred to as a cohort, with cohort 1 identifying matings from 2011 and so on), a genetically diverse range of bulls were nominated by breeders from all states of Australia and New Zealand. Sires from the USA and the UK were also included in some cohorts. Sires represented in each cohort were predominately young bulls (2 – 3 years of age), with some older influential sires also included.

Relationship metrics. Numerator relationship matrices (NRM) were constructed with unpublished AGBU nrmblock software as per Moore *et al.* (2022), based on algorithms by Aguilar *et al.* (2011) and Sargolzaei *et al.* (2005). For each sire in the breed's pedigree which produced progeny in each year from 2010 to 2021, the relatedness to animals generated for the eleven ASBP cohorts was calculated based on the off-diagonal elements of the NRM. This component of the study focused on three relationship metrics, 1; the sires' relationship to their closest relative, 2; the sires' average relationship with their 10 closest relatives, and 3; the sires' average relationship with the animals in the reference population cohort. Summary statistics across sire groups were weighted by the number of progeny sired by the individual within the Trans-Tasman pedigree.

Accuracy estimates. Breeding values for Angus Australia's TransTasman Angus Cattle Evaluation (TACE) are estimated using BREEDPLAN software which applies ssGBLUP models as per Johnston *et al.* (2018), with the accuracy estimations for this study based on the BREEDPLAN methodology reported by Li *et al.* (2017). To test the influence of ASBP data on the accuracy of breeding values for sires represented in the TACE pedigree, a series of modified evaluations were conducted where the genetic evaluation was completed with subsets of the ASBP data excluded based on the TACE pedigree, genotypes and data available in August 2022. The analyses were 1; no ASBP data, 2; Cohort 1-3 data only, 3; Cohort 1-6 data only, 4; Cohort 1-9 data only, and 5; All ASBP data.

RESULTS AND DISCUSSION

The relationship of the progeny in Cohort 1 with the sires which had progeny present in the TACE pedigree declined over time. The average relationship remained reasonably consistent between the cohort progeny and the industry sires (blue line, Figure 1), and this is a by-product of the effective population size and that the top 10 genetically influential ancestors explain 42% of the genetic diversity in the population (Clark *et al.* 2019). However, whilst the average relationship remains relatively constant, the relationship metrics focusing on the strength of the relationship with the closest relatives were shown to noticeably decline (Figure 1). This rate of decline, while not uniform, was relatively consistent across all the cohorts. This suggested that the evolution of the Trans-Tasman Angus population is largely constant as a result of the effective population size and limitations on sourcing outside genetics. The merit of the ASBP ultimately depends on its ability to produce accurate breeding values for hard to measure and economically important traits among future selection candidates.

The importance of the ASBP reference population to the accuracy of selection candidate estimated breeding value (EBV) accuracy is largely governed by the baseline accuracy which, in turn, is driven by the size of the reference population and the effective population size (Clark *et al.* 2012). It should be noted that within a ssGBLUP analysis the reference expands beyond the ASBP and includes all animals from the broader industry which have both phenotypes and genotypes. Consequently, for highly recorded traits like 400-day weight, the contribution of the ASBP data is minimal. For the sires used across the Angus breed in 2012, 2016 and 2020, the mean change in accuracy was less than 1% (Figure 2). In contrast, for carcass intramuscular fat the mean impact of the ASBP data for single trait accuracy of the sires from the same three years was an accuracy increase of 5.7%, 7.5% and 8.2% (Figure 2), respectively. These estimates are inclusive of the

contribution to EBV accuracy of correlated traits, which is a feature of the BREEDPLAN multi-trait analysis. After accounting for this, the impact of the ASBP data to carcass intramuscular fat EBV accuracy was reduced for the three drops to +1.5%, +2.4% and +3.8%, respectively. The value of the ASBP data was most noticeable for net feed intake, where there is minimal recording outside of the reference, with the ASBP data leading to an average change in single trait accuracy (BREEDPLAN reported multi-trait analysis in brackets) of +8.7% (+2.0%), +10.3% (+3.2%) and +11.3% (+4.8%) for the 2012, 2016 and 2020 sires (Figure 2), respectively.



Figure 1. The average relatedness metrics, weighted by the sires progeny count within year, between ASBP cohort progeny and sires of calves born n years after the cohort mating: Cohort 1 (2011) = blue, Cohort 4 (2014) = red, Cohort 7 (2017) = green with other cohorts in grey

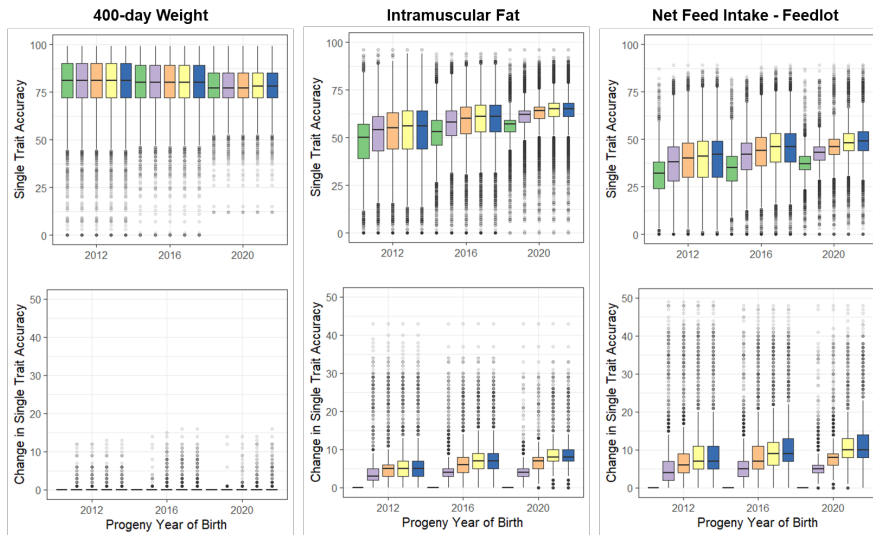


Figure 2. Impact of including ASBP phenotypes from Cohorts 1-3 (purple), Cohorts 1-6 (orange), Cohorts 1-9 (yellow) and All Cohorts (blue), compared to when no ASBP phenotypes (green) are available on the single trait accuracy of breeding values of the sires of the 2012, 2016 and 2020 progeny for 400-day weight, carcass Intramuscular Fat and Net Feed Intake – Feedlot

The impact on EBV accuracy of the decline in relatedness between ASBP cohorts and sires appearing in the TACE pedigree in later years is most clearly observed for net feed intake (Figure 2). For industry sires used in 2012, the inclusion of ASBP data provided an extra 8.7% accuracy, however if the ASBP had concluded after either the 3rd, 6th or 9th cohort this gain would have only been +5.6%, +7.5% and +8.5%, respectively. As expected, the majority of the accuracy gain observed in the 2012 sires comes from the earlier cohorts with cohorts 1-3 accounting for 67% of the overall accuracy improvement. In comparison, for 2020 sires, cohorts 1-3 only provide 46% (+5.2%) of the overall accuracy improvement observed when including the ASBP data, with 94% of the gains in accuracy achieved from cohorts 1-9 data. This suggests that, for traits which Angus breeders aren't able to readily measure on farm, the ASBP recording makes a valuable contribution and shows that investment in the reference needs to continue to reflect the diversity of genetics represented in the current selection candidates.

CONCLUSIONS

To maximise the contribution to EBV accuracy provided by reference population projects, this study demonstrates that relationships between reference animals should be low, but that they need to be sufficiently genetically diverse that their relationship to the broader population is high. As relatedness between ASBP cohorts and subsequently used industry sires declined, there was a corresponding fall in accuracy gains from the ASBP phenotypes. This shows that for traits which are lowly recorded in the broader Angus population, the ASBP remains highly valuable. It also clearly demonstrates that investment in reference populations needs to be ongoing to reflect the diversity of genetics represented within selection candidates.

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