ANNUAL ENHANCEMENTS TO THE TRANSTASMAN ANGUS CATTLE EVALUATION

December 2023

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Dear Angus Breeders,

This document includes details of the annual enhancements that are scheduled to the TransTasman Angus Cattle Evaluation. The enhancements are scheduled for implementation in the December 2023 analysis, being the analysis where the EBVs are released on approximately November 30th, 2023.

The annual enhancements that are made to the TransTasman Angus Cattle Evaluation ensure that the EBVs published for Angus animals continue to be the best possible estimate of an animal's breeding value, maximising the genetic improvement that is being achieved in Angus breeding programs.

The enhancements scheduled for implementation in 2023 are particularly focussed on the optimal use of genomics in genetic evaluation, while also introducing evaluation efficiencies that will ensure the long-term viability of the genetic evaluation, which is important with a rapidly growing pedigree, genotype, and phenotype database.

The enhancements scheduled for implementation in 2023 broadly fall into three categories:

Please contact staff at Angus Australia if you have any questions. A list of contacts is provided on page 6.

Regards

Scott Wright
Chief Executive Officer

Christian Duff
General Manager Genetic Improvement

1. OPTIMAL USE OF GENOMICS

Angus Australia has observed exponential growth in the number of genotypes submitted for genetic evaluation purposes in recent years (Figure 1). With over 300,000 genomic profiles now available, it is important to continually review how to optimally utilise the genomic information within the evaluation, with the aim of providing the highest accuracy EBVs possible.
The following two enhancements focus on the optimal use of genomics within the TransTasman Angus Cattle Evaluation.
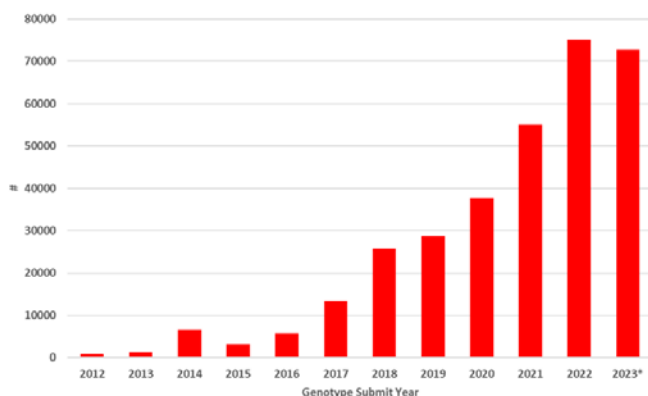

Figure 1. Genotype Submission Per Year for Angus Australia's Genetic Evaluations. *Note — in 2023, to October 31st 2023 only.

1.1 Increase in Genomic Relationship Weighting

Key Points:

· The genomic relationship weighting will increase (from 0.5 to 0.95).

· Some individual animals will show EBV re-ranking, however the correlations are strong and positive on a population level.

· EBV accuracy will generally increase, particularly for young, genotyped animals.

· Selection accuracy of EBVs increases substantially when compared to pedigree and 0.5 genomic relationship weightings.

Within TACE, EBVs are derived from several sources of information, including pedigree, trait measurements and genomic information. One important consideration for current day evaluation is the weighting applied to genomic relationships versus pedigree relationships.

Understanding the relationship between animals is imperative for all genetic evaluations, which can be determined at the pedigree (i.e. animal) level or genotype (i.e. DNA) level. Determining relationships at the DNA level generally provides more precision. For example, Figure 2 shows an assumed relationship of 0.25 of animals with a common grand sire through the pedigree, or 25% shared DNA. With the benefit of genomic information however, we can get a much more accurate picture, and in this stylized example the genomic relationships vary from 0.23 to 0.27.

Further, using genomic relationship allows connection to other animals (and their performance data), that are not connected through pedigree. For example, connection to shared DNA from animals in Angus Australia refence population program, the Angus Sire Benchamrking Program, and the associated hard-to-measure traits (e.g. fertility, abattoir carcase, meat grading, feed intake).

The genomic relationship weighting value (known as "lambda") is currently applied at 0.5 (i.e. 50% to genomic relationship and
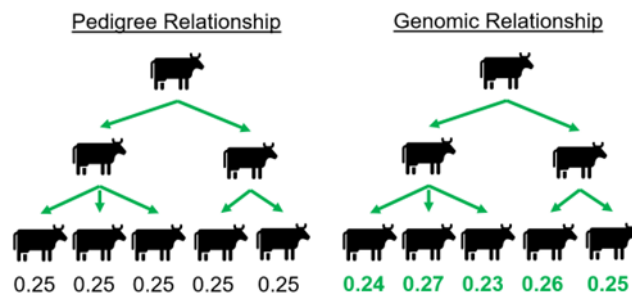
Relationship to Grand Sire

Figure 2 — Pedigree and Genomic relationship to a common grand sire (Source: AGBU).
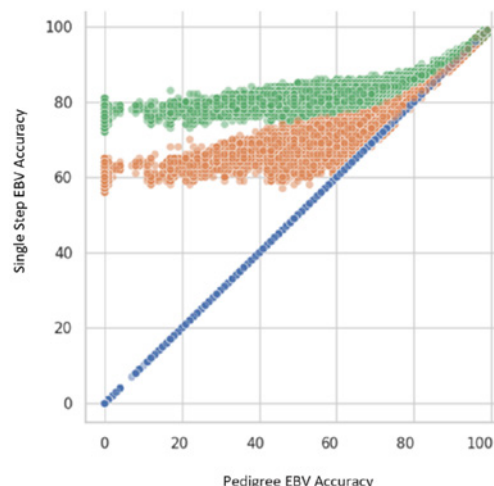

Figure 3. 200 Day Weight EBV Accuracy comparison between pedigree and single-step analysis at 0.5 weighting (brown) and 0.95 weighting (green) (Source: AGBU)

50% to pedigree relationship), which was the optimal level when the TACE Single Step genetic evaluation was introduced in 2017.

With over 300,000 genotypes now available for TACE (and growing), this weighting factor was the focus of a review over the past 12 months by scientists at the Animal Genetics and Breeding Unit at the University of New England. Based on this review, the weighting on genomic relationships can now be increased to 0.95. This means the genomic relationship between animals will have a larger influence on an animal's EBVs calculation, compared to the pedigree relationships, for those animals that have both pedigree and a genotype available. This change reflects the robustness of modern genotyping platforms available to breeders, and the use of genotypes in assigning and verifying pedigree through parentage tests.

With the genomic relationship weighting factor increased to 0.95, the enhanced EBVs, when compared to the EBVs at the current 0.5 weighting, show some re-ranking, however the correlations are strong and positive on a population level. Across the EBVs, the correlations range from 0.978 to 0.995 for sires and 0.962 to 0.976 for 2 year-old bulls. Additionally, there is a similar spread in values observed across the EBVs.

Importantly, there will be a noticeable and significant increase in EBV accuracy resulting from the increase in genomic relationship weighting, particularly for young, genotyped animals. An example of this is shown in figure 3 for the 200 day weight EBV.

Validation of this enhancement shows the increase in genomic relationship weighting (to 0.95) provides a substantial increase in selection accuracy, less bias, and more stability across all EBVs, when compared to both traditional EBVs (pedigree based) and single step EBVs with a genomic relationship weighting of 0.5 (Figure 4).
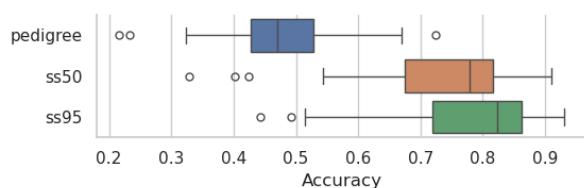

Figure 4 — Selection accuracy comparison between pedigree, single-step with 0.50 lambda, and single-step 0.95 lambda across all multi-trait EBVs Source: AGBU

For further information on the methodology used to calculate validation selection accuracy refer to Johnston et al (2023)

"BREEDPLAN Single-Step Genomic Evaluations Delivers Increased Accuracies Across All Breeds and EBVs", Proc. Assoc. Advmt. Anim. Breed. Genet. 25: 111 — 114.

As an additional note, this enhancement applies to the EBVs provided to TACE from the BREEDPLAN pipeline. For single-step EBVs provided through alternative pipelines (e.g. Structural Soundness EBVs through AGI, or RBVs through Angus Australia) the genomic relationship weightings are currently set at the higher level of 0.9 to 0.95.

1.2 Incorporation of Genomics in Docility

Key Points:
· Pedigree to single-step evaluation (pedigree and genomics)
· Categorical (aka threshold) to continuous (aka linear) trait model
· Docility EBVs will remain reported on the same scale.
· Significant re-ranking of EBVs will be observed, at both the individual and population level, along with less spread in the EBVs.
· EBV accuracy will increase, particularly for young, genotyped animals.
· Selection accuracy is substantially higher.

Selection for temperament is consistently a high or the highest priority for most cattle producers when selecting bulls. In response, Angus Australia members have been active in collecting Docility scores which underpin the TACE Docility EBV evaluation, allowing accurate genetic description of Angus animals.

Angus Australia members have collectively contributed to an overall database with 298,583 docility scores on Angus animals, with more than 24,000 animals scored each year since 2018 (Figure 5). Importantly, a significant proportion (42%) of those animals also have a genotype available for genetic evaluation, which increases to >70% in recent observation years.

To enhance the Docility EBV evaluation, an obvious area is to transition from a pedigree to a single-step (pedigree plus genomics) relationship model. This brings the Docility EBV evaluation in-line with all other TACE EBVs, being genomically enhanced.

For the single-step enhancement to occur, the docility score evaluation was also changed from a categorical (aka Threshold)
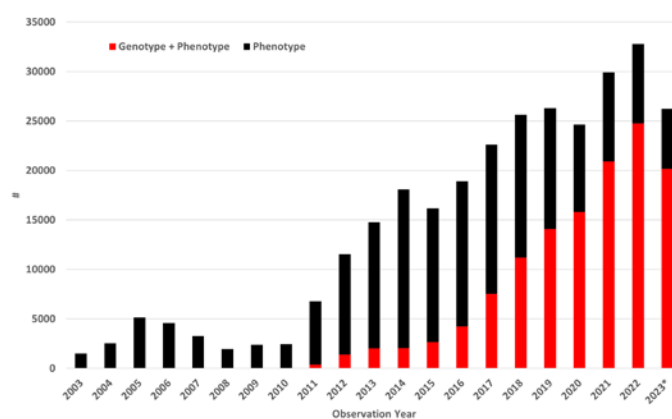

Figure 5 — Docility Score Recording Trends for TACE
*Note — in 2023, to October 31st 2023 only.

to a continuous (aka linear) model. This means each of the nine possible docility scores (i.e. 1 to 5, with half scores) will be included in the evaluation, rather than being grouped in distinct categories. This also ensures the single-step Docility EBV evaluation can be run efficiently to meet commercial schedule expectations. Testing has shown a 20-hour reduction in evaluation time with this enhancement.

Importantly, to provide consistency in interpretation, the underlying linear based EBVs will be transformed so the reported Docility EBVs remain on the same scale, being differences in percentage of progeny with acceptable temperament, with higher EBVs being preferable.

The enhanced Docility EBVs, when compared to the current EBVs, show significant re-ranking, at both the individual and population level. For example, the Docility EBV correlations for sires with at least 75% accuracy (n=2,275) is 0.86 and 2021 drop bulls with at least 50% accuracy (n=19,581) is 0.65. A slight reduction in the spread in Docility EBVs will also be observed. Testing has shown that the EBV changes are mainly the result of transitioning to a genomically enhanced single-step evaluation, rather than the change to the underlying linear model.

Docility EBV accuracies will substantially increase because of this enhancement, particularly for young, genotyped animals (Figure 6). For example, for a genotyped animal with a current Docility EBV accuracy of 50% accuracy, an increase to approximately 70% should be observed.

The EBV accuracies of young, genotyped animals will increase because of this enhancement. Additionally, validation shows a substantial increase in selection accuracy (improvement from 0.4 to 0.6 being a 50% increase), less bias, and more stability for the enhanced Docility EBV, when compared to the current pedigree based EBV.
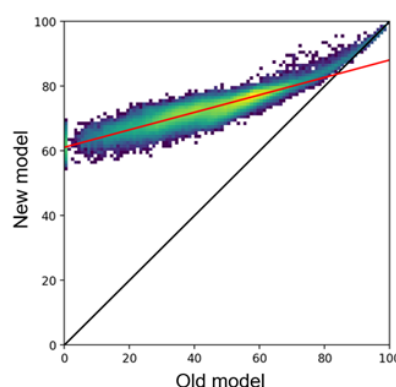

Figure 6 — Docility EBV accuracy will increase as a result of the enhancements (Source: AGBU)

2. ENHANCED RESEARCH BREEDING VALUES

Angus Australia provides several Research Breeding Values (RBVs) as a pathway to understanding and enhancement, prior to becoming a recognised Estimated Breeding Value (EBVs). TACE currently includes six RBVs including Mature Body Condition, Mature Cow Height, Coat Type, ImmuneDEX, MSA Marbling and Shear Force.

This section outlines enhancements that will be made to three of the RBVs currently published in TACE. These have been made possible through the significant increase in associated phenotypes that have been recorded and submitted for genetic evaluation in recent years (Figure 7). Of note is the increase in the recording of the mature cow body compositions traits in recent years off the back of the "Breeding Better Breeders" initiative including the publication of the associated RBVs.
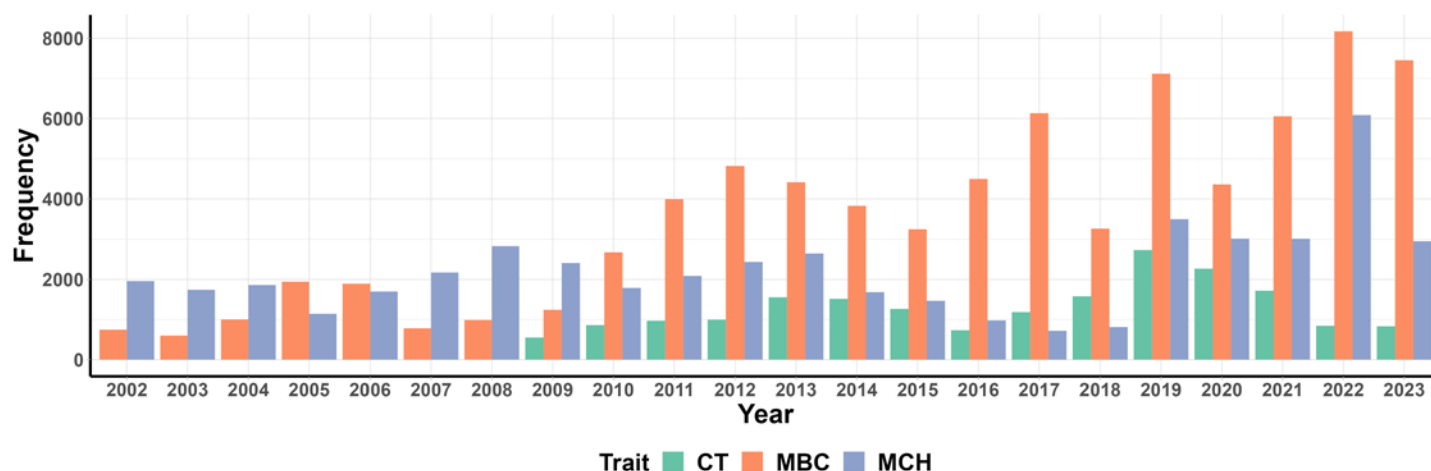

Figure 7 — Recording trends for Coat Type, Mature Body Condition and Mature Cow Height by observation year.

2.1 Cow Body Composition RBVs

Key Points:

· Significantly more animals will display the Mature Body Condition and Mature Cow Height RBVs.

· The variance components, including the heritabilities, for both traits have been re-estimated.

· Genomics is now included through a single step evaluation model for both RBVs.

· Some individual animals will show RBV re-ranking, however the correlations are strong and positive on a population level, while RBV accuracy will generally increase.

Three significant enhancements have been made to the calculation of the RBVs for Mature Body Condition (MBC) and Mature Cow Height (MCH). The first enhancement is the use of new software for RBV estimation. This new software allows all relevant data to be analysed (i.e. pedigree, phenotypes and genotypes) resulting in RBVs on more animals (Table 1).

RBV*	Pre-enhancement	Post-enhancement
MBC	69,140	1,223,312
MCH	32,682	1,348,859
CT	32,363	840,287

Table 1 — Animals with RBV published pre and post enhancement. MBC = Mature Body Condition, MCH = Mature Cow Height, CT = Coat Type.
* Animals with a published RBV that meets the minimum 25% accuracy threshold

The second enhancement involves updated variance components including heritabilities. These genetic parameters underpin the RBV evaluation (like all EBVs) and are required to be updated periodically to ensure they match the contemporary data and animals available for breeding. This is like the variance component re-estimates that were applied to the TACE EBVs in the December 2022 annual enhancements. The updated heritabilities for Mature Body Condition and Mature Cow Height are included in Table 2.

The third enhancement being the transition from a pedigree to a single step evaluation model. This will provide model consistency across all EBVs and RBVs. This is possible through

	OLD		NEW	
Trait	# Records	Heritability*	# Records	Heritability
MBC	4,915	0.10	38,111	0.21
MCH	2,952	0.49	16,831	0.52
CT	3,044	0.28	9,195	0.20

Table 2 - Variance components estimated between the old and new analyses for MBC, MCH and CT

*Note — Old heritability estimates for MBC and MCH were based on pedigree models. All NEW heritability estimates are based on single-step (combined pedigree and genomic relationship) models.

the increase in genomic testing observed (Figure 1) and with the associated reference population size i.e. genotyped and phenotyped animals (Table 3).

Trait	#
MBC	22,980
MBH	10,237
CT	13,799

Table 3 –Reference Population Size (i.e. Genotyped and Phenotyped Animals)

2.2 Coat Type RBVs

Key Points:
- Significantly more animals will display the Coat type RBV.
- The variance components, including the heritabilities have been re-estimated.
- Some individual animals will show RBV re-ranking, however the correlations on a population level are strong and positive, while RBV accuracy will generally increase.

Two significant enhancements have been made to the calculation of the Coat Type (CT) RBV. The first enhancement is the use of new software for RBV estimation. This new software allows all relevant data to be analysed (i.e. pedigree, phenotypes and genotypes) resulting in CT RBVs on more animals (Table 1).

The second enhancement involves updated variance components including heritabilities. The updated heritabilities for Coat Type are included in Table 2.

For further information on the Coat Type RBV variance component research please refer to Samaraweera et al (2023) "Genetic evaluation of coat type for Australian Angus" Proc. Assoc. Advmt. Anim. Breed. Genet. 25: 290 − 293

3. GENETIC EVALUATION EFFICIENCY AND MAINTENANCE

In addition to the enhancements noted above, several other enhancements will also be implemented. These enhancements are less significant but form an important part of the ongoing maintenance and efficiency gains of the TransTasman Angus Cattle Evaluation.

3.1 Calving Ease EBV Analysis Efficiency

Updated software will be implemented to improve the efficiency of the single-step calving ease analysis. Testing has shown that this enhancement will reduce the time taken to run the full single-step calving ease analysis from 2.8 days to 1.3 days.

This software enhancement will have no noticeable impact on the Calving Ease EBVs, however changes to the genomic relationship weighting (section 1.1) may result in Calving Ease EBV changes for some individual animals.

3.2 Days to Calving EBV Software Modification

Software modifications will be implemented to better handle Days to Calving data, particularly for females that have been transferred (changed ownership) and with mating records in more than one herd. Importantly, this enhancement will ensure the Days to Calving EBV more accurately reflects records over the lifetime of the animal. This may lead to a change in EBVs for some animals, though is a more accurate representation of the data.

3.3 Maintenance of genomic pipeline

The pipeline for including genomic information into the calculation of EBVs have been updated as standard, including:

- Re-estimation of the reference haplotype library:
  The reference haplotype library that is used when converting (imputing) the raw genotypes from different genotyping platforms into a standard set of SNPs for use in the genetic evaluation has been updated. Some changes in EBVs may be observed for animals with low density genotypes (i.e. <20K) or their close relatives as a result of this enhancement.
- Incorporation of additional SNPs:
  The single nucleotide polymorphisms (SNPs) that are used in the genetic evaluation have been updated to include additional SNPs from the latest genotyping platforms.
- Re-estimation of the allele frequencies:
  Allele frequencies are used to assess whether an animal is sufficiently related to the genomic reference population.

The genomics pipeline enhancements have resulted in only minor changes in EBVs and EBV accuracies.
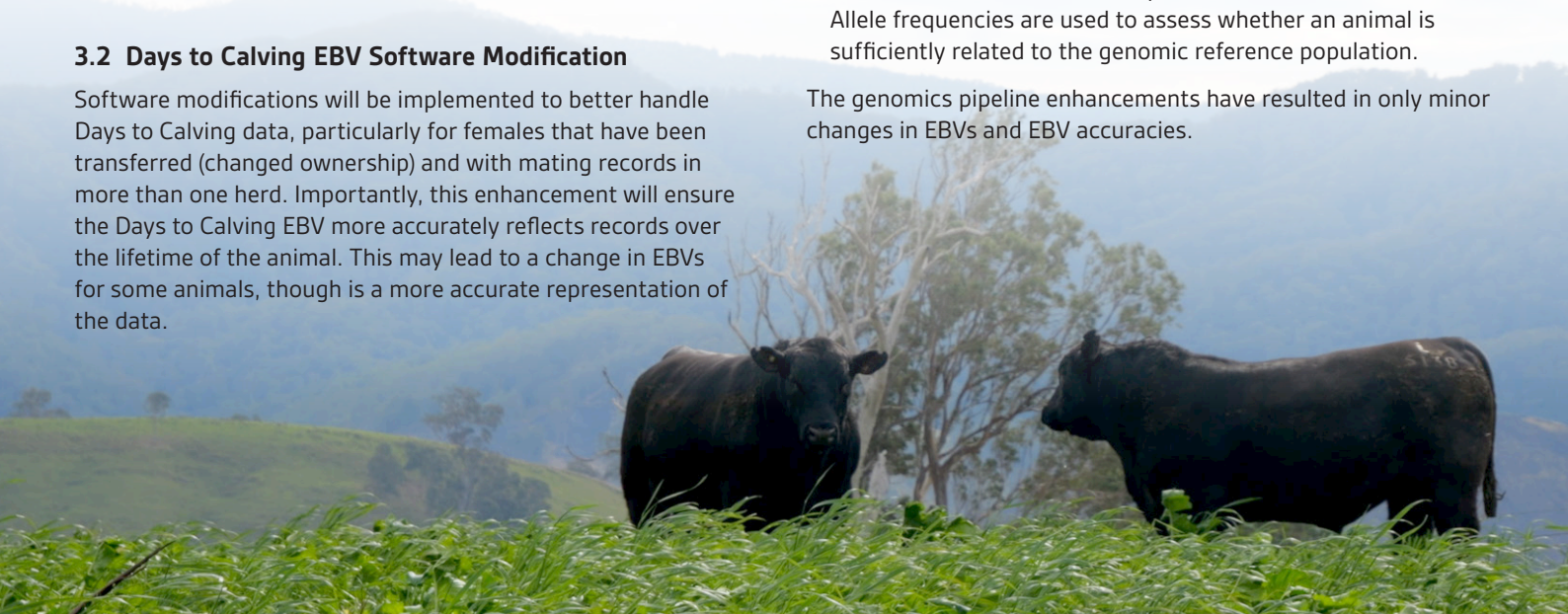
CONTACTS FOR FURTHER INFORMATION

To further discuss any of the enhancements implemented in the December 2023 TransTasman Angus Cattle Evaluation, please contact members of Angus Australia's Genetic Improvement and Extension team.

Christian Duff General Manager - Genetic Improvement
Ph: +61 2 6773 4620
Mob: 0457 457 141
E: christian@angusaustralia.com.au

Jake Phillips
Extension Manager
Ph: +61 2 6773 4625
Mob: 0401 261 217
E: jake.phillips@angusaustralia.com.au

Nancy Crawshaw
Extension Officer
Ph: +61 2 6773 4643
Mob: 0436 337 652
E: nancy.crawshaw@angusaustralia.com.au

www.angusaustralia.com.au

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