THE ANGUS SIRE BENCHMARKING PROGRAM – A MAJOR CONTRIBUTOR TO FUTURE GENETIC IMPROVEMENT IN THE AUSTRALIAN BEEF INDUSTRY

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SUMMARY

This paper describes the Angus Sire Benchmarking Program (ASBP) and quantifies the contribution that the program has made to the development of a comprehensive genomic reference population for Angus cattle in Australia. Data from the ASBP has enabled the effective use of genomic information in single-step genetic evaluation in the Trans-Tasman Angus Cattle Evaluation, particularly for difficult-to-measure traits. The program has also enabled validation of the effectiveness of genetic evaluation and provided a valuable resource for R&D contributing to the development of new phenotypes for traits of commercial importance.

INTRODUCTION

In recent decades Angus breeders in Australia have achieved world-leading rates of genetic improvement in profitability traits through the application of performance-based selection programs using a highly effective genetic evaluation pipeline underpinned by BREEDPLAN software (Parnell 2015). Coinciding with the emergence of genomic technology as a potential tool to enhance the rate of future genetic improvement, Angus Australia commenced the Angus Sire Benchmarking Program (ASBP) in 2010. This program was part of a portfolio of industry Beef Information Nucleus (BIN) projects initiated by various breeds with funding support from the Meat and Livestock Australia Donor Company (Banks 2011).

The key objective of the ASBP was to establish a contemporary reference population of phenotypes and genotypes to facilitate the application of genomic technology in the Angus breed. A target of the program was to achieve 4,000-6,000 animals measured for difficult-to-measure traits to achieve reasonable accuracy from genomics assisted selection, with ongoing input of contemporary data to account for the decay in linkage disequilibrium over time (Porto-Neto *et al*. 2014). Further objectives included the assembly of high-quality structured progeny test data on contemporary Angus bulls, particularly for difficult-to-measure traits; to evaluate the effectiveness of the current Angus genetic evaluation; and, the development of a resource for the extension and validation of future genetic evaluation models. This paper provides an overview of the ASBP and quantifies its early contribution to genetic improvement in the Angus breed in Australia.

MATERIALS AND METHODS

The ASBP commenced in 2010, with 35 Angus bulls joined by fixed-time AI to 1,640 cows across 5 co-operator herds. Additional cohorts of between 21 to 47 bulls joined to 1,000 to 2,500 cows have been initiated each year up to and including 2019. In each cohort, a genetically diverse range bulls were nominated by breeders from all states of Australia and New Zealand. Sires from 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 bulls also included. Table 1 shows the numbers of sires used and the total numbers of progeny recorded in each cohort.

Birth and early growth performance traits were measured on all calves in the co-operator herds. Male progeny were castrated and grown to feedlot entry age prior to measurement of feed intake over a 70-day test period, followed by finishing in a commercial feedlot. Following slaughter, steer carcases were assessed for a range of meat quality traits, with samples taken for meat science assessment (e.g.

IMF%, shear force). Heifer progeny were grown out in the commercial co-operator herds and joined by natural service to obtain first-parity reproductive and calving performance. Ultrasound scanning was conducted on all progeny, along with recording of temperament, coat scores and structural assessment. In addition, samples of progeny across various cohorts were measured for a range of novel traits, including immune competence, methane emissions, heat tolerance, retail beef yield and carcase fatty acid profile. Blood samples were collected on all progeny for analysis to determine genomic profiles (>8,000 SNP).

All relevant ASBP data was included in the Trans-Tasman Angus Cattle Evaluation (TACE) to contribute to the calculation of Estimated Breeding Values (EBVs) of the sires and their relatives. Sire Performance Reports were produced at the completion of each cohort, including average progeny performance for each trait adjusted for herd, contemporary group, age of dam and progeny recording age.

Table 1. Building the Angus reference population

Cohort	Joining Year	Number of sires Aust.	O'seas	Total	Average ABI†	Total progeny	Progeny per sire Average (Min, Max)
1	2010	31	4	35	$102	906	26.3 (15, 36)
2	2011	37	10	47	$104	1,303	25.8 (17, 41)
3	2012	32	8	40	$105	1,255	24.3 (14, 37)
4	2013	19	2	21	$117	608	26.4 (10, 37)
5	2014	36	10	46	$108	1,311	27.2 (16, 47)
6	2015	40	1	41	$126	1,323	27.6 (19, 46)
7	2016	30	4	34	$132	1.091	27.0 (12, 42)
8	2017	33	2	35	$142	1.047	25.5 (10, 40)
9	2018	19	3	22	$148	565‡	NA
Total		277	44	321		9409	

†Angus Breeding Index (Angus Australia 2019a ‡ estimate from pregnancy scan results

At the commencement of each cohort, the average EBV differences between the top 10 sires and the bottom 10 sires were calculated for a sample of key traits included in the TACE analysis to determine the expected variation in their average progeny performance (i.e. ½ EBV difference). These expected differences were subsequently compared with the actual average progeny performance differences to evaluate the predictive power of the sire's EBVs.

The contribution of the ASBP to the Angus reference population was assessed by comparing the estimated accuracy of genomic estimated breeding values (GEBVs) for a range of traits with ASBP animals only included, with industry animals only, and with all animals included. The estimated GEBV accuracy was calculated using the methods described by Goddard et. al. (2011) with the effective number of chromosome segments calculated according to Daetwyler *et al*. (2008) and an assumed effective population size of 90 (Clark *et. al*. 2019).

RESULTS AND DISCUSSION

Contribution of progeny test data to sire EBVs: Table 1 shows the numbers of progeny in each cohort with data contributed to the TACE analysis. Sire Progeny Performance Reports and EBV listings for all ASBP sires were published on the Angus Australia website following completion of each cohort (Angus Australia, 2019b). In May 2019, the 321 sires included in cohorts 1 to 9 also had 90,876 progeny recorded in 808 Angus seedstock herds, with 171 of the sires having 100 or more progeny recorded.

Differences in the average performance of the progeny of different sires were used in Angus Australia publications and extension programs to highlight the impact of genetic variation. For

example, differences between the highest and lowest average progeny carcase values of $619 and $695, were calculated for steers in cohort 4 and cohort 5, respectively.

Validation of Angus EBVs: As shown in Figure 1, the EBV differences between the top 10 sires and the bottom 10 sires were reliable predictors of the subsequent average progeny performance differences for key traits included in the TACE analysis.

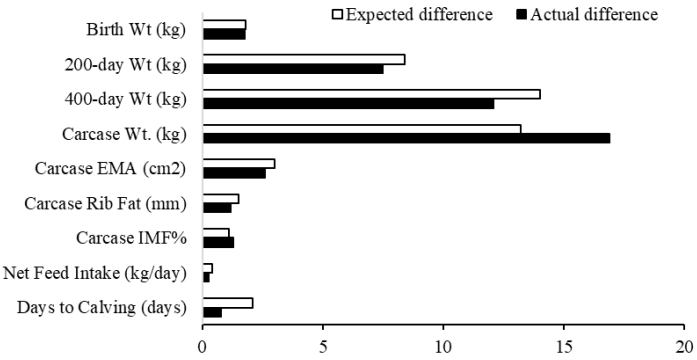

Figure 1. Validation of Angus EBVs, via difference between highest 10 and lowest 10 sires based on initial EBV (average for sires in ASBP cohorts 1 to 6, excluding cohort 4 due to low sire numbers)

Contribution to the Angus reference population: As shown in Table 2, the ASBP has contributed significantly to the Angus reference population, especially for difficult-to-measure traits. This has increased the accuracy of genomic information and enabled the implementation of "single-step" genetic evaluation for Angus incorporating genomic, pedigree and performance data.

Table 2. Contribution of the ASBP to the Angus reference population and accuracy of genomic selection

	Reference population†			Estimated GEBV accuracy‡		
	All animals	ASBP only	ASBP %	All animals	ASBP only	Industry only
Calving Ease	20,364	1,718	(8%)	0.48	0.16	0.46
Birth Wt	44,481	7,813	(18%)	0.79	0.50	0.76
200-day Wt	41,094	8,009	(19%)	0.78	0.51	0.75
400-day Wt	30,124	5,114	(17%)	0.74	0.43	0.71
Days to Calv.	2,220	1,881	(85%)	0.18	0.17	0.07
Carcase Wt	2,890	2,811	(97%)	0.34	0.33	0.06
Carcase EMA	2,802	2,802	(100%)	0.33	0.33	0.00
Carcase Rib Fat	2,876	2,797	(97%)	0.34	0.33	0.06
Carcase RBY%	385	385	(100%)	0.11	0.11	0.00
Carcase IMF%	2,826	2,796	(99%)	0.28	0.28	0.03
Net Feed Intake	2,950	2,833	(96%)	0.34	0.34	0.07
Temperament	26,908	7,908	(29%)	0.72	0.51	0.66

†*animals born since 2010 with phenotypes and genomic profiles (> 5,000 SNP)*
‡*after Goddard et al. (2011) – see text for methodology used*

The ASBP has proven to be an effective model of co-investment by members of Angus Australia, with support from partner organisations, to assemble and maintain a reference population representing contemporary Angus genetics to underpin genomics assisted selection. The full reference population used in the TACE analysis also includes genotypes and phenotypes from New Zealand, along with some historical records from prior research programs.

Contribution to additional research outcomes: The ASBP population has been used for several other research programs such as derivation of genetic parameters for methane emissions (Bird-Gardner et al., 2017), retail beef yield (Donoghue et al., 2019) and alternative ultrasound methods for predicting carcase traits from the live-animal (Duff et al., 2019). The resource has also been used to evaluate new carcase measurement technologies (ALMTech, 2019) and the development of novel phenotypes for traits of future commercial importance such as immune competence (Hine et al. 2014) and heat tolerance.

CONCLUSIONS

The ASBP has been an important ongoing initiative to develop an effective reference population, particularly for difficult-to-measure traits, underpinning current and future genetic evaluation of Angus cattle utilising genomic information. In addition, the program has provided an important industry resource for the validation of contemporary genetic evaluation models, demonstration of the effectiveness of Angus EBVs and the development of new phenotypes for traits of commercial significance.

ACKNOWLEDGEMENTS

The Angus Sire Benchmarking Program receives co-funding through the MLA Donor Company program, along with essential support from various partners including co-operator herds, bull owners, Rangers Valley Feedlot, University of New England, CSIRO, ALFA, Vetoquinol, Bayer, Kerwee Feedlot and genotyping companies (Zoetis, Neogen).

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