Evaluating the effect of ssGBLUP on a composite beef cattle population with limited pedigree completeness

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Introduction

Established through importing semen + live animals from herds associated with the BBU

Ratified as a true breed in South Africa in 1987

The 2\textsuperscript{nd} largest stud breed associated with SASB

Parentage Summary of Active Animals

<table>
<thead>
<tr>
<th>Category</th>
<th>Known</th>
<th></th>
<th>Verified</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Number</td>
<td>Percentage</td>
<td>Number</td>
<td>Percentage</td>
</tr>
<tr>
<td>Both Parents</td>
<td>54,981</td>
<td>86 %</td>
<td>5,022</td>
<td>8 %</td>
</tr>
<tr>
<td>Neither Parent</td>
<td>8,345</td>
<td>13 %</td>
<td>48,603</td>
<td>76 %</td>
</tr>
<tr>
<td>Only Sire</td>
<td>404</td>
<td>1 %</td>
<td>9,950</td>
<td>16 %</td>
</tr>
<tr>
<td>Only Dam</td>
<td>75</td>
<td>0.01 %</td>
<td>171</td>
<td>0.01 %</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Category</th>
<th>Count</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Animals</td>
<td>63,805</td>
<td>-</td>
</tr>
<tr>
<td>Registered Animals</td>
<td>34,017</td>
<td>53 %</td>
</tr>
<tr>
<td>Total Animals</td>
<td>29,788</td>
<td>47 %</td>
</tr>
</tbody>
</table>
Any foundation cows (FS) with Brahman background can be upgraded to SA Beefmaster

Using Stud Book Proper (SP) bulls on crossbred cows (FS/A/B)
Problem Statement

1) Widespread use of SP Multiple Sires (MS) across all Beefmaster herds:
   a) Low parentage verification + progeny never allocated to bulls
   b) High % of Section B offspring with unknown sire pedigrees

2) Upgrading introduces FS + Section A cows with:
   a) Limited to no pedigree depth
   b) Lack production + fertility measurements
Problem Statement

Poor pedigree depth results in lower accuracy of breeding values (Clark et al., 2012)

Upgrading practices result in around 50% of calves registered as Section B annually.
Aim & Objectives

Aim: To assess the change in breeding value estimation and accuracy when using genomic data on a breed with limited pedigree completeness

1) Compare depth of pedigree across levels of upgrading
   (OptiSel; Wellman + Bennewitz, 2019: Poprep; Groeneveld, 2009)

2) Compare EBVs vs GEBVs and their respective accuracies
   (MiX99; Lidauer et al., 2016: R; RStudio Team, 2014)

• Traits: Birth, Weaning, Yearling and 18-Month Weights
  Heifer Fertility + first three Inter-Calving Periods
Materials: Pedigree

451 009 animals in the SA Beefmaster pedigree

With around 48% of animals being Section B

<table>
<thead>
<tr>
<th>Herd Book Population</th>
<th>Number Genotyped</th>
<th>Birth Year Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total</td>
<td>1 353</td>
<td>1985-2020</td>
</tr>
<tr>
<td>Stud Proper</td>
<td>487</td>
<td>1999-2020</td>
</tr>
<tr>
<td>Section C</td>
<td>463</td>
<td>1994-2020</td>
</tr>
<tr>
<td>Section B</td>
<td>298</td>
<td>1985-2020</td>
</tr>
<tr>
<td>Section A</td>
<td>103</td>
<td>1997-2020</td>
</tr>
</tbody>
</table>

Genomic population built via Beef Genome Project
Materials: Growth

\[ y_{ijklmnop} = \mu + cg_i + sex_j + age_k + parity_l + age_of_dam_m + PE_n + mat_o + animal_p + e_{ijklmnop} \]

- \( y \) = birth, weaning, 12- or 18-month weights of animal \( p \)
- \( \mu \) = mean weight
- \( cg_i \) = contemporary group \( i \) (herd x year x season x treatment group x birth status) of animal \( p \)
- \( sex_j \) = sex \( j \) of animal \( p \)
- \( age_k \) = age \( k \) of animal \( p \)
- \( parity_l \) = parity status (1 or >1) \( l \) of dam of animal \( p \)
- \( age_{of\_dam}_m \) = linear and quadratic regressions on age of the dam of animal \( p \)
- \( PE_n \) = random permanent environmental effect \( n \) associated with the dam of animal \( p \)
- \( mat_o \) = random maternal additive genetic effect of dam \( o \) of animal \( p \)
- \( animal_p \) = random direct additive genetic effect of animal \( p \)
- \( e_{ijklmnop} \) = random residual effect
$y_{ijklmno} = \mu + c_g_i + h_{erd_j} + s_e_x_k + a_{ge_l} + a_{ge_of_dam_m} + P_{E_n} + a_{nimal_o} + e_{ijklmno}$

$y =$ weaning weight, heifer fertility or one of the first three inter-calving periods of animal $o$

$\mu =$ mean of weaning weight, heifer fertility or one of the first three inter-calving periods of animal $o$

$c_g_i =$ contemporary group $i$ (herd x year x season x treatment group for weaning weight, birth herd x year x season for heifer fertility, herd x year x season x previous calving group for inter-calving periods) of animal $o$

$h_{erd_j} =$ herd $j$ of animal $o$ (weaning weight only)

$s_e_x_k =$ sex $k$ of animal $o$ (weaning weight only)

$a_{ge_l} =$ age $l$ at which animal $o$ was weaned (weaning weight only)

$a_{ge_of_dam_m} =$ linear and quadratic regressions on age of the dam of animal $o$ (weaning weight only)

$P_{E_n} =$ permanent environmental effect $n$ associated with the dam of animal $o$ (weaning weight only)

$a_{nimal_o} =$ random direct additive genetic effect of animal $o$

$e_{ijklmno} =$ random residual effect
Methods

1) Genotyped population
   • Quality control and imputation to density of 120,000 SNPs (Fimpute v3; Sargolazei, 2014)
   • Gmatrix and subsequent blending of G and A matrix to create $H^{-1}$ matrix (RelaX2)

2) Breeding values
   • Estimated using MiX99 (Lidauer et al., 2016)
   • ssGBLUP inclusion of $H^{-1}$ matrix

3) Accuracies
   • Estimated the Misztal and Wiggans approach (Misztal and Wiggans, 1988)
   • ssGBLUP uses the full $H^{-1}$ matrix
Results: Pedigree

Expected from the known upgrading system in place

SA Beefmaster Pedigree Investigation

<table>
<thead>
<tr>
<th>Herd Book Population</th>
<th>Pedigree Completeness</th>
<th>Complete Generational Equivalent</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total</td>
<td>38 %</td>
<td>2.07</td>
</tr>
<tr>
<td>Stud Proper</td>
<td>86 %</td>
<td>4.46</td>
</tr>
<tr>
<td>Section C</td>
<td>66 %</td>
<td>3.45</td>
</tr>
<tr>
<td>Section B</td>
<td>24 %</td>
<td>2.10</td>
</tr>
<tr>
<td>Section A</td>
<td>6 %</td>
<td>0.47</td>
</tr>
</tbody>
</table>
Results: WW Direct

R² observed: 73% Section A | 94% Section C
95% Section B | 91% Stud Proper

EBV plotted against GEBV for genotyped animals

Accuracy plotted against genomic accuracy
Results: WW Maternal

R² observed: 93% Section A | 91% Section C
93% Section B | 89% Stud Proper

EBV plotted against GEBV for genotyped animals

Accuracy plotted against genomic accuracy
Results: ICP1

$R^2$ observed: 73% Section A | 85% Section C
90% Section B | 81% Stud Proper

Accuracy plotted against genomic accuracy

EBV plotted against GEBV for genotyped animals
Discussion

Observed pedigree completeness + CGE in SA Beefmaster:
- Similar to indigenous + localised admixed breeds*
- Low in comparison to established beef + dairy breeds#

Greatest changes in EBV to GEBV seen for:
- Section A animals with limited pedigree depth + no phenotypes
- Sex-limited, maternal and lowly heritable traits+

Genotyping increases accuracy of EBV estimation, especially for animals that:
- Have low pedigree completeness as a consequence of the upgrading process
- Multiple Sires with little to no verified progeny

*Garrido et al., 2008; Santana et al., 2011; Pienaar et al., 2012; Cortés et al., 2019; Invankovic et al., 2022.
#Gutierrez et al., 2002; Gallego et al., 2020; Paim et al., 2020; Rios-Utrrear et al., 2021; Hay et al., 2022; Visser et al., 2023.
+Hayes et al., 2009; Saatchi et al., 2012; Hayes et al., 2019; Olasege et al., 2021; Facy et al., 2023.
Conclusion

Genotyping in the SA Beefmaster is a viable tool to overcome low accuracy of breeding value estimation due to limited pedigree depth.

Complement animals that come from an upgrading background and/or to reveal the true genetic merit of bulls used as Multiple Sires.

In the absence of pedigrees, genomics can be a solution to improve selection for new breeders joining the society and/or for breeders with large herds with a low parentage verification rate.
Thank You!