SOUTHERN MULTI-BREED RESOURCE POPULATION: GENERATION OF COHORTS ONE AND TWO

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SUMMARY

This paper describes the generation of the first and second cohort of animals in a large 5-year breeding project being conducted across New South Wales involving five temperate beef breeds and the Brahman breed. Females were joined to 154 sires via artificial insemination and back-up matings in 2019 to generate the first cohort of calves, which were born in 2020. Calves were born and raised in mixed breed groups and will be intensively recorded head-to-head for current BREEDPLAN traits and new economically important traits. Birth data have been collected for Cohort One, with records available for 1,398 calves. Traits recorded at birth included birth weight, calving ease, calf fate, calf bellow and calf vigour. Traits to be collected at weaning include weaning weight, hip height, muscle score, docility (crush-side and flight speed), horn/poll phenotype and worm egg count. Relationships between calf bellow and calf vigour scores at birth and subsequent measures of behaviour and production will be assessed. Steers will be backgrounded at one of two locations before entering Tullimba feedlot and subsequently slaughtered, while females will be retained at each site to be joined naturally. Generation of Cohort Two has begun with females joined to 202 sires via artificial insemination and back-up matings in 2020, with 1,535 calves expected to be born in 2021. Data generated from the project will enhance current within-breed genetic evaluations through collection of data for traits that are currently poorly recorded, and by expanding the suite of traits available for selection.

INTRODUCTION

Currently, beef producers making selection decisions regarding the genetic merit of potential parents of the next generation of progeny in their herds are only able to utilise estimated breeding values (EBVs) and selection indexes generated from within-breed genetic evaluations (Graser *et al*. 2005). In addition, there is interest to enhance current within-breed genetic evaluations by conducting intensive collection of traits that are currently poorly recorded (such as fertility and eating quality), and by expanding the suite of traits to include behaviour, health and welfare traits. A new project is being conducted over the next 5 years (2020 to 2025) known as the Multi-Breed Genomic Beef Cattle Resource or Southern Multi-Breed (SMB) project. This project will collect phenotypes and genotypes on animals from six breeds that have been managed in mixed breed

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[*] AGBU is a joint venture of NSW Department of Primary Industries and University of New England

groups at sites across New South Wales (NSW) for existing BREEDPLAN and new economically important traits, such as early-in-life reproduction. This paper provides a description of the generation of the first two cohorts of animals in the project.

MATERIALS AND METHODS

Generation of Cohort One. The animals used in this project were calves born in the first Cohort of the Southern Multibreed Resource population in five NSW Department of Primary Industries (DPI) research herds (Trangie Agricultural Research Centre, Trangie; Grafton Primary Industries Institute, Grafton; Tocal Agricultural Centre, Tocal; Glen Innes Agricultural Research and Advisory Station, Glen Innes; Elizabeth MacArthur Agricultural Institute (EMAI); Menangle) (Walmsley *et al*. 2021). Calves in Cohort One were from six different breeds (Angus, Brahman, Charolais, Hereford, Shorthorn and Wagyu), and all breeds were managed and recorded in mixed groups at each location. Females at each site were mated via a single synchronised artificial insemination (AI) program in late 2019, with back up bulls introduced five days after insemination. A total of 94 sires were represented in the AI program (Angus=21; Brahman=12; Charolais=10; Hereford=25; Shorthorn=13; Wagyu=13) and 60 sires in the natural joinings (Angus=20; Brahman=3; Charolais=6; Hereford=15; Shorthorn=8; Wagyu=8). Purebred joinings were undertaken at all locations except Grafton, where a small amount of crossbreeding involving Brahman reciprocal matings to Angus and Herefords occurred. Matings were allocated using MateSel based on coancestry to limit inbreeding, with a small amount of emphasis placed on the index (Walkom *et al*. 2021). The joining program was staggered across the five sites, with calving occurring from June (Trangie) to October (EMAI) in 2020. Cohort One calves were fully pedigreed and had a comprehensive suite of traits measured at birth based on BREEDPLAN collection protocols. All Cohort One calves were assessed for horn/poll phenotype at marking time (approximately 10 to 12 weeks of age), with dehorning undertaken for those with the horn phenotype. Calves will be serially assessed for horn/poll phenotype in the project (Conners *et al*. 2021). The number of female and male calves by breed of calf at each location is found in Table 1. There were 1,398 calves born in Cohort One.

Table 1 Number of female (F) and male (M) calves by breed and site in Cohort One

Site[b]	AA[a]		BB		CC		HH		SS		WY		
	F	M	F	M	F	M	F	M	F	M	F	M	Total
TR	37	38	-	-	-	-	37	31	-	-	29	30	202
GR	64	58	62[c]	67[d]	-	-	47	54	-	-	-	-	352
TO	48	40	-	-	6	14	-	-	44	40	-	-	192
GI	38	26	-	-	-	-	28	28	-	-	19	26	165
EMAI	41	49	-	-	56	57	44	44	52	57	47	40	487
Total	228	211	62	67	62	71	156	157	96	97	95	96	1398

[a] AA=Angus; BB=Brahman; CC=Charolais; HH=Hereford; SS=Shorthorn; WY=Wagyu
[b] TR=Trangie; GR=Grafton; TO=Tocal; GI=Glen Innes; EMAI=Menangle
[c] BBxBB (n=22), AAxBB (n=13), BBxAA (n=4), BBxHH (n=12) and HHxBB (n=11) calves
[d] BBxBB (n=19), AAxBB (n=10), BBxAA (n=11), BBxHH (n=22) and HHxBB (n=5) calves

At birth, the calves were tagged, and several traits were recorded following standard BREEDPLAN collection procedures, including birth weight, calving ease and calf fate. In addition, measures of calf bellow and calf vigour were recorded for calves at two locations

(Grafton and EMAI). Calf bellow scores were collected in the following categories: 0 (no bellow); 1 (single bellow less than 1 sec) and 2 (single bellow longer than 1 sec or multiple bellows). Calf vigour scores were collected in the following categories: 1 (extremely weak); 2 (weak); 3 (healthy); 4 (vigorous) and 5 (extremely vigorous). Summary statistics across the project for the traits recorded at birth can be found in Table 2, with variation observed in all traits. All traits collected at calving were recorded by farm staff at the research station.

Table 2 Summary statistics for birth traits in Cohort One

Trait	Number of records	Mean	SD	Minimum	Maximum
Birth weight (kg)	1,398	38.6	7.5	18	61
Calving ease	1,398	1.1	0.5	1	5
Calf fate	1,398	0.09	0.4	0	2
Calf bellow	838	0.59	0.79	0	2
Calf vigour	839	3.25	0.79	1	5

Most calves emitted no bellow (60%) during the recording process, while 21% of calves emitted a single bellow of less than 1 second in duration, and 19% emitted either a single bellow longer than 1 second or multiple bellows (Figure 1). The relationship between calf bellow scores at birth and subsequent measures of behaviour (all animals will have crush-side and flight speed docility measures taken at weaning) will be assessed.
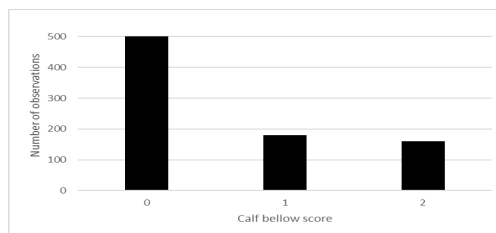

Figure 1. Distribution of calf bellow scores in Cohort One

Most calves were healthy or vigorous (87%), with a small number of calves observed to be extremely vigorous (6%) and extremely weak (4%) (Figure 2). The relationship between calf vigour scores at birth and subsequent measures of behaviour and production will be assessed.
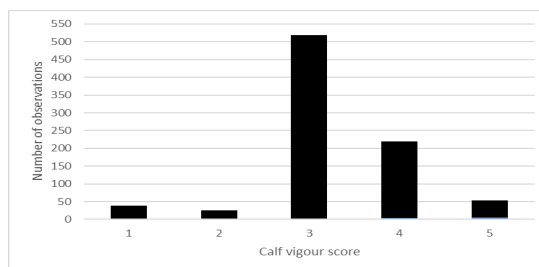

Figure 2. Distribution of calf vigour scores in Cohort One

Cohort One animals will be weaned at approximately 8 months of age, with a wide range of traits to be recorded at this time including weaning weight, hip height, muscle score, docility (crush-side and flight speed), horn/poll phenotype (as a repeated record of their phenotype

collected at marking) and worm egg count. Steers from Cohort One will be backgrounded at one of two locations before entering Tullimba feedlot and subsequently slaughtered. Cohort One females will be retained at each site to be naturally joined in late 2021. Serial ovarian scans will be undertaken on the females in the lead-up to joining to identify the presence of a corpus luteum as a measure of puberty.

Generation of Cohort Two. Females at each site were mated via a single synchronised AI program in late 2020, with back up bulls introduced five days after insemination. A total of 135 sires were represented in the AI program (Angus=36; Brahman=19; Charolais=15; Hereford=29; Shorthorn=16; Wagyu=20) and 67 sires in the natural joinings (Angus=20; Brahman=4; Charolais=8; Hereford=17; Shorthorn=8; Wagyu=10). The joining program was staggered across the five sites, with calving anticipated to occur from June (Trangie) to October (EMAI) in 2021. Females were pregnancy scanned in January/February 2021, and the predicted number of calves in Cohort Two by calf breed and site is contained in Table 3.

Table 3 Predicted number of calves by breed and site in Cohort Two

Site[b]	AA[a]	AAxBB	BB	BBxAA	BBxHH	CC	HH	HHxBB	SS	WY	Total
TR	71	-	-	-	-	-	62	-	-	55	188
GR	90	12	77	46	40	-	106	40	-	-	411
TO	95	-	-	-	-	55	-	-	92	-	242
GI	77	-	-	-	-	-	73	-	-	40	190
EMAI	104	-	-	-	-	112	84	-	108	96	504
Total	437	12	77	46	40	167	325	40	200	191	1535

[a] AA=Angus; BB=Brahman; CC=Charolais; HH=Hereford; SS=Shorthorn; WY=Wagyu
[b] TR=Trangie; GR=Grafton; TO=Tocal; GI=Glen Innes; EMAI=Menangle

CONCLUSIONS

Data collection on the first cohort of animals in the Southern Multibreed resource population has commenced, with birth data recorded the first cohort of calves. Intensive data collection is planned on these animals at weaning, followed by collection of production and carcase data on steers in the feedlot and abattoir, and on heifers prior to joining and subsequent calving. This information, along with genotypes on sires, dams and calves, will be available to enhance current within-breed genetic evaluation as well as provide records for animals from multiple breeds managed in mixed breed groups.

ACKNOWLEDGEMENTS

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