Re-ranking of Imported Angus Sires Following Integration of Foreign Genotypes into a National Genomic Evaluation

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Abstract

In South Africa, imported Angus sires are frequently introduced into the national genetic evaluation with little to no local progeny records, limited pedigree depth, and typically without own or progeny performance data recorded under local production conditions. Historically, interim evaluations incorporated country-of-origin genetic merit information, expressed as percentile rankings and blended them into the South African evaluation until sufficient local progeny records became available. This avoids an initial underestimation of their EBVs. Such approaches may not fully account for genotype-by-environment interactions, population-specific allele frequencies, differences in genetic parameters, or divergent selection pressures between source and recipient populations. Single-step multiple-trait genomic BLUP (MT ssGBLUP) enables direct integration of SNP genotypes, allowing imported sires to be evaluated relative to a locally genotyped reference population. This study compared EBVs from the national pedigree-based BLUP evaluation incorporating percentile adjustments with EBVs from MT ssGBLUP without percentile adjustments for 194 imported Angus sires across pre-weaning traits. Pearson correlations between evaluation methods were 0.92 for Birth Weight Direct (BWD), 0.80 for Weaning Weight Direct (WWD), and 0.71 for Weaning Weight Maternal (WWM). Despite the high correlation for BWD, individual re-ranking averaged 21 positions. Greater re-ranking was observed for WWD (maximum −117 to +139 positions) and WWM (−145 to +147 positions), likely reflecting lower data density and the delayed accumulation of maternal information. Across traits, incorporation of genomic information resulted in substantial redistribution of ranking, with most imported sires improving relative position, while others declined depending on genomic relationships with locally measured and genotyped animals. These results indicate that MT ssGBLUP does not uniformly inflate evaluations but reallocates merit according to realized genomic similarity within the South African reference population. Strengthening genomic connectedness between imported sires and locally measured animals is therefore essential to reduce uncertainty during early evaluation stages and to improve the reliability of selection decisions under production environments distinct from those of origin.

Key Words: genetic evaluation, single-step GBLUP, imported sires

Introduction

The genetic improvement of beef cattle populations increasingly depends on the exchange of genetic material and genetic information across national borders. In South Africa, as in many countries with comparatively small registered seedstock populations, breeders routinely import semen and live animals from established Angus populations in North America, Australia and elsewhere to broaden the genetic base and accelerate the rate of genetic gain (Guarini et al., 2019; Adekale et al., 2025). These imported sires typically enter the national pedigree with little to no local progeny records, shallow pedigree ties to the resident population, and, in many cases, no performance data recorded under South African production conditions. To avoid the systematic underestimation of breeding values that would

otherwise result from evaluating such animals on parent-average information alone, national genetic evaluation systems have historically relied on interim procedures that translate country-of-origin genetic merit, often expressed as within-breed percentile rankings, into the local evaluation until sufficient local progeny records accumulate.

While practical, percentile-based blending of foreign genetic merit does not explicitly account for several biological and statistical realities that distinguish the source and recipient populations. Chief among these is genotype-by-environment (G×E) interaction, which has repeatedly been shown to cause the re-ranking of sires and a decline in the genetic correlation between the same trait expressed in different environments as those environments diverge. Breeders must carefully assess the performance of sires and their offspring in the target environment before making selection decisions, because the average performance of progeny sired by bulls selected under more favourable conditions can deviate substantially from expectation when commercial conditions differ from those under which the sires were originally evaluated. In beef cattle, sire-by-region and sire-by-system interactions have been reported for growth and reproductive traits using both classical multi-trait and reaction-norm approaches, with several studies showing that these interactions can substantially alter the ranking of sires for growth traits based on their estimated breeding values. Multi-trait analyses of fertility traits in tropical beef populations have similarly shown that genetic correlations for the same trait measured in different environments tend to decline as those environments diverge, with correlations below approximately 0.8 taken as evidence of genotype-by-environment interaction and an indication that splitting selection by environment would be beneficial for the breeding program. More recently, reaction-norm studies in Nellore cattle have reported genotype-by-environment interactions for feed intake traits with genetic correlations between extreme environmental levels as low as 0.22–0.26, resulting in selection coincidences of only 40–53% between environments, underscoring how substantially sire merit can be redistributed when evaluated across divergent production environments (Silva Neto et al., 2023). Beyond G×E, differences in population-specific allele frequencies, linkage disequilibrium patterns, genetic parameters, and historical selection pressure between the exporting and importing populations further complicate the direct transfer of foreign genetic merit into a national evaluation (Silva Neto et al., 2024; Adekale et al., 2025).

Multi-step approaches that address these issues by deregressing foreign estimated breeding values (EBVs) and blending them with national information, as implemented for Multiple Across-Country Evaluation (MACE) proofs in dairy cattle and Interbeef proofs in beef cattle, have been shown to improve reliability and reduce bias relative to pedigree-only evaluations, but they remain vulnerable to double-counting of information and to loss of accuracy inherent in the deregression process itself (Guarini et al., 2019; Adekale et al., 2025). Single-step genomic BLUP (ssGBLUP) offers an alternative that avoids these intermediate steps by combining pedigree, phenotypic, and genomic information into a single evaluation, connecting genotyped imported sires directly to the local reference population through realized genomic relationships rather than through expected pedigree relationships or externally derived proofs (Aguilar et al., 2010; Christensen and Lund, 2010). This approach has been implemented successfully in large national beef cattle evaluations, where the increase in ability to predict future performance for birth weight, weaning weight, and post-weaning gain with single-step genomic BLUP was 25% in a 2014 dataset and 36% in a 2017 dataset compared with traditional BLUP, with genetic trends revealing that multistep evaluations had overestimated merit, especially for traits with fewer phenotypic records (Lourenco et al., 2018).

Despite these developments, it remains unclear how imported Angus sires with limited South African performance records would be re-ranked if evaluated through a multi-trait ssGBLUP system that draws directly on realized genomic connectedness with the local reference population, rather than through the percentile-adjusted pedigree-based system currently in use. Understanding the magnitude and direction of this re-ranking, and the traits for which it is most pronounced, is essential for assessing whether the current interim evaluation approach remains fit for purpose and for guiding future investment in genomic connectedness between imported and locally measured animals. The objective of this study was therefore to compare EBVs for pre-weaning growth traits obtained from the current national pedigree-based evaluation, with EBVs obtained from a multi-trait single-step genomic evaluation, for a sample of 194 imported Angus sires within the South African Angus population.

Materials and Methods

Data

The phenotypic data were acquired from the LOGIX Genetic Evaluation System (SA Stud Book). Records for birth weight (BW) and weaning weight (WW) used in the evaluation are summarised in Table 1. The Angus cattle breeders' society of South Africa has a recording rate of 99% for birth weight and 74% for weaning weight.

Table 1: Total number of weight records for birth weight (BW) and weaning weight (WW).

Trait	Number of Male Records	Number of Female Records	Total Number of Records
BW	55 892	83 281	139 173
WW	41 690	64 530	106 220

Pedigree information on 280 194 animals dating back to 1931, of which 20 853 were registered as active animals, consisting of 6 244 males and 14 609 females.

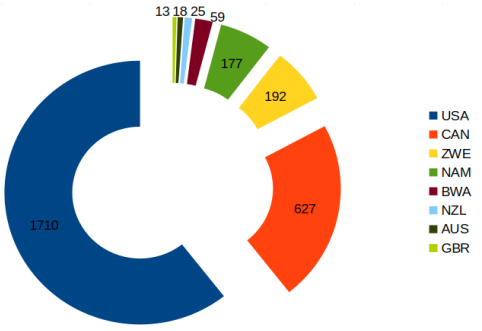


Figure 1. The top eight countries of imported Angus sires (USA: United States of America; CAN: Canada; ZWE: Zimbabwe; NAM: Namibia; BWA: Botswana; NZL: New Zealand; AUS: Australia; GBR: Great Britain)

The pedigree contained 2,847 imported sires from 18 countries, with the top eight countries shown in Figure 1. Of these, 194 imported Angus sires had genomic profiles available and were included in the evaluation.

Furthermore, the genomic profiles of 1,427 South African born Angus animals, comprising 63% males and 37% females, were used in this study. Animals were genotyped across four commercial single nucleotide polymorphism (SNP) arrays of varying densities. Genotyping was done on commercial variants of the Illumina BovineSNP50 v.3; namely the SASB 50k, ICBF IDB v.2, Versa 50k and the newer Versa 80k. Quality control of genomic SNP data, performed in PLINK v1.90b6.10 (Purcell et al. 2007), retained only autosomal SNPs with a known base-pair position, a call rate ≥0.90, a MAF ≥0.01, and no significant deviation from Hardy–Weinberg equilibrium ($p>0.001$). Animals were required to have a call rate ≥0.90 while individuals with ≥0.95 identical genotypes were discarded. Genotypes were imputed with FImpute v3 (Sargolzaei et al. 2014), using pedigree information, to a density of approximately 51,000 SNPs.

Models

In order to predict estimated breeding values in multiple scenarios the same multi-trait animal linear model was used. The model was defined as follows:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e},$$

where **y** is the vector of phenotypes, **b** is the vector of fixed effects, **u** is a vector of random genetic effects, including direct and maternal additive genetic effects; the model also accounted for the relevant (co)variances among genetic effects and other random effects, with **u** ~ N(0,A σ_u^2), where A is the pedigree-based matrix and σ_u^2 is the direct-genetic variance, **e** represents the residual, where e ~ N(0,I σ_e^2), with σ_e^2 representing the residual variance, **I** the identity matrix while **X** and **Z** are incidence matrices for **b** and **u** respectively.

Fixed effects in **b** for the model included herd x year x season x treatment group x birth status with age adjustment within contemporary group, sex, dam parity (1 or >1) and linear (α) and quadratic (α^2) regression coefficients for age of dam. Estimation of variance components for the above model was calculated using restricted maximum likelihood (REML) optimised with quasi-Newton procedure using analytical gradients in Variance Component Estimation (VCE) (Groeneveld, 2010) software. MiX99 (MiX99 Development Team, 2017) was used to predict both traditional EBVs and GEBVs using the same model. The ssGBLUP model utilises the inverse of the joint relationship matrix $\mathbf{H^{-1}}$ (Aguilar et al. 2010; Legarra et al. 2014).

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{pmatrix},$$

where $\mathbf{A}^{-1}$ is the inverse of the pedigree-based matrix, A_{22} is the overlapping part of A for the genotyped animals and **G** is the genomic relationship matrix (GRM). The GRM was constructed using VanRaden Method 1 of (VanRaden, 2008). This was achieved using a weighting factor of 0.1, with the resulting matrix blended with the pedigree-based relationship matrix (A_{22}) using the RelaX2 HGInv program (Strandén, 2014) to produce the G^{-1} matrix. The resulting matrix was then used in MiX99 for the internal construction of H^{-1} in ssGBLUP.

Results & Discussion

A total of 194 imported Angus sires were included in the comparison of estimated breeding values (EBVs) derived from pedigree-based BLUP and multi-trait single-step GBLUP (MT ssGBLUP) across three traits: Birth Weight Direct (BWD), Weaning Weight Direct (WWD), and Weaning Weight Maternal (WWM).

The mean EBV difference revealed a consistent upward shift across all three traits upon the integration of genomic information, with BWD (Figure 2) increasing by a mean of 0.82 kg (SD = 0.41), WWD (Figure 3) by 21.87 kg (SD = 3.79), and WWM (Figure 4) by 3.34 kg (SD = 2.11). This systematic upward shift is consistent with the genomic reference population capturing realised genetic relationships between animals that were not accounted for in the pedigree BLUP run. Where pedigree-based evaluation assumes Mendelian sampling is zero on average across non-relatives, the genomic relationship matrix reflects the actual proportion of the genome shared between individuals, thereby capturing realised genetic relationships that pedigree information alone cannot resolve.

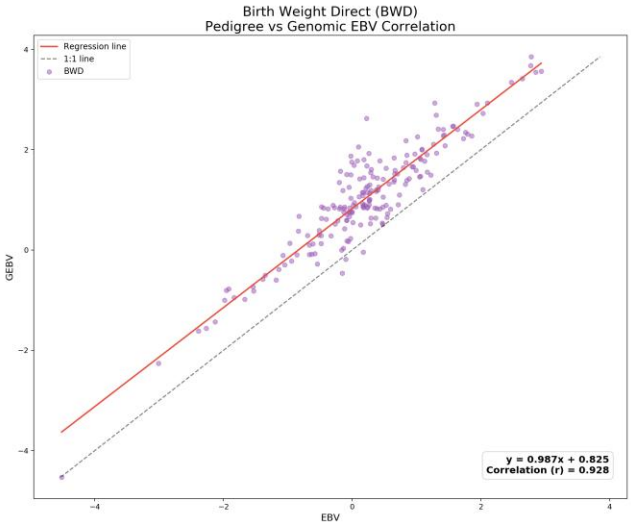


Figure 2. Pearson correlation for birth weight

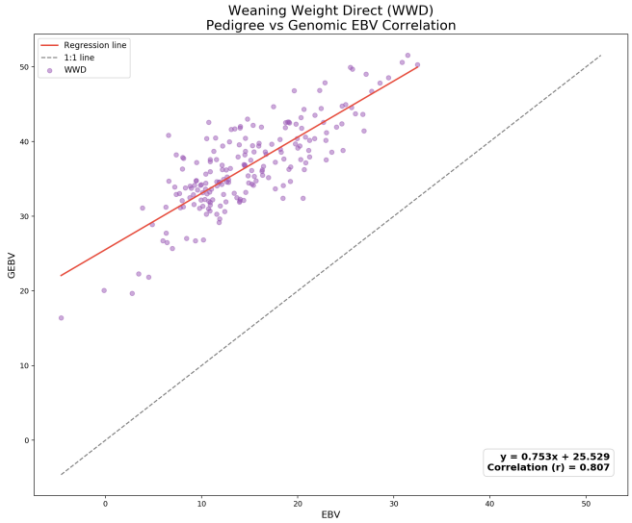


Figure 3. Pearson correlation for weaning weight direct

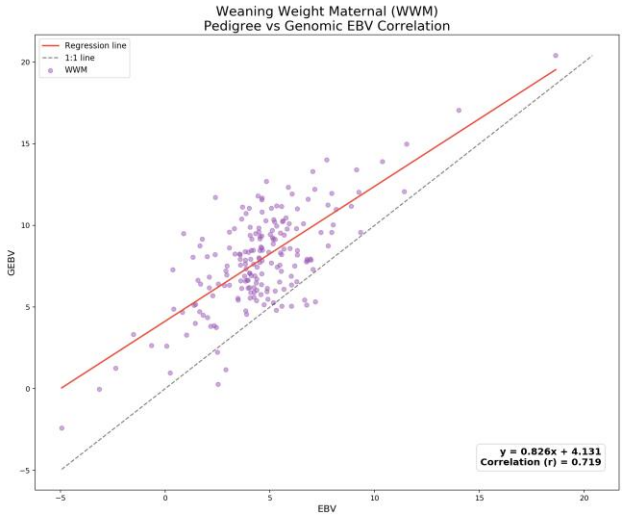


Figure 4. Pearson correlation for weaning weight maternal

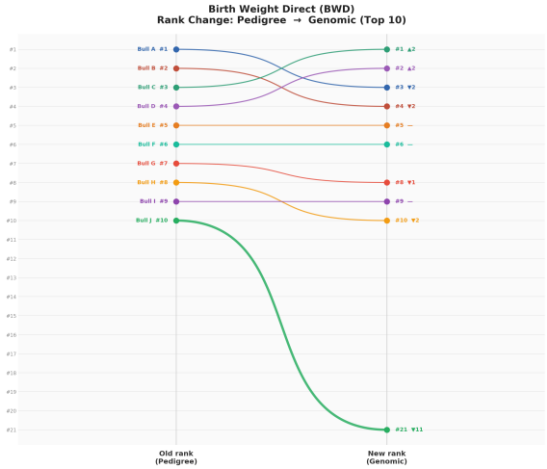


Figure 5. Rank shuffle for top 10 animals by old rank for birth weight

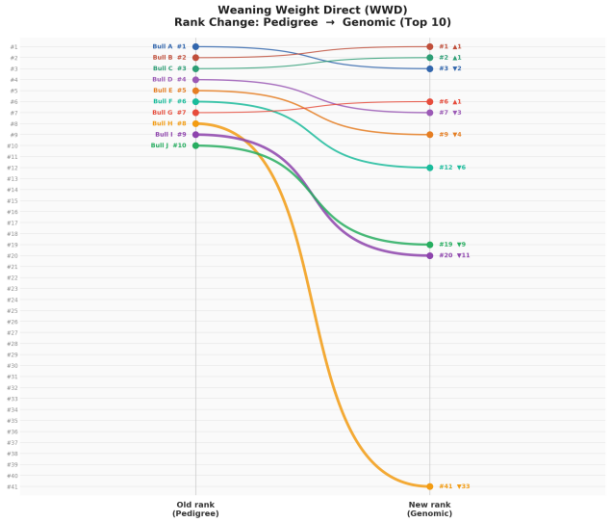


Figure 6. Rank shuffle for top 10 animals by old rank for weaning weight direct

Pearson correlations between pedigree and genomic EBVs were high and significant for all traits (BWD: r = 0.928; WWD: r = 0.807; WWM: r = 0.719; all p<0.0001), indicating broad consistency between the two evaluation systems. The lower correlation for WWM compared with the direct growth traits is consistent with greater dependence of maternal EBV prediction on the availability and structure of maternal information.

The objective of this study was to determine how the rankings of imported Angus sires would change with the inclusion of genomic information. Despite the high EBV correlations, substantial re-ranking of sires occurred across all traits following the transition to ssGBLUP. Mean absolute rank movement was 20.8 positions for BWD (Figure 5), 29.7 for WWD (Figure 6), and 39.7 for WWM (Figure 7), with maximum movements of 91, 139, and 147 positions respectively. Approximately half of all animals declined in rank for BWD (50.8%) and WWD (50.3%), while 51.3% improved in rank for WWM, suggesting a slight directional shift in maternal rankings under the genomic evaluation.

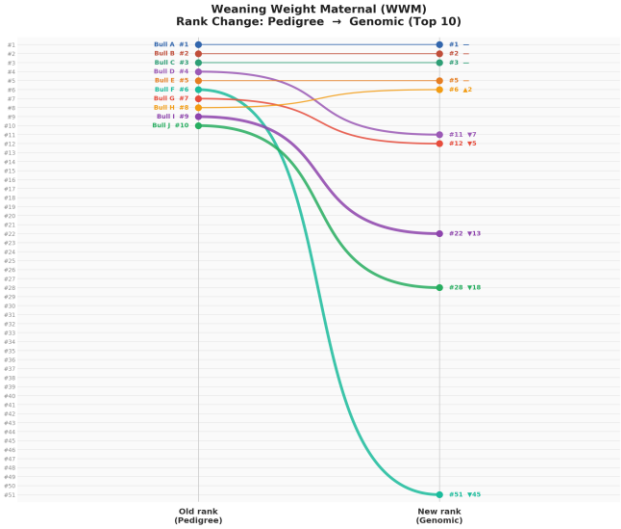


Figure 7. Rank shuffle for top 10 animals by old rank for weaning weight maternal

Movement of the 194 imported bulls within the entire population of genotyped males showed varied results across traits. For BWD, the group overall remained in the bottom two-thirds of the population, although three additional bulls entered the top 25% under the genomic evaluation, indicating some upward movement while confirming that these imported bulls generally transmit lighter birth weights. The most notable improvement was observed for WWD, where the group shifted from the bottom half to the top half of all genotyped males in the population. Bulls in the top 10% more than doubled in number, as did those in the top 25%, with 159 out of 194 bulls improving their rank for WWD under the genomic run. For WWM, the group moved closer to the population median, with 140 out of 194 bulls improving their rank, suggesting a broad upward re-evaluation of maternal genetic merit when genomic information was included.

These results indicate that while the overall genetic landscape was broadly preserved between evaluations, individual sire rankings were considerably affected, with practical implications for sire selection decisions made based on pedigree BLUP rankings alone.

A significant negative relationship between number of progeny and absolute rank movement was observed for BWD (Spearman p=-0.449, p<0.0001) and WWD (p=-0.296, p<0.0001), as well as for the average movement across traits (p=-0.313, p<0.0001). Animals with no recorded progeny showed the largest mean absolute rank movement across traits (35.7 positions on average), nearly double that of animals with 51 or more progeny (19.5 positions) as seen in Table 2.

Table 2: Average change in rank according to the number of progeny with performance records

Progeny group	Number in group	Average rank movement (positions)
0	67	35.7
1 – 5	32	32.8
6 – 20	44	29.8
21 - 50	28	22.2
51 +	22	19.5

This pattern is consistent with the theoretical expectation of ssGBLUP, where the genomic relationship matrix effectively provides additional information for animals with limited phenotypic data in young or unproven animals by capturing realised allele sharing that the pedigree cannot account for (Misztal et al., 2013). In the pedigree-only evaluation, EBVs for animals without progeny are derived almost entirely from parent averages and pedigree relationships, which carry considerably less information than direct performance records. The inclusion of genomic data therefore disproportionately updates EBVs, and consequently rankings, for these animals. The majority of the ten largest rank movers across traits carried two or fewer progeny, further supporting this interpretation and highlighting the particular susceptibility of imported bulls with limited local performance records to re-ranking under genomic evaluation.

In contrast to the direct growth traits, WWM showed no significant relationship between progeny count and rank movement (ρ=-0.051, p=0.482). Mean absolute rank movement for WWM remained consistently high across all progeny groups, ranging from 37.3 positions in the zero-progeny group to 32.0 positions in animals with 51 or more progeny, a far smaller decline than observed for BWD, where movement dropped from 29.3 to 4.2 positions

across the same progeny range. This suggests that an increase in direct progeny records does not stabilise maternal EBVs the way it does for direct growth traits.

This trait-specific pattern reflects the biological complexity of estimating maternal ability in bulls. Maternal EBVs rely heavily on female relatives' performance records, such as those from dams, grandams, and sisters with calves recorded in the local evaluation environment (Mrode, 2014). Following first importation, many of the relevant records of their female relatives reside in foreign databases that the local evaluation does not have access to. This means that these sires have limited access to the specific daughter and female-relative information needed for reliable maternal estimation, even when their number of direct progeny increases. This effect is further compounded by the composition of the South African Angus genomic reference population, which comprises 37% females and may therefore provide less information for maternal traits, potentially contributing to the persistently high rank instability observed for WWM.

The large rank movements observed for WWM should therefore be interpreted with caution, as they may reflect instability in the estimation process as much as genuine genetic re-ranking and underscore the need for an expanded and more sex-balanced genomic reference population to improve the reliability of maternal EBV prediction for imported sires in the South African Angus evaluation.

Conclusions

In conclusion, the results show that the inclusion of genomic information via ssGBLUP resulted in a systematic upward shift in EBVs across all three traits, reflecting the capture of realised genetic relationships that pedigree-based BLUP alone was unable to account for. Genomic information had the greatest impact on animals with limited progeny records. The results also showed that maternal EBVs proved uniquely resistant to stabilisation by progeny count, reflecting the biological requirement for locally recorded daughter performance data, and highlighting the need for continued development of the maternal genomic reference population.

Overall, incorporation of genomic information resulted in substantial re-ranking of the imported sires within the South African Angus population, with the magnitude and direction of change varying among traits.

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