BULL DISCOVERY POWERED BY GENOMICS – A PRACTICAL CASE STUDY

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SUMMARY

The benefits of genomic testing are widely understood but the initial cost of investing in the technology can be daunting for many producers. This case study examines the impact of genomics in a real beef herd by comparing the Estimated Breeding Values (EBVs) of animals with and without genomic information included. The study demonstrated that the ranking of some selection candidates will change with the inclusion of genomic information, which could significantly affect selection decisions and rates of potential genetic gain. On average across the reported traits 5.33 new animals, based on Genomic Breeding Values (GEBV), replaced existing bulls in the top 15 when based on EBVs.

INTRODUCTION

Having led the Australian beef industry with the adoption of numerous reproductive and genetic improvement technologies, Australian Angus breeders are now embracing genomic technology in increasing numbers. When combined with pedigree and performance information, genomic information adds an additional source of information in the Angus BREEDPLAN analysis resulting in the generation of EBVs with additional accuracy, and ultimately enabling more accurate selection decisions. (Johnston *et al*. 2018).

The incorporation of genomic information is of most value when an animal's existing EBV has low accuracy (Dehnavi *et al.* 2018). For example, (i) when an animal is very young; (ii) for traits that are hard to measure, or traits that cannot be measured prior to an animal entering the breeding herd; (iii) for traits that have a low heritability; (iv) in situations where collecting effective performance information is problematic, such as in small herds, or when an animal has been removed from its contemporary group; and (v) in situations where little information is recorded with Angus BREED-PLAN for the animal, such as recently imported overseas sires.

The study will examine the impact of the incorporation of genomic information into the calculation of EBVs for a group of Angus bulls to determine the potential impact to selection decisions.

MATERIALS AND METHODS

The Angus BREEDPLAN genetic evaluation includes pedigree, performance and genomic information from the Angus Australia and New Zealand Angus Association databases to evaluate the genetics of Angus and Angus-influenced animals across Australia and New Zealand, using analytical software developed by the Animal Genetics and Breeding Unit (AGBU) (Graser *et al*. 2005). Over 17,500 animals were genomically tested through Angus Australia during 2018, and over 50,000 Australian Angus animals now have genomic information analysed within the Angus BREEDPLAN genetic evaluation.

To evaluate the effect that the inclusion of genomic information has on the calculation of EBVs, the mid-September 2018 Angus BREEDPLAN analysis was conducted twice, initially with all available pedigree, performance and genomic information included (GEBV), as per the EBVs published to industry, and secondly, with only the available pedigree and performance information included, but with the available genomic information removed (EBV).

From within the results of the two analyses, GEBVs and EBVs for a group of selection candidates were extracted for analysis, being 138 bulls born in 2016 from the herd of a current Angus Australia

member who has a long history of performance recording for genetic analysis. The 138 bulls represented the entire group of male calves present in the herd at the time of DNA sample collection, which is 93% of the 149 male calves born in the herd in that birth year.

All 138 bulls were genotyped with the Zoetis i50K for Angus product, containing 29,834 SNPs after genotype QA has been applied.

RESULTS AND DISCUSSION

Summary of Data. A summary of the performance information analysed, in the GEBV and EBV analyses, for the 138 bulls is included in Table 1

Table 1. Count of performance measurements for the 138 analysed bulls

Traits Observed	BWT (kg)	200 (kg)	400 (kg)	600 (kg)	SC (cm)	Scan EMA (cm2)	Scan RIB (mm)	Scan P8 (mm)	Scan IMF (%)
Bulls	135	134	130	106	121	119	119	115	119

BWT: Birth weight, 200: 200-day weight, 400: 400-day weight, 600: 600-day weight, MCW: Mature cow weight, SC: Scrotal circumference, Scan EMA: Scanning measurement of Eye muscle area, Scan RIB: Scanning measurement of rib fat, Scan P8: Scanning measurement of fat at the P8 site, Scan IMF: Scanning measurement of the intramuscular fat

Change in Average EBVs. Across the 138 bulls, little movement in the average EBVs for the selection candidates was observed. The inclusion of genomic information increased the average accuracy of the EBVs for the bulls, with the magnitude of the increase varying for different traits (Table 2).

Table 2. Average EBV and accuracy change in 138 bull with the incorporation of genomic information

	BWT (kg)	200 (kg)	400 (kg)	600 (kg)	MCW (kg)	SS (cm)	CWT (kg)	EMA (cm2)	RIB (mm)	P8 (mm)	RBY (%)	IMF (%)
EBV	3.9	48	85	111	86	1.7	62	5.8	-0.1	-0.4	0.4	2.1
EBV Accuracy	64	60	60	62	58	55	52	50	52	52	48	47
GEBV	4.1	49	87	114	88	1.6	64	5.8	-0.1	-0.4	0.4	2.1
GEBV Accuracy	71	69	67	69	64	64	60	58	62	59	54	57
BV Difference	+0.2	+1	+2	+3	+2	-0.1	+2	0	0	0	0	0
Accuracy Difference	+7%	+9%	+7%	+7%	+6%	+9%	+12%	+8%	+10%	+7%	+6%	+10%

BWT: Birth weight, 200: 200-day weight, 400: 400-day weight, 600: 600-day weight, MCW: Mature cow weight, SS: Scrotal size, CWT: Carcase Weight, EMA: Eye muscle area, RIB: Rib fat, P8: Rump fat, RBY: Retail beef yield, IMF: Intramuscular fat

Change in EBV Spread. While the average EBVs for the bulls did not change substantially, there was an increase in the spread of EBVs for all traits with the inclusion of genomic information. (Table 3). The increase in EBV spread observed from the incorporation of genomic information aids in better identifying genetic differences between individuals.

Change in Ranking of Individuals. Likewise, while the average EBVs for the bulls did not change substantially, there was a considerable re-ranking observed in EBVs when genomic information was included. The correlation between EBVs and GEBVs is listed in Table 4. The reported change is the

result of an increase in the genetic linkage between individual bull and the reference population and the replacement of assumptions around pedigree relationships with genomic information.

Table 3. Standard deviation of EBVs in 138 bulls with the incorporation of genomic information

	BWT (kg)	200 (kg)	400 (kg)	600 (kg)	MCW (kg)	SS (cm)	CWT (kg)	EMA (cm2)	RIB (mm)	P8 (mm)	RBY (%)	IMF (%)
EBV	1.4	5.4	8.3	13.1	16.5	0.7	7.6	1.2	1.1	1.4	0.8	0.5
GEBV	2.0	6.9	10.7	17.4	23.6	1.0	10.8	2.1	1.5	1.9	1.1	0.7
Difference	43%	28%	29%	33%	43%	43%	42%	75%	36%	36%	38%	40%

Refer to Table 2 for breeding value descriptions

Table 4. Correlation between EBVs and GEBVs for 138 bulls with the incorporation of genomic information

	BWT	200	400	600	MCW	SS	CWT	EMA	RIB	P8	RBY	IMF
Correlation	0.85	0.85	0.84	0.88	0.87	0.87	0.86	0.71	0.84	0.85	0.79	0.78

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At a practical level, the implementation of selection within a commercial beef breeding program requires the identification of selection candidates that best meets the breeding objective. Whilst movement in individual breeding value may be significant enough to affect whether an animal meets the required breeding objective thresholds, the individual re-ranking has a far more significant effect on an individual's selection. Therefore, it was more significant for the within herd selection of an individual, where they rank within contemporary the group of selection candidates, rather than their reported breeding value.

Table 5 displays bulls, in green, not ranked in the top 15 prior to inclusion of genomic information. Genomic testing has enabled these bulls to be ranked higher and considered for selection. Without genomics they ranked lower and outside the top 15. On average across the reported traits 5.33 new animals, based on GEBV, replaced existing bulls in the top 15 when based on EBV. Bulls marked in red, are those individuals which were replaced within the top 15 and if selected could have resulted in a loss in potential genetic gain.

The paper highlights the value genomic information delivers to the EBV calculation, in addition to the potential risk breeders take implementing selection decisions without the incorporation. The significant movement and potential losses in genetic gain represent expected movement, as a result genomic testing. This feature validates the growing trend seen within registered Angus cattle in Australia around the increased utilisation of genomic technologies.

CONCLUSION

This case study has provided a real beef herd example illustrating the effect of genomic testing on the EBVs for a group of selection candidates. The inclusion of genomic information did not substantially change the EBVs of the selection candidates on average, but a considerable increase in the spread of EBVs and considerable re-ranking of the selection candidates was observed. The accuracy of the EBVs for the selection candidates increased on average, but the magnitude of accuracy increase varied by trait. Most importantly, in a practical context, the inclusion of genomic information changed the candidates selected for use within the breeding program. It must be noted that the observations in this case study may vary with a different group of selection candidates.

Table 5. Ranking top 15 bulls for each trait, with and without the inclusion of genomic information (Red=dropped outside top 15 with genomic inclusion, Yellow= changed rank order but remained in the top 15, Green=moved into the top 15 with genomic inclusion)

						EBV						
Rank	BWT	200	400	600	MCW	SS	CWT	EMA	RIB	P8	RBY	IMF
1	M63	M223	M149	M81	M81	M174	M81	M149	M42	M249	M300	M197
2	M289	M198	M223	M223	M287	M307	M177	M242	M8	M53	M131	M167
3	M8	M81	M198	M333	M250	M109	M149	M153	M29	M238	M271	M188
4	M212	M225	M225	M198	M46	M263	M103	M131	M308	M307	M214	M90
5	M20	M148	M148	M149	M333	M298	M225	M177	M249	M42	M202	M289
6	M162	M149	M118	M225	M223	M65	M148	M163	M65	M38	M133	M82
7	M165	M102	M81	M245	M225	M223	M248	M214	M20	M308	M149	M225
8	M53	M118	M248	M46	M198	M321	M83	M111	M176	M120	M89	M102
9	M169	M186	M237	M148	M186	M315	M46	M202	M45	M29	M328	M80
10	M89	M237	M102	M83	M83	M142	M237	M300	M145	M20	M242	M117
11	M140	M248	M186	M287	M156	M328	M8	M38	M238	M145	M156	M140
12	M141	M240	M103	M102	M323	M275	M223	M248	M307	M118	M275	M240
13	M14	M257	M240	M257	M220	M333	M165	M99	M53	M117	M248	M63
14	M155	M197	M257	M156	M6	M57	M257	M81	M120	M315	M64	M198
15	M179	M188	M290	M118	M257	M259	M98	M148	M54	M198	M174	M223
						GEBV						
Rank	BWT	200	400	600	MCW	SS	CWT	EMA	RIB	P8	RBY	IMF
1	M63	M225	M148	M245	M287	M307	M81	M300	M65	M249	M300	M104
2	M8	M81	M225	M81	M245	M54	M103	M214	M29	M145	M64	M167
3	M329	M102	M245	M225	M250	M275	M83	M242	M35	M315	M214	M197
4	M289	M240	M102	M46	M81	M65	M149	M274	M308	M307	M280	M188
5	M89	M245	M81	M287	M46	M177	M225	M153	M8	M29	M242	M90
6	M212	M223	M103	M333	M83	M315	M148	M111	M42	M212	M237	M53
7	M179	M103	M248	M83	M333	M333	M177	M156	M120	M53	M275	M82
8	M155	M148	M46	M156	M156	M32	M46	M163	M249	M123	M99	M117
9	M14	M198	M118	M148	M234	M194	M245	M64	M145	M308	M131	M236
10	M106	M149	M223	M102	M6	M321	M156	M21	M53	M8	M89	M156
11	M321	M248	M149	M38	M220	M142	M248	M148	M176	M38	M285	M323
12	M141	M333	M240	M103	M80	M109	M86	M202	M45	M238	M217	M80
13	M169	M83	M198	M6	M280	M263	M287	M99	M162	M65	M274	M125
14	M99	M287	M83	M223	M320	M298	M21	M42	M179	M162	M170	M243
15	M311	M118	M142	M149	M186	M89	M142	M321	M63	M179	M272	M35

Refer to Table 2 for breeding value descriptions

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