

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 2nd largest stud breed associated with SASB

Parentage Summary of Active Animals

Category	Known		Verified	
	Number	Percentage	Number	Percentage
Both Parents	54 981	86 %	5 022	8 %
Neither Parent	8 345	13 %	48 603	76 %
Only Sire	404	1 %	9 950	16 %
Only Dam	75	0.01 %	171	0.01 %

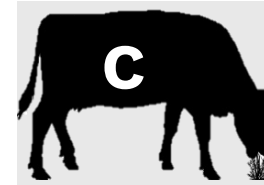
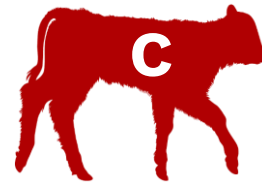
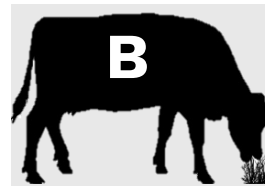
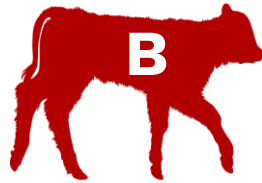
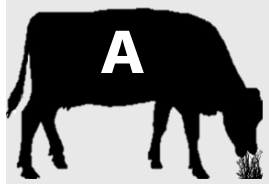
Category	Breed	
	Count	Percentage
Total Animals	63 805	-
Registered Animals	34 017	53 %
Total Animals	29 788	47 %



Introduction

Any foundation cows (FS) with Brahman background can be upgraded to SA Beefmaster

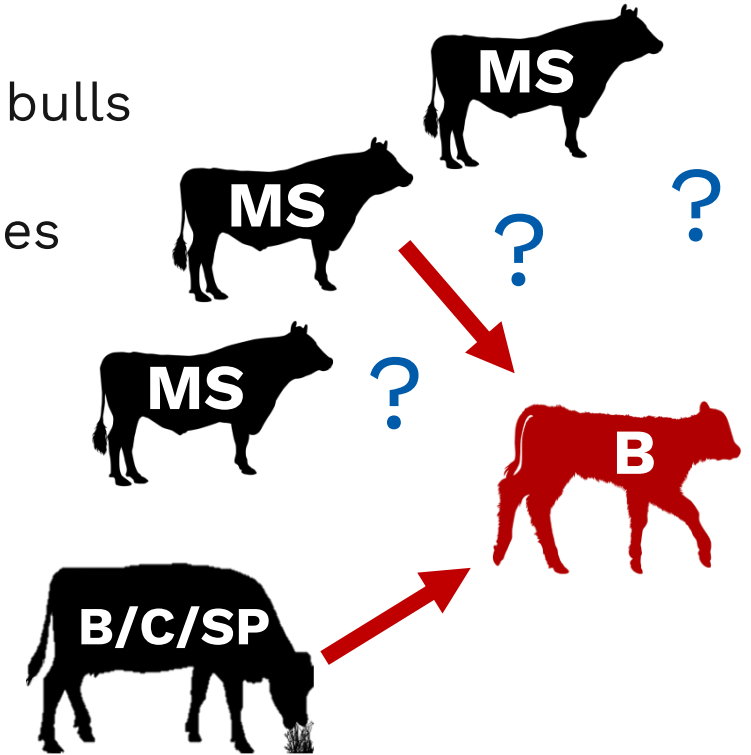
Using Stud Book Proper (SP) bulls on crossbred cows (FS/A/B)



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

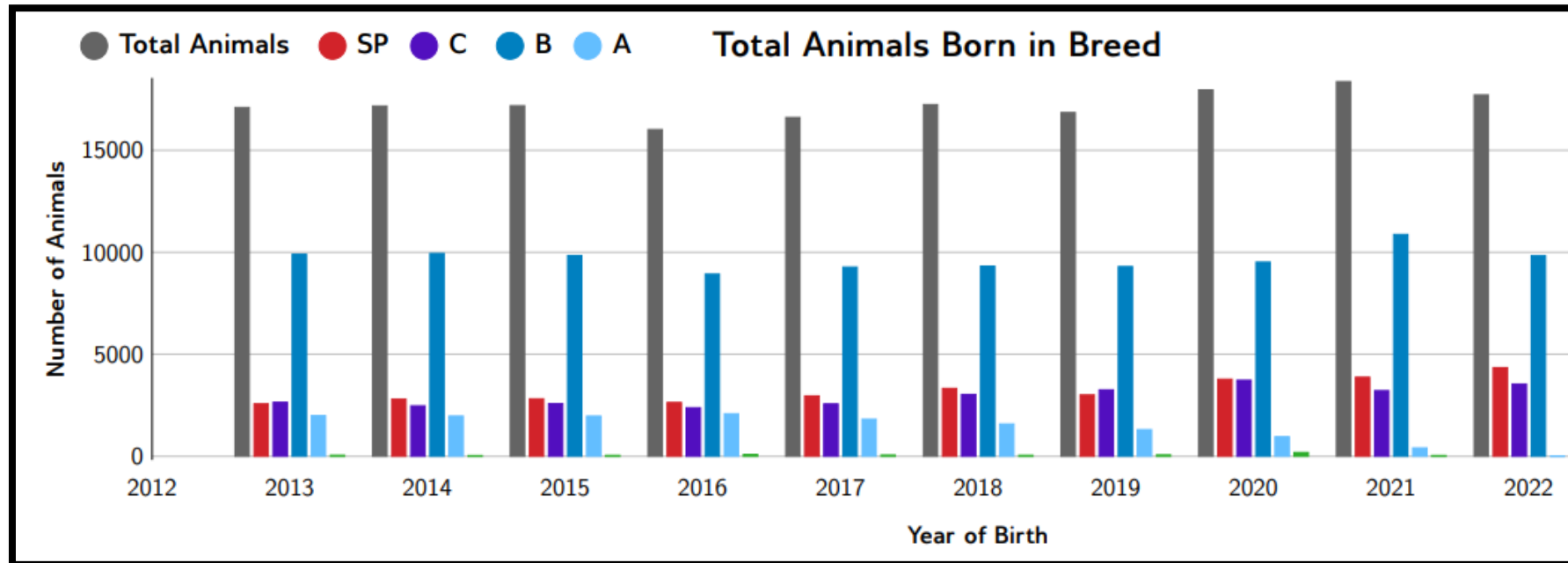


2) Upgrading introduces FS + Section A cows with:

- 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**



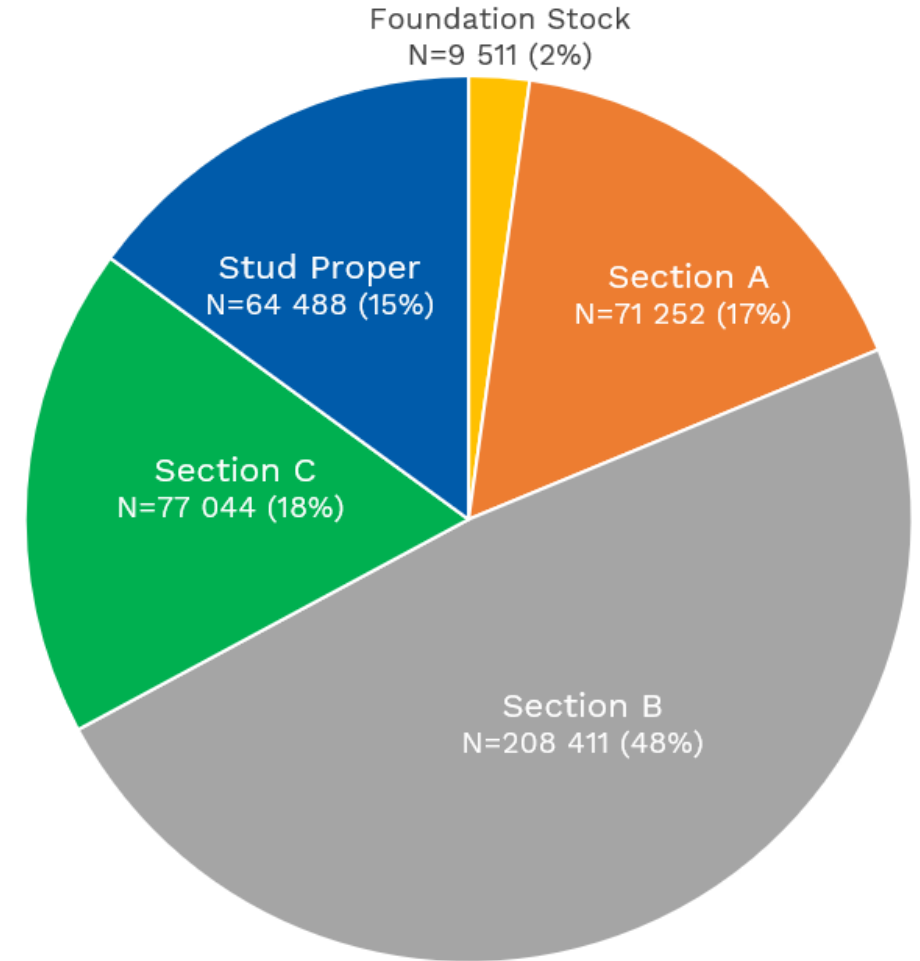
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Materials: Pedigree

451 009 animals in the SA Beefmaster pedigree

With around **48%** of animals being Section B

Herd Book Population	Number Genotyped	Birth Year Range
Total	1 353	1985-2020
Stud Proper	487	1999-2020
Section C	463	1994-2020
Section B	298	1985-2020
Section A	103	1997-2020



Genomic population built via Beef Genome Project



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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

μ = 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

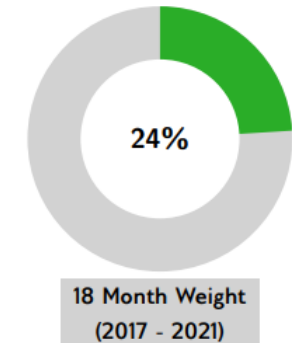
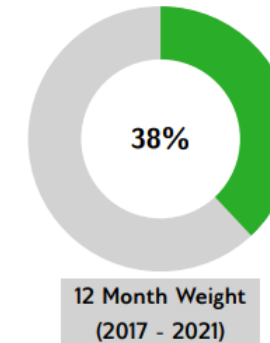
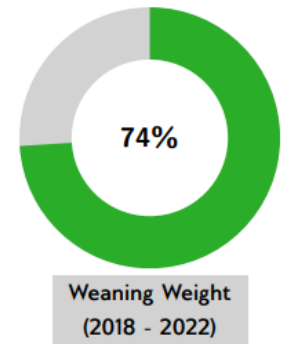
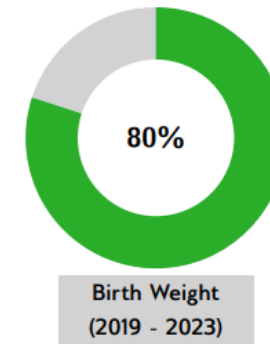
$age_of_dam_m$ = linear and quadratic regressions on age of the dam of animal p

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



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Materials: Fertility

$$Y_{ijklmno} = \mu + cg_i + herd_j + sex_k + age_l + age_of_dam_m + PE_n + animal_o + e_{ijklmno}$$

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

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

cg_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

$herd_j$ = herd j of animal o (weaning weight only)

sex_k = sex k of animal o (weaning weight only)

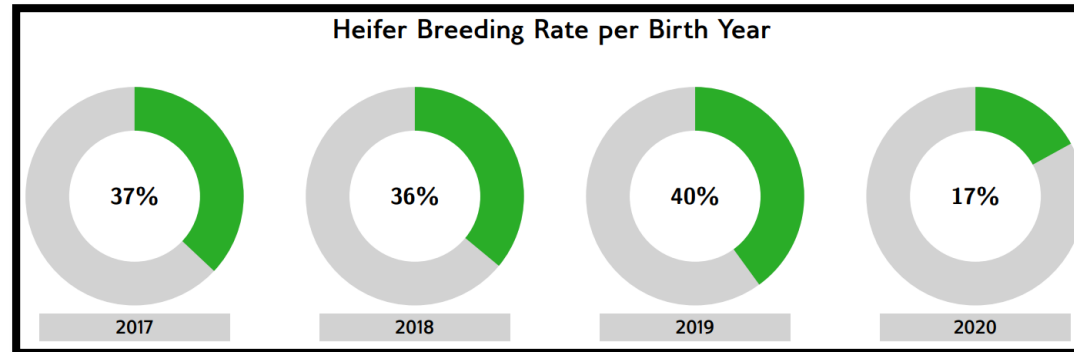
age_l = age l at which animal o was weaned (weaning weight only)

$age_of_dam_m$ = linear and quadratic regressions on age of the dam of animal o (weaning weight only)

PE_n = permanent environmental effect n associated with the dam of animal o (weaning weight only)

$animal_o$ = random direct additive genetic effect of animal o

$e_{ijklmno}$ = random residual effect



Methods

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} + A_{22}^{-1} \end{bmatrix}$$

1) Genotyped population

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

2) Breeding values

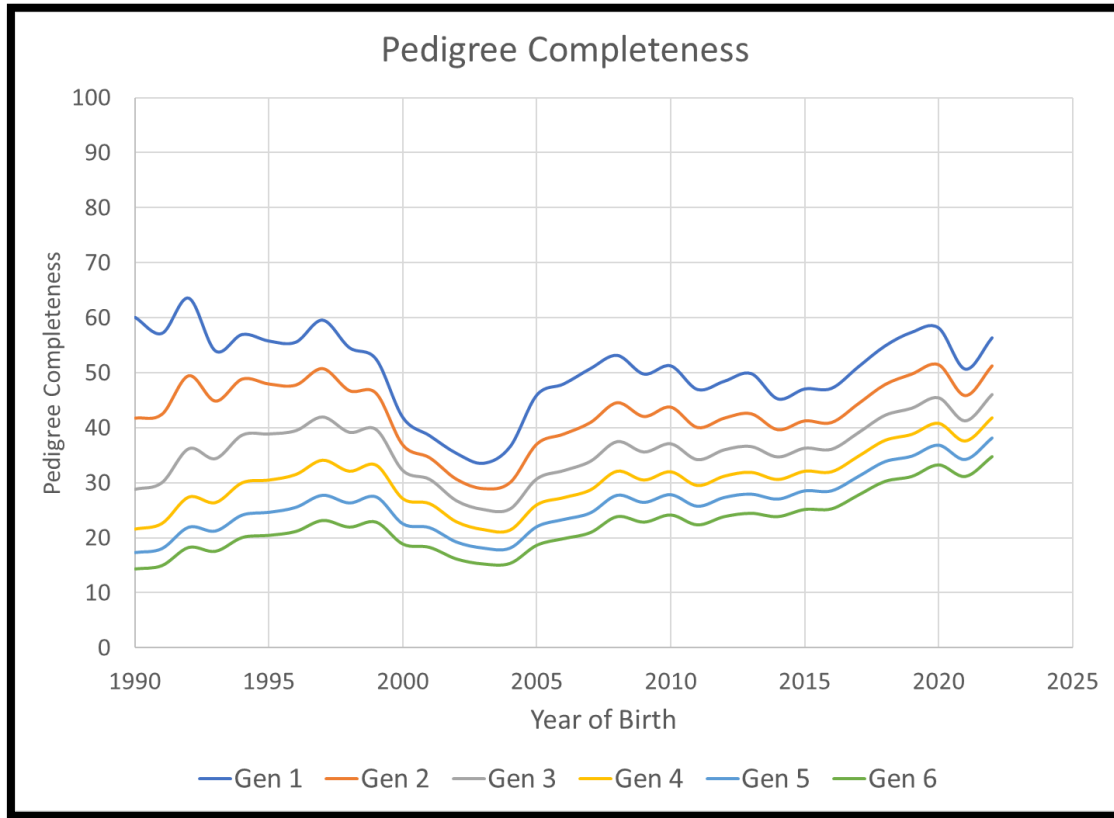
- Estimated using MiX99 (Lidauer *et al.*, 2016)
- ssGBLUP inclusion of H^{-1} matrix

$$accuracy = \sqrt{1 - SEP^2 / \sigma_a^2}$$

3) Accuracies

- Estimated the Misztal and Wiggans approach (Misztal and Wiggans, 1988)
- ssGBLUP uses the full H^{-1} matrix

Results: Pedigree



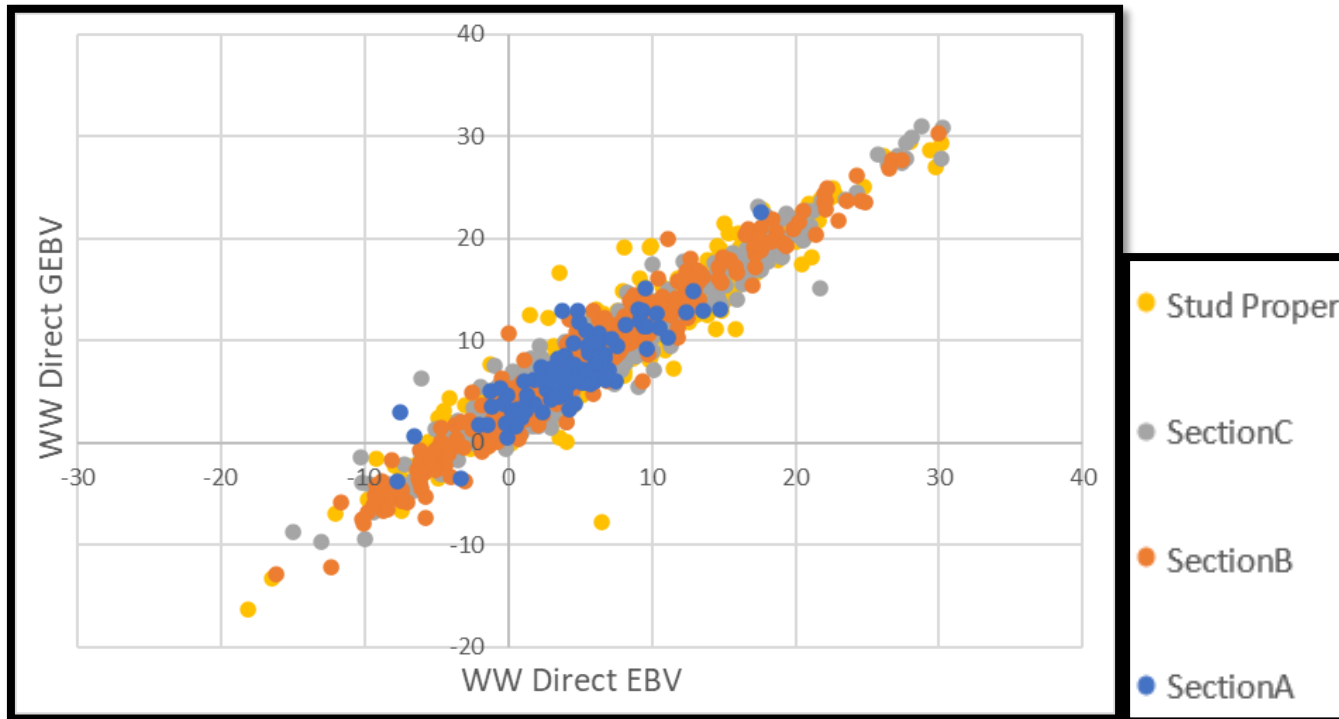
SA Beefmaster Pedigree Investigation

Herd Book Population	Pedigree Completeness	Complete Generational Equivalent
Total	38 %	2.07
Stud Proper	86 %	4.46
Section C	66 %	3.45
Section B	24 %	2.10
Section A	6 %	0.47

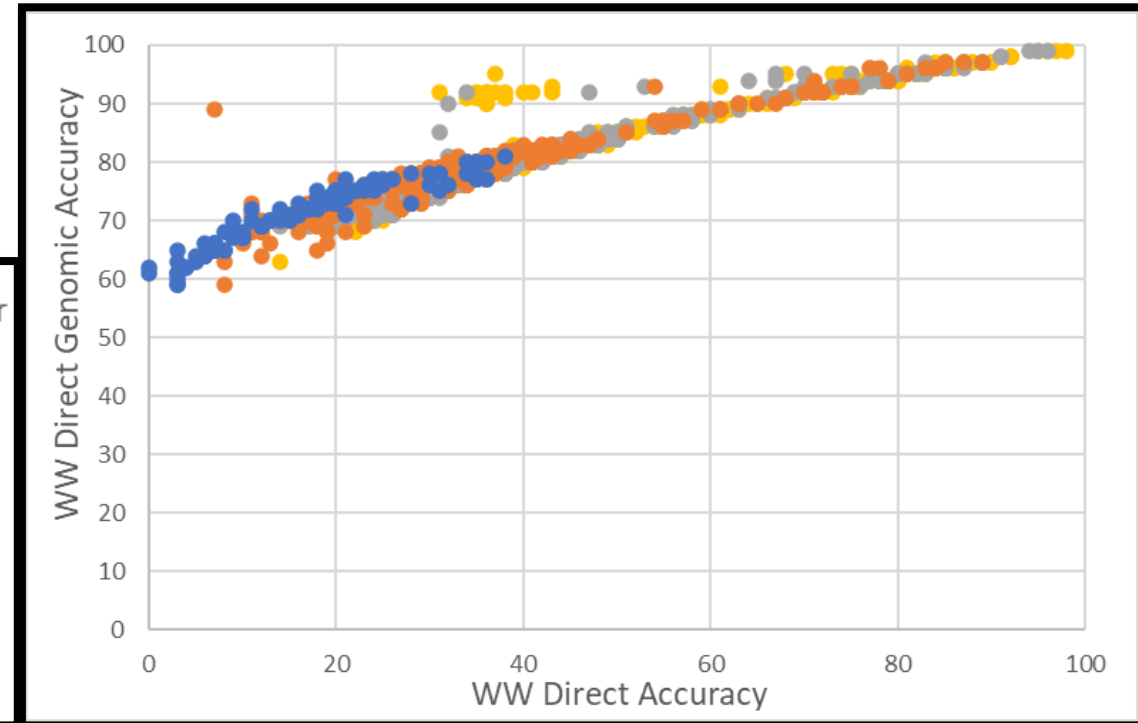
Expected from the known upgrading system in place

Results: WW Direct

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



Accuracy plotted against genomic accuracy

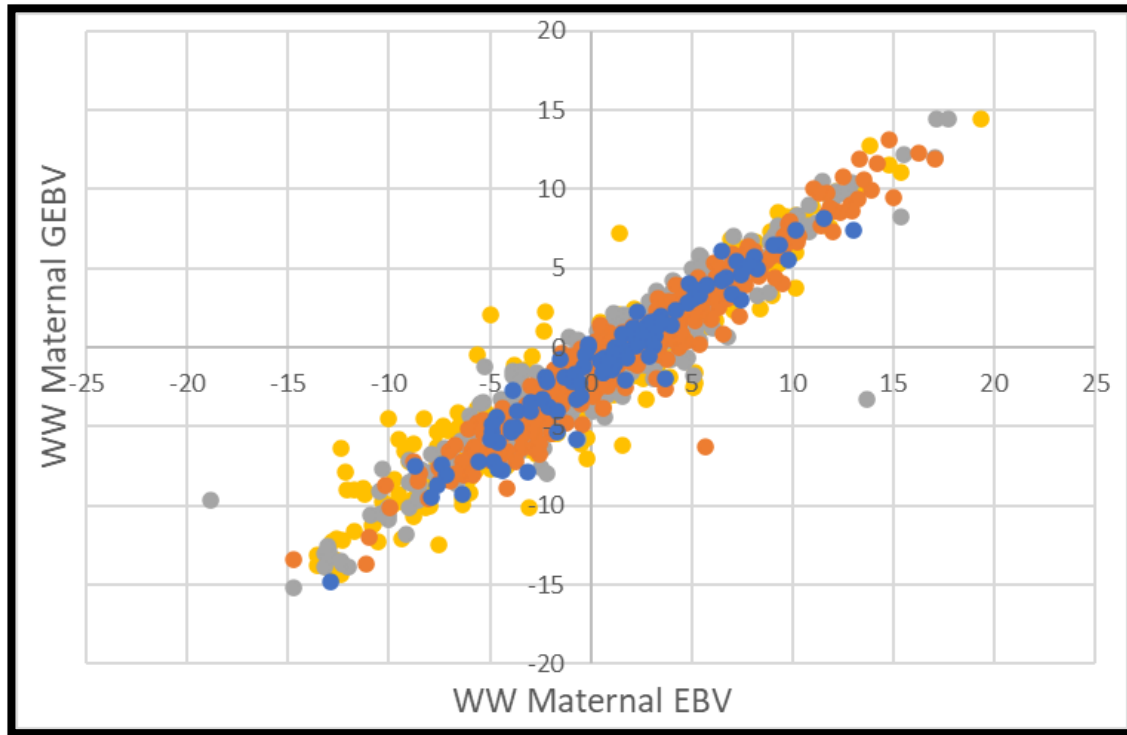


EBV plotted against GEBV for genotyped animals

Results: WW Maternal

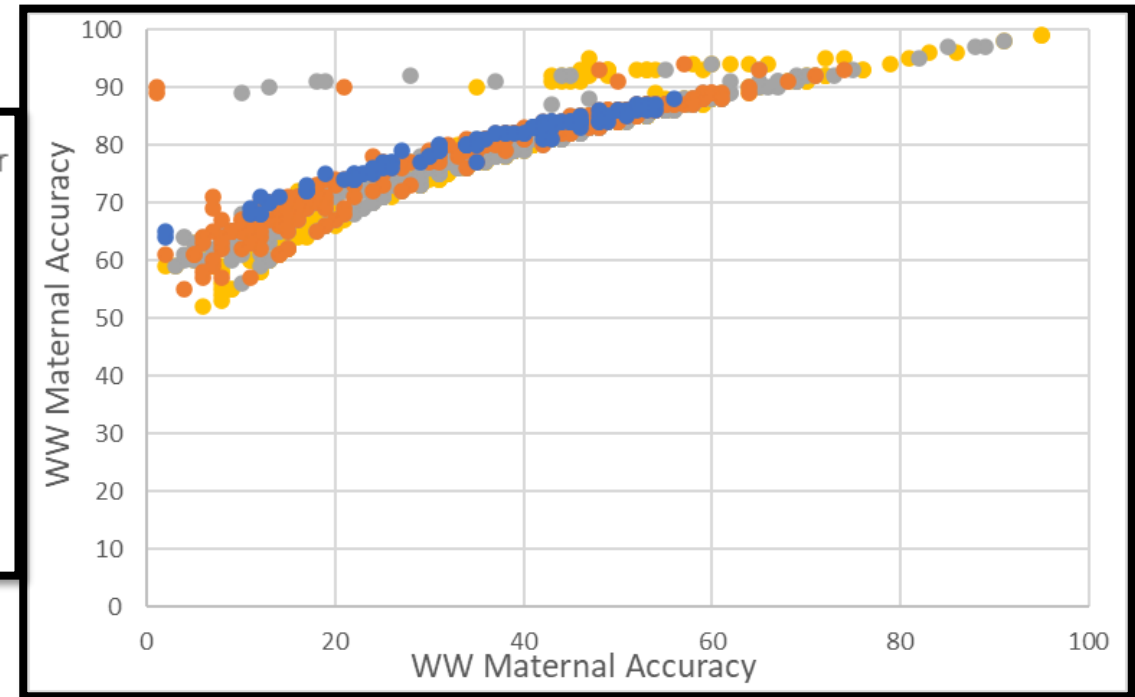
R² observed: 93% Section A | 91% Section C

93% Section B | 89% Stud Proper



EBV plotted against GEBV for genotyped animals

Accuracy plotted against genomic accuracy

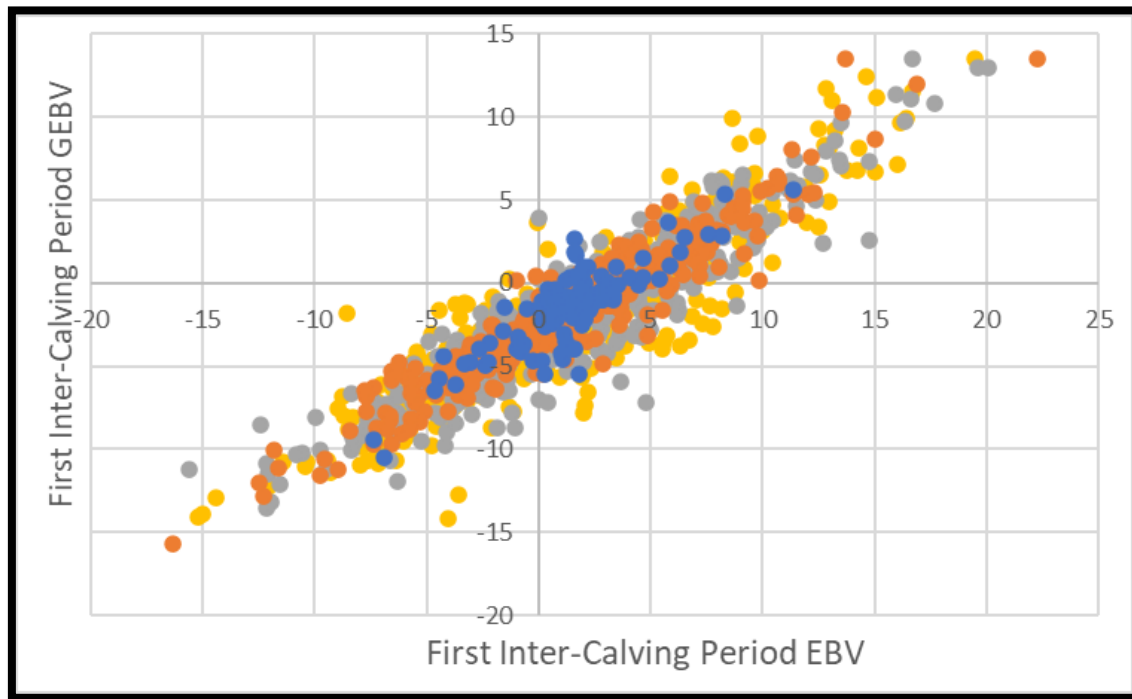


Results: ICP1

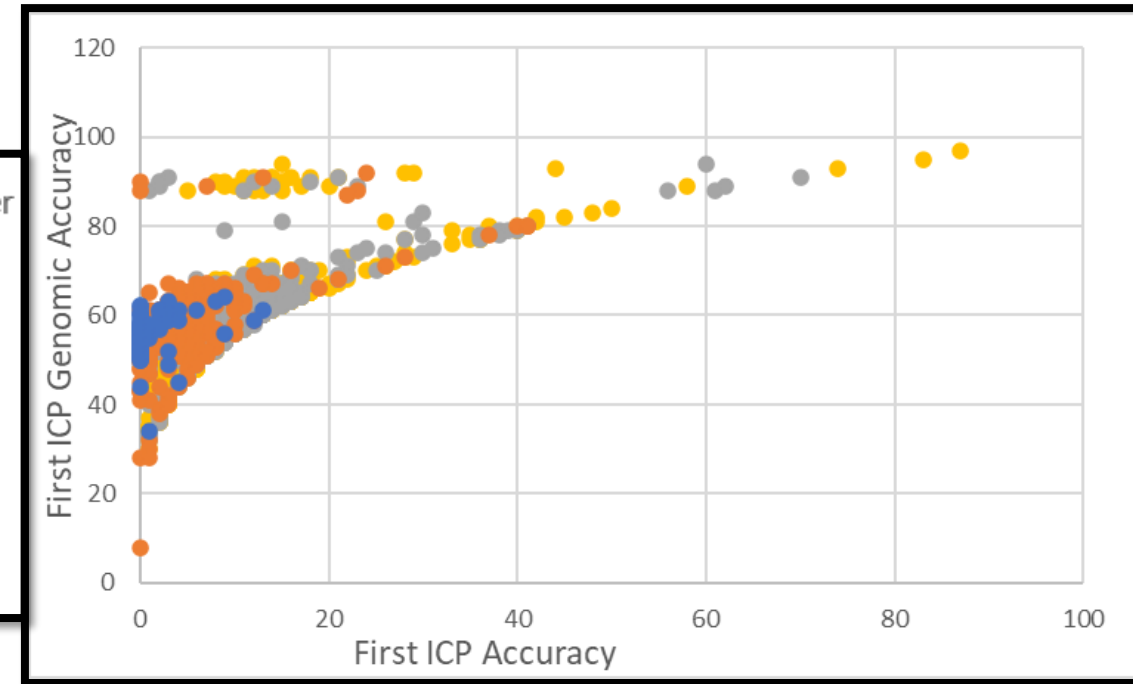
R² observed: 73% Section A | 85% Section C

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.

#Gutiérrez *et al.*, 2002; Gallego *et al.*, 2020; Paim *et al.*, 2020; Rios-Utrear *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



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