

ANGUS BREEDCHECK – VALIDATION USING INDUSTRY DATA

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SUMMARY

Angus BREEDCHECK is a genomic based tool that predicts breed composition for 11 breeds with a focus on Angus content. In this study we compare the Angus BreedCHECK genomic breed composition (GBC) estimates to pedigree-based breed content estimates (PBC) for five animal classes (AC) recorded on the Angus Australia database. The AC populations being Herd Book Register (HBR), Angus Performance Register (APR), Angus Commercial Register (ACR), Angus HeiferSELECT (AHS) and the Multi Breed Register (MBR), including 143,879, 75,369, 6,379, 25,710, and 2,780 animals, respectively. Additionally, comparisons were made within a subset of Angus cross *Bos indicus* (n=1,201) and Angus cross Hereford (n=365) cattle, as determined by PBC, from the MBR. Across the 254,117 animals in this study, there is close alignment in the mean and standard deviation of Angus content as derived by GBC and PBC, with a mean of 99.3% and 99.4% and standard deviation of 3.6 and 4.1, respectively. While 97.7% of the study animals fell within $\pm 10\%$ in Angus content when comparing GBC to PBC. Within the AC populations, and across the sub-set of Angus cross *Bos indicus* and Angus cross Hereford cattle, close alignment was also observed in the comparative statistics. Using a large industry dataset, this study has validated the precision of Angus BreedCHECK to estimate beef cattle breed content, with an emphasis on Angus content.

INTRODUCTION

Understanding breed composition is important in many beef cattle breeding programs, such as those linked to beef supply chains with branded beef schemes or with structured crossbreeding programs. This information is also important for understanding the potential effectiveness of genomic breeding values that are based on breed specific reference populations, like those provided in the Angus HeiferSELECT product (Alexandre *et al.* 2022; Angus Australia 2023).

Breed composition of beef cattle is historically assessed by documenting the breed of foundation sires and dams (usually pure-bred), which facilitates the calculation of breed composition in subsequent generations through simple mode of inheritance i.e. 50% of the breed from the sire and 50% breed from the dam (Sölkner *et al.* 2010). More recently, genomic prediction of breed composition, based on a breed-based genomic reference population, has allowed for breed composition estimation where breed composition is unknown through documentation, particularly where no or limited pedigree is available (i.e., commercial animals or beef products). Importantly, current studies have shown that genomic prediction can offer precision to breed composition estimation in livestock (Sölkner *et al.* 2010; Gurman *et al.* 2017; Reverter *et al.* 2020; Ryan *et al.* 2022).

Angus BREEDCHECK is a genomic based tool that predicts breed composition for 11 breeds with a focus on Angus content. It was developed by Angus Australia in collaboration with the CSIRO, Australia's national science agency. It is currently available via Angus HeiferSELECT which is a genomic selection tool to help inform the selection of Angus replacement females (of 87.5% Angus content or greater) in a commercial beef breeding operation.

The objective of this study is to compare the breed composition values from Angus BreedCHECK on a large industry dataset of genotyped Angus influenced animals, to their known

breed background.

MATERIALS AND METHODS

Data for the 254,117 animals in this study was accessed from the Angus Australia database. For each animal the data included genomic estimates of breed composition from Angus BreedCHECK (GBC), pedigree estimated breed composition (PBC) and the animal class (AC).

The method used to estimate the GBC values (%) is described in detail by Reverter *et al.* (2020). In short, a linear regression model was used to estimate the GBC of individuals where the SNP genotypes are regressed on the allele frequencies from a reference population of 11 breeds. More specifically, this is based on a genomic profile for each animal containing 45,364 autosomal SNPs and a breed based genomic reference population including Angus (n=868), Brahman (n=330), Charolais (n=71), Hereford (n=111), Holstein (n=144), Limousin (n=53), Murray Grey (n=62), Santa Gertrudis (n=53), Shorthorn (n=88), Simmental (n=27) and Wagyu (n=43).

The method used within the Angus Australia database to estimate the PBC values (%) involves breeders and Angus Australia staff documenting the breed of foundation sires and dams in the pedigree, followed by calculating breed composition in subsequent generations by summing 50% of the breed content inherited from the sire and dam.

The AC categories extracted for this study are Herd Book Register (HBR), Angus Performance Register (APR), Angus Commercial Register (ACR), Angus HeiferSELECT (AHS) and Multi Breed Register (MBR). The ACs are applied within the Angus Australia database to primarily cater for service delivery flexibility, however they also broadly categorise the levels of expected Angus breed purity. For example, HBR animals, considered the highest purity of Angus, can only be bred from HBR sires and dams. APR or ACR animals can be bred from foundation (or base) Angus animals, AHS are wholly commercially bred Angus, while MBR, as the name suggests, includes components of non-Angus breeds.

To validate Angus BreedCHECK, this study compared the GBC values to the PBC values for the different AC populations. Additionally, a similar comparison was made in a subset of Angus cross *Bos indicus* cattle (n=1,201) and Angus cross Hereford cattle (n=365), as determined by PBC, recorded on the MBR.

RESULTS AND DISCUSSION

Across the 254,117 animals in this study, there is close alignment in the mean and standard deviation of Angus content as derived by GBC and PBC, with a mean of 99.3% and 99.4% and standard deviation of 3.6 and 4.1, respectively (Table 1). This also highlights the high Angus content represented in the overall study population. Additional to the summary statistics, the proportion of animals with an Angus content difference equal to or less than 10%, when comparing GBC to PBC estimates, were calculated. Accordingly, 97.7% of the study animals fell within $\pm 10\%$ when comparing Angus contents.

Close alignment is also observed for mean and standard deviation values between GBC and PBC within the AC groups (Table 1). The largest difference being between the MBR GBC and PBC Angus content means of 84.2% and 79.8%, respectively, but with similar standard deviations. This may be explained by limitations in the current breed reference population underpinning the GBC estimates or, more likely, inaccurate PBC values stemming from incorrect foundation breed allocations for some animals in the MBR study group.

When comparing the mean GBC and PBC values by AC (Table 1), the findings follow industry expectations of the HBR being the highest mean Angus content followed closely by the APR. The ACR and AHS have marginally lower means, and are in close alignment with one another, which is expected given the commercial nature of both animal classes (i.e., non-seedstock). Also as expected, the MBR, which is a multi-breed population, has the lowest mean Angus content and largest standard

deviation by both GBC and PBC estimation methods. This is further outlined in Table 2 showing 99.9% of HBR animals are at least 87.5% Angus content by GBC estimation. Conversely, and as expected, a significantly lower 46.6% of MBR animals are categorised in the highest Angus content level.

Table 1. Angus content statistics by animal class (AC) and estimation methods of genomic breed content (GBC) and pedigree breed content (PBC)

AC ^a	# Animals	GBC (%) Mean	GBC SD	PBC (%) Mean	PBC SD	Difference (<±10%)
HBR	143,879	99.8	1.2	99.9	1.0	99.8 %
APR	75,369	99.5	2.5	99.1	5.5	96.4 %
ACR	6,379	98.2	6.9	99.2	3.5	91.1 %
AHS ^b	25,710	98.0	6.1	-	-	-
MBR	2,780	84.2	14.3	79.8	14.9	81.2 %
All	254,117	99.3	3.6	99.4	4.1	97.7 %

^aAC: Animal Class, HBR: Herd Book Register, APR: Angus Performance Register, ACR: Angus Commercial Register, AHS: Angus Heifer Select, MBR: Multi Breed Register.

^bPBC is not calculated on AHS animals.

Table 2. Proportion of animals by animal class (AC) and Angus content levels from genomic breed content estimation (GBC)

AC ^a	Angus Content Levels			
	≥87.5%	≥75%	≥50%	<50%
HBR	99.9%	100.0%	100.0%	0.0%
APR	99.1%	99.9%	100.0%	0.0%
ACR	95.5%	98.5%	99.6%	0.4%
AHS	94.8%	98.4%	99.8%	0.2%
MBR	46.6%	75.4%	98.6%	1.4%
All	98.5%	99.5%	100.0%	0.0%

^aSee Table 1.

There was also close alignment of mean and standard deviation values when comparing GBC to PBC estimates for Angus (Table 3), *Bos indicus* or Hereford (Table 4) content within the subset of MBR animals. For example, in the Angus cross *Bos indicus* group the Angus breed content mean by GBC and PBC was 78.0% and 77.1% respectively (Table 3). For the *Bos indicus* component (Table 4) in the same animals, the means were 22.9% and 21.4% respectively. Similar results were observed in the Angus cross Hereford population.

Additionally, most animals (93%) had Angus breed content estimates that fell within the ±10% difference range (Table 3). A similar result was observed for the *Bos indicus* and Hereford content estimates (Table 4) with 90.2% and 99.7% respectively falling with the ±10% difference range. The correlations presented (Table 3 and 4) between the GBC and PBC estimates also support general alignment with the values being moderate to strong and positive in direction.

Table 3. Angus content statistics by estimation methods of genomic breed content (GBC) and pedigree breed content (PBC) for multi breed register (MBR) animals

Breed ^a	# Animals	GBC (%) Mean	GBC SD	PBC (%) Mean	PBC SD	Difference (<±10%)	Correlation
AA*BI	1201	78.0	9.1	77.1	7.4	89.3%	0.69
AA*HH	365	91.8	3.0	93.9	3.5	99.4%	0.66
All	1566	81.2	10.0	81.0	9.8	93.0%	0.86

^aAA*BI: Angus Cross *Bos indicus* (Brahman or Santa Gertrudis), AA*HH: Angus Cross Hereford.

Table 4. Bos Indicus or Hereford content statistics by estimation methods of genomic breed content (GBC) and pedigree breed content (PBC) for multi breed register (MBR) animals

Breed ^a	# Animals	GBC (%) Mean	GBC SD	PBC (%) Mean	PBC SD	Difference (<±10%)	Correlation
AA*BI	1201	21.4	7.4	22.9	8.7	90.2%	0.72
AA*HH	365	6.9	3.8	6.1	3.5	99.7%	0.63

^a See Table 3.

CONCLUSIONS

This study has validated the precision of Angus BreedCHECK to estimate beef cattle breed content, with a close alignment of the comparative statistics when comparing GBC to PBC estimates, as well as an alignment with industry expectations of the Angus content differences across the ACs from the Angus Australia database. Therefore, Angus BreedCHECK provides potential value as a tool for the estimation of breed content in Angus or Angus influenced breeding programs, particularly commercial herds, or within Angus beef supply chain initiatives. Angus BreedCHECK can also be used in the assessment of the effectiveness of the genomic breeding values provided from Angus HeiferSELECT.

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