PROGRESS OF THE SOUTHERN MULTIBREED RESOURCE POPULATION: HARD-TO-MEASURE PHENOTYPES TO DRIVE GENOMIC SELECTION

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SUMMARY

This paper describes the progress in the first half of a large, 5-year breeding project run across New South Wales involving five temperate beef breeds and the Brahman breed. The project's purpose is to generate up to 8,000 progeny that allows the benefits of genomic selection to be captured, particularly for traits that are lowly recorded due to being difficult or costly to record or which are yet to be routinely included in genetic evaluations, e.g., fertility, health, and resilience. The project has generated 4,886 progeny from three cohorts, with another 1,990 females to calve in mid-2023. Cohort one, born in 2020, has now had all steers complete feedlot finishing with carcass traits recorded, with the heifers having completed their first calving and subsequent rebreed. Details concerning the recording of hard-to-measure traits to this point in the project are provided. The high-density SNP genotypes collected, and the recording of these traits will contribute to the genomic reference populations and BREEDPLAN evaluations of the breeds involved.

INTRODUCTION

The potential exists to significantly increase profitability in the Australian beef industry using EBVs and selection indexes by capturing the benefits of genomic selection. In 2018, the BREEDPLAN genetic evaluation system implemented single-step GBLUP (Johnston *et al.* 2018), which was a significant step toward realising these gains. Achieving the full benefits of genomic selection is contingent on a number of other factors. The impacts effective population size, relative size of the reference population, trait heritability (Goddard and Hayes 2009), the relatedness within the reference population and its relatedness to selection candidates (Pszczola *et al.* 2011) have on the success of genomic selection have been well described. To successfully improve profitability, genomic selection must provide predictive accuracy for all traits that impact profitability and form the basis of current and future selection indexes. For this reason, the size of the reference population required is a function of not only the number of animals with genotypes and phenotypes but also the types of phenotypes recorded. This is particularly the case for traits that are difficult or costly to record or are economically important but yet to be routinely included in genetic evaluations, e.g., fertility, health, and resilience traits. The Southern Multi-breed project (SMB: Walmsley *et al.* 2021), initiated in 2020, and the Repronomics^{TM} project (Johnston *et al.* 2017), initiated in 2013, are two industry research initiatives that have been developed to address

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these needs across multiple breeds. The relatedness of the animals in the SMB project to the wider respective Australian breed populations has been examined by Moore *et al.* (2023). This paper provides a brief update on the progress of the SMB Project with a focus on the hard-to-measure and lowly recorded BREEDPLAN traits that are being evaluated as part of SMB.

BRIEF OVERVIEW

The SMB project is being conducted across the New South Wales Department of Primary Industries research facilities; Trangie Agricultural Research Centre; Grafton Primary Industries Institute; Tocal Agricultural Centre; Glen Innes Agricultural Research and Advisory Station; Elizabeth MacArthur Agricultural Institute (EMAI); Menangle and the University of New England (UNE) research feedlot, "Tullimba" (Kingstown). The project is focused on the five numerically largest temperate breeds (viz. Angus, Charolais, Hereford, Shorthorn, and Wagyu) in southern Australia and the Brahman breed, which is commercially relevant in the sub-tropics of NSW and links SMB to the Repronomics^{TM} project (Johnston *et al.* 2017). A critical design feature is that all breeds are managed in mixed breed groups, which allows valid breed comparisons to be made. Walmsley *et al.* (2021) describe the design and initiation of the SMB project.

PROGENY GENERATED

The aim was to generate up to 8,000 progeny across the project's lifetime. To date, the project has generated progeny in 2020, 2021, and 2022, with a fourth cohort due to begin calving in mid-2023. The number of calves in cohorts 1 to 3 are shown in Table 1. The progeny were generated by a combination of artificial insemination (AI) programs followed by natural mate back-ups over the base cows and natural mate bulls over all female progeny generated by the project. In total, AI programs included 265 sires (Angus=74; Brahman=30; Charolais=30; Hereford=55; Shorthorn=33; Wagyu=43) with 141 natural mate sires used (Angus=46; Brahman=10; Charolais=16; Hereford=34; Shorthorn=15; Wagyu=20).

Table 1. Number of progeny generated by year (cohorts 1 to 3) and sex, in the Southern Multibreed project, and the number of pregnancies for cohort 4

		Progeny generated			Confirmed Pregnancies
Year	2020	2021	2022	Total	2023
Steers	710	784	965	2459	-
Heifers	694	758	975	2427	-
Overall	1404	1542	1940	4886	1990

TRAITS RECORDED

All calves are intensively recorded from birth following BREEDPLAN protocols for the current standard BREEDPLAN traits. These include birth (BW), weaning (WW), yearling (YW) and finished (FW) weights, calving ease (CE), ultrasound scan traits (eye muscle area (EMA), rib fat (RIB), rump fat (RUMP) and intramuscular fat (IMF)), carcass traits (Carcass Weight, EMA, RIB, RUMP and IMF) including retail beef yield (RBY), days-to-calving (DTC) and temperament (TEMP – docility and crush scores). Table 2 presents the number of records for these traits across all breeds for the first three cohorts. Birth weight and calving ease are the first traits recorded in an animal's life and as such have the largest number of records to date (n=4,880 and 4,886, respectively). Both traits relate to the probability of calf survival through the birthing process and as such have important impacts on profitability. Mean birth weight was 38 kg (±7.9 SD) and ranged between 8.5 kg and 69.5 kg, with 88% of records between 25 and 50 kg. Although the majority of calving ease scores were category 1, all five categories have been observed.

In addition to those in Table 2, other traits are important for improving profitability. The increasing importance of animal welfare and pressure to reduce dehorning means that poll status has the potential to be an important economic trait. Horn/poll status has been recorded at marking (n = 4,545), with assessments also conducted at weaning (n = 2,700) to capture late developing horns/scurs. Phenotypes have been observed for all horn/poll classifications described by Connors *et al.* (2021). Animal health traits that impact welfare and productivity have also been recorded. Worm egg counts (WEC) have been measured at weaning (n = 2,681) as well as prior to heifer joining and steers entering the feedlot (n = 2,487) in the first two cohorts. Figure 1 shows the average cube root transformed WEC for sites and years at weaning. Immune competence (Wilkie and Mallard, 1999) has been proposed as a trait that could increase general disease resistance through selection to reduce the incidence of diseases such as bovine respiratory disease. Currently, only cohort two has been recorded for immune competence (n = 1,412) at weaning.

Table 2. Number of progeny per cohort recorded* for current BREEDPLAN traits in the Southern Multibreed project for the first three cohorts

Cohort	BW	CE	WW	YW	FW	Scan	Carc.	RBY	DTC	TEMP.
2020	1402	1403	1291	1278	1248	1278	628	157	505	1282
2021	1541	1543	1412	1394	170	868	-	-	-	1138
2022	1937	1940	-	-	-	-	-	-	-	-

*See text for trait descriptions.

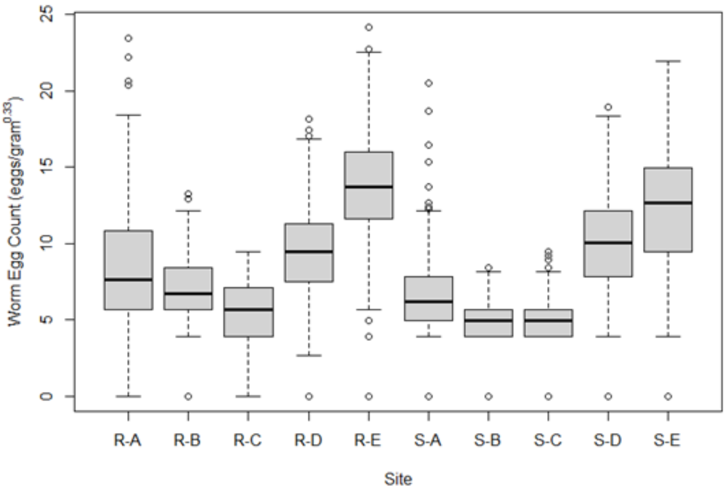

Figure 1. Average weaning worm egg count (cube root transformed) for each research site (designated A to E) and years (R-2020 and S-2021) for the first two cohorts of Southern Multibreed calves (n=2,681)

The importance of fertility as a driver of profitability, and the relatively low levels of DTC recording in the beef industry (Gudex and Millen, 2019) have created the need to examine new traits for inclusion in genetic evaluations. Regular ovarian scans have been conducted using real-time ultrasound to identify puberty in heifers or return to oestrous in first-lactation females by the presence of a *corpus luteum*. Currently, 1,321 heifers have had puberty assessments conducted, with 465 first-lactation females assessed for return to oestrous. Analysis of ovarian activity records is described by Donoghue *et al.* (2023). Prior to joining, heifers and first-lactation females have had body condition score assessments, hip height measurements and ultrasound body composition scans taken, following the protocols described by Wolcott *et al.* (2023), for evaluation as potential indicators of the capacity to maintain body condition during periods of high energy demand. McKiernan (1990) described a muscle score scale that has a significant association with RBY and can be used to assess live animals for increasing profitability. Progeny (n = 2,703) were assessed using this scale when ultrasound scanning has been conducted. Feed is the major direct cost in beef production meaning that profitability is a direct function of changes in feed efficiency. In an effort to address this steer feed intake has been recorded (n = 628) in the feedlot (Torres-Varquez *et al.* 2018).

CONCLUSIONS

The SMB project has produced 4,886 progeny in the first 2.5 years with another 1,990 pregnant females to calve in mid-2023. An extensive recording program has focused not only on traits routinely recorded in BREEDPLAN but also those which are difficult or costly to record or are yet to be routinely included in genetic evaluations, e.g., health and resilience. A significant body of high-quality data is being produced from the investment made by industry and government. This represents a valuable resource to benchmark across-breed performance and capture the benefits of genomic selection, particularly for hard-to-measure traits. As such, the project will enable more effective selection for those traits contributing to value chain profit.

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