

BENEFITS OF GENOMIC INFORMATION IN THE ANGUS INDUSTRY – THE RENNYLEA EXPERIENCE

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SUMMARY

Performance data, pedigree and genotype information from Rennylea Angus stud was used to estimate pedigree-based estimated breeding values (EBV) and single-step genomic breeding values (GEBV). Pedigree-based EBV and GEBV and their accuracies were compared. For closely related animals, GEBV are more powerful in differentiating animals' genetic potential compared to EBV. The greatest benefit of GEBV for providing an estimate of the underlying genetics was for young sires, even more so, when only a small proportion of animals are being selected for breeding.

INTRODUCTION

Genomic selection was rapidly adopted in the dairy compared to the beef industry, due to advantages, such as implementation in a single breed and a large reference population (Goddard 2012). The use of genomic information is gaining momentum in the Australian Angus industry and Angus Australia is establishing a well-recorded reference population with the Angus Sire Benchmarking Program, which is essential for effective industry application (Angus Australia 2017). Some leading breeders, including Rennylea Angus stud, have been whole-herd genotyping with high density genomic profiles for several years. In this study we explored the Rennylea data with the aim to demonstrate the potential benefit of genomic information for Rennylea Angus, based on a within-herd analysis.

MATERIALS AND METHODS

Data. Data from Rennylea Angus stud were obtained from the Angus Australia database. Data included records of animals born between 1987 and 2017 with 7,758 animals in the pedigree. Three traits were analysed for this study: weaning weight (WW, in kg, 7,325 records), intra-muscular fat from ultrasound scanning at 500 days (IMF, in mm, 5,239 records) and scrotal circumference at 400 days (SS, in cm, 2,086 records).

Rennylea commenced genotyping animals born in 2014. We found 337 sires with 22.6 progeny genotyped on average and progeny numbers per sires ranged from 1 to 338 progeny. For the comparison of EBV to GEBV we will focus on the 74 large sires with at least 25 progeny.

Genotype information was generated with a number of different genotyping platforms with varying SNP densities, ranging from 18K to 778K. Most animals were genotyped with a SNP density of 29,834. However, only 15,388 SNP were in common to the SNP chip with the second largest number of animals (18,815 SNP with 1,679 animals). These SNP were kept for further analyses. An imputation step was carried out, to impute scattered missing genotypes to the set of 15,388 common SNP. After merging all SNP platforms, the imputed genotype file contains 15,388 SNP genotypes for 3,954 animals. The frequency of the first allele averages 0.486 and ranges from 0.0 to 1.0 and 92.5 % of SNP have a minor allele frequency > 1 %.

Statistical analysis. Variance components and heritabilities were estimated in linear mixed animal models from pedigree using ASReml (Gilmour *et al.* 2009). Fixed effects included sex (male / female), birth year (1987 – 2017), birth month (February-April and July – September), artificial insemination

(yes/no), embryo transfer (yes / no), recording dates and management groups (35 groups). Significant effects were retained in the model. Animals from multiple births and management groups with less than 10 animals were excluded. Using the same models, EBV and GEBV were estimated using QXPAK (Perez-Enciso and Misztal 2004). The accuracies were calculated as:

accuracy (ACC) = $\sqrt{1 - \frac{s_i^2}{V_g}}$, with s_i = standard error of the estimated breeding value for the *i*th individual and V_g = genetic variance. Correlations between EBV and GEBV were calculated for all animals, all sires and young sires only to establish the concordance of the ranking. The proportion of agreement between animals selected at top 1% or 10% on EBV versus GEBV from all animals, sires and young sires were established.

RESULTS AND DISCUSSION

Trait heritabilities from pedigree were low to moderate (Table 1). Compared with heritabilities published by Angus Australia the $h^2=0.58$ for SS was high and the other heritabilities were within the range of the published estimates (Angus Australia 2019).

Table 1. Mean (\pm standard deviation (stddev)), minimum (Min) and maximum (Max), phenotypic and genetic variances (V_p and V_g) and heritability h^2 (\pm standard error (stderr)) for weaning weight (WW, kg), scrotal circumference (SS, cm) and intramuscular fat (IMF, %)

Trait	Mean \pm stddev	Min	Max	V_p	V_g	$h^2 \pm$ stderr
WW	229.50 \pm 43.54	201.00	421.00	674.64	164.28	0.27 \pm 0.03
SS	37.05 \pm 2.67	26.00	47.00	6.22	3.58	0.58 \pm 0.07
IMF	4.39 \pm 1.55	0.20	8.40	1.75	0.52	0.30 \pm 0.03

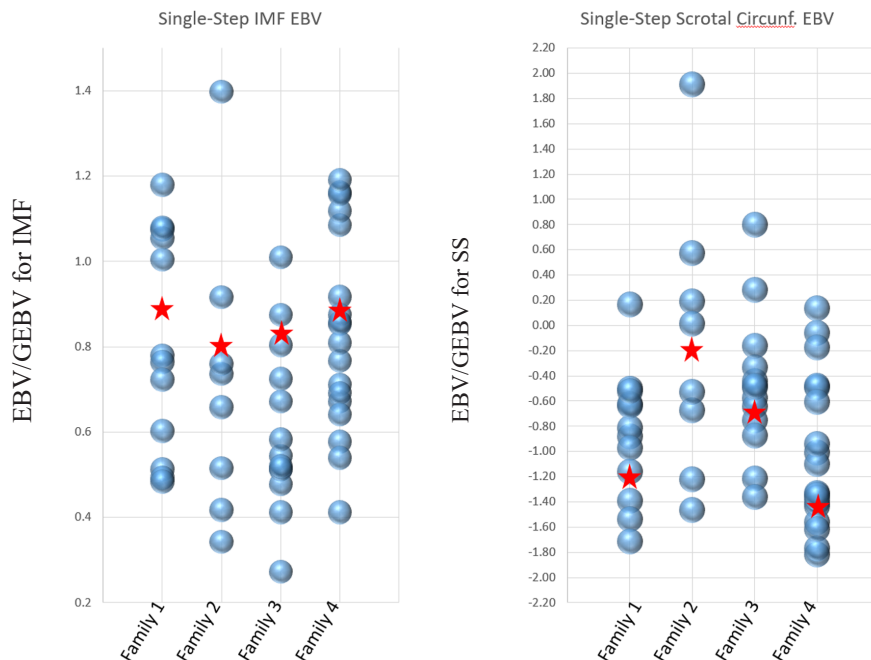


Figure 1. Distribution of GEBV (bubbles) for IMF (left) and SS (right) for the four largest full-sib families. Marked with a star is the value for EBV of full-sibs from the same family

The comparison of EBV and GEBV for the four largest full-sib families for IMF and SS demonstrates that GEBV are different for the members of the same family (Figure 1), because the genomic relationship matrix accounts for different relationships than 0.5 for members of full-sib families. For closely related animals, GEBV are more powerful in differentiating animals' genetic potential, compared to EBV and enables better within-family selection.

A comparison of pedigree-based EBV and GEBV for all 7,460 animals, all 3,020 sires and all 1,450 young bulls showed high concordance of ranking, expressed as correlation (Table 2). The correlations for young bulls were higher for WW, a trait that the animals themselves have a phenotype for, compared to IMF. This means that, for young bulls, GEBV provide a better estimate of the underlying genetics.

Table 2. Correlations between estimated breeding values (EBV) and genomic breeding values from single step (GEBV) for all 7,460 animals, all 3,020 sires and 1,450 young 2016-17 bulls

	All animals	All sires	Young bulls
WW	0.88	0.85	0.80
SS	0.89	0.90	0.66
IMF	0.91	0.85	0.70

The concordance between animals selected on EBV versus GEBV from all animals, all sire or young bulls was higher at 10% selected compared to 1% (Figure 2). We previously demonstrated that GEBV provide a better estimate of an animal's genetic potential (Figure 1), consequently, the lower the concordance the higher the benefit from selecting on GEBV. Figure 2 shows the benefit of selecting on GEBV, particularly for higher selection intensities (1%) and for the WW trait.

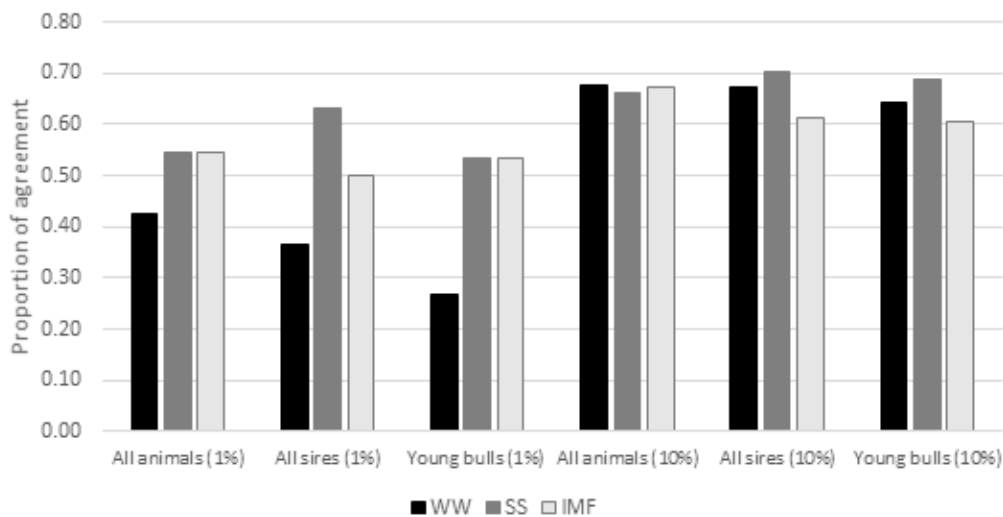


Figure 2. Concordance, expressed as the proportion of agreement, of all animals, all sires and young bulls if selected on GEBV and EBV at 1% (left to middle) and 10% (middle to right)

The plots in Figure 3 show the close alignment of the accuracies of EBV and GEBV. It also demonstrates that the younger bulls (red) are getting the most benefit of higher accuracies from GEBV compared to EBV with the “cloud” of accuracies for the GEBV of young bulls being distinctly higher. This benefit is least obvious for WW.

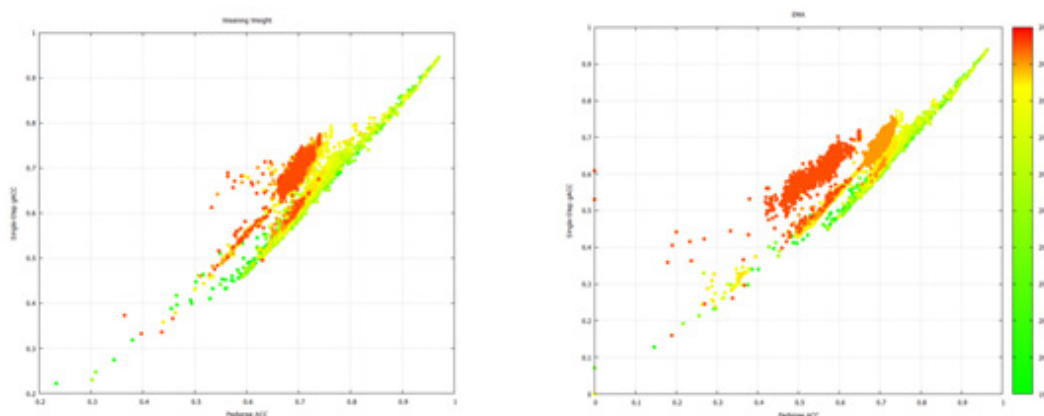


Figure 3. Plots of accuracies for EBV (x-axis) and GEBV (y-axis) for WW (left) and IMF (right). Scale on the right shows colour by age with younger animals are coloured in red and older animal in green

CONCLUSION

The within-herd analysis of the Rennyalea data demonstrates the benefit of using genomic information for more accurate estimates of individual animal breeding values only for this particular data set. To generate whole industry benefit from genomic information well recorded reference populations such as the Angus Sire Benchmarking Program are required to deliver the best tools for industry application.

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